

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:18:32 ; Search time 14.1 Seconds
(without alignments)
15.119 Million cell updates/sec

Title: US-09-258-947-38
Perfect score: 61
Sequence: 1 WNWRYREYV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	9	1 W15299	Human platelet gly
2	61	100.0	9	1 W17558	Mimotope capable o
3	61	100.0	10	1 W32624	Human platelet gly
4	61	100.0	10	1 W17552	Mimotope capable o
5	45	73.8	10	1 W32625	Human platelet gly
6	45	73.8	10	1 W17559	Mimotope capable o
7	38	62.3	10	1 W32627	Human platelet gly
8	38	62.3	10	1 W17554	Mimotope capable o
9	38	62.3	505	1 W06481	Helicobacter CP2 a
10	38	62.3	505	1 W06482	Helicobacter CP2-P
11	38	62.3	505	1 W06483	Helicobacter CP2-P
12	38	62.3	505	1 W52810	Helicobacter pylori
13	38	62.3	505	1 W54146	Helicobacter pylori
14	38	62.3	505	1 W98423	H. pylori GHPO 358
15	36	59.0	10	1 W32626	Human platelet gly
16	36	59.0	10	1 W17553	Mimotope capable o
17	36	59.0	627	1 Y00235	Enterococcus faeca
18	36	59.0	726	1 W95636	Rhodothermus marin
19	36	59.0	1313	1 Y00234	Enterococcus faeca
20	36	59.0	1313	1 Y00236	Enterococcus faeca
21	35	57.4	15	1 W12276	Synthetic library
22	35	57.4	15	1 W17334	A glycolipid sugar
23	35	57.4	15	1 W94702	Lipoteichoic acid
24	35	57.4	19	1 W94729	Sequence 15mer 2nd
25	35	57.4	19	1 W94710	Sequence 15mer 2-8/
26	35	57.4	19	1 W94721	Sequence 15mer 2-19
27	35	57.4	19	1 W94705	Sequence 15mer 2-1/
28	35	57.4	19	1 W94709	Sequence 15mer 2-7/
29	35	57.4	37	1 W12287	Synthetic template
30	35	57.4	422	1 R67688	S. pombe spauris g
31	35	57.4	422	1 R67687	S. pombe spauris g
32	35	57.4	422	1 R88130	Aureobasidin resis
33	35	57.4	422	1 R88131	Aureobasidin sensi
34	35	57.4	739	1 R54613	Delta24-34 CD26. P

35	35	57.4	759	1 R54612	Delta3-9 CD26. Pol
36	35	57.4	760	1 W27438	Human fibroblast a
37	35	57.4	766	1 R40909	Sequence encoded b
38	35	57.4	766	1 R54611	Native CD26. Polyp
39	35	57.4	3079	1 R59926	GAP protein Ira2.
40	34.5	56.6	49	1 R68717	CLTB-56/CLTB-97A f
41	34.5	56.6	49	1 W25887	Chimaeric T/B cell
42	34.5	56.6	49	1 W67403	Hiv-1 peptide epit
43	34.5	56.6	49	1 W99919	Hiv-1 vaccine synt
44	34.5	56.6	51	1 R77767	CLTB-56/CLTB-97A f
45	34.5	56.6	168	1 W89845	Protein encoded by

ALIGNMENTS

RESULT 1
W15299
ID W15299 standard; peptide; 9 AA.
AC W15299;
DT 30-JAN-1998 (first entry)
DE Human platelet glycoprotein Ib/IX complex epitope mimotope consensus.
KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
KW anti thrombotic drug; ristocetin.
OS Synthetic.
OS Homo sapiens.
PN W09718236-A1.
PD 22-MAY-1997.
PF 08-NOV-1996; U17882.
PR 13-NOV-1995; US-556597.
PA (UUNY) UNIV NEW YORK STATE RES FOUND.
PI Lyle VA, Miller JL;
DR WPI; 97-289227/26.
PT Peptide which mimics human platelet glycoprotein Ib/IX complex
PT epitope - also anti-mimotope molecule capable of binding to the
PT peptide and useful to modulate platelet adhesion, aggregation or
PT agglutination
PS Claim 4; Page 98; 115pp; English.
CC The present sequence represents the consensus sequence for a mimotope
CC which functionally mimics a binding site for a monoclonal antibody (Mab)
CC which recognises an epitope within the human platelet glycoprotein (gp)
CC Ib/IX complex. More specifically the Mab is C-34. the mimotope peptide
CC can be used for raising antibodies, as probes to search for anti-
CC mimotopes and to neutralise the inhibitory activity of those antibodies
CC which recognise the epitope which is mimicked by the peptide. Anti-
CC mimotopes can be used to modulate the adhesion, aggregation or
CC agglutination of platelets by affecting von Willebrand factor
CC interaction with the platelets through the gp Ib/IX receptor, e.g. as an
CC anti-thrombotic drug which inhibits the ristocetin induced aggregation
CC of platelets.
SQ Sequence 9 AA;

Query Match 100.0%; Score 61; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 WNWRYREYV 9
| | | | | | | | | |
DB 1 WNWRYREYV 9

RESULT 2
W17558
ID W17558 standard; peptide; 9 AA.
AC W17558;
DT 08-DEC-1998 (first entry)
DE Mimotope capable of binding to monoclonal antibody C-34 #38.
KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
KW binding site; platelet epitope; neutralise; aggregation; inhibition;
KW von Willebrand factor interaction; adhesion; agglutination.

OS Synthetic.
 OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UYN) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 98-556458/47.
 PT Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1: Column 48; 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 9 AA;

Query Match 100.0%; Score 61; DB 1; Length 9;
 *Best Local Similarity 100.0%; Pred. NO. 1.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNNRYREYV 9
 D5 1 WNNRYREYV 9

RESULT 3
 W32624
 ID W32624 standard; peptide; 10 AA.
 AC W32624;
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope; mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.
 PF 08-NOV-1996; U17882.
 PR 13-NOV-1995; US-558597.
 PA (UYN) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 97-289227/26.
 PT Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide - also anti-mimotope molecule capable of binding to the
 PT agglutination
 PS Claim 3; Page 96; English.
 CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (Mab) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the Mab is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through

CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 61; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.00026;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNNRYREYV 9
 D5 2 WNNRYREYV 10

RESULT 4
 W71752
 ID W71752 standard; peptide; 10 AA.
 AC W71752;
 DT 08-DEC-1998 (first entry)
 DE Mimotope capable of binding to monoclonal antibody C-34 #1.
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UYN) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 98-556458/47.
 PT Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1: Column 47; 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 61; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. NO. 0.00026;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNNRYREYV 9
 D5 2 WNNRYREYV 10

RESULT 5
 W32625
 ID W32625 standard; peptide; 10 AA.
 AC W32625;
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.

OS Synthetic.
OS Homo sapiens.
PN W09718236-A1.
PD 22-MAY-1997.
PF 08-NOV-1996; U17882.
PR 13-NOV-1995; US-556597.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
PI Lyle VA, Miller JL;
DR WPI; 97-289227/26.
PT Peptide which mimics human platelet glycoprotein Ib/IX complex
PT epitope - also anti-mimotope molecule capable of binding to the
PT peptide and useful to modulate platelet adhesion, aggregation or
PT agglutination
PS Claim 3; Page 96; 115pp; English.
CC The present sequence represents a mimotope which functionally mimics a
CC binding site for a monoclonal antibody (MAB) which recognises an epitope
CC within the human platelet glycoprotein (gp) Ib/IX complex. More
CC specifically the MAB is C-34. The mimotope peptide can be used for
CC raising antibodies, as probes to search for anti-mimotopes and to
CC neutralise the inhibitory activity of those antibodies which recognise
CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
CC to modulate the adhesion, aggregation or agglutination of platelets by
CC affecting von Willebrand factor interaction with the platelets through
CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
CC the ristocetin induced aggregation of platelets.
SQ Sequence 10 AA;

Query Match 73.8%; Score 45; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 0.09;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNWRYREYV 9
Db 2 NNWRNKKYV 10

RESULT 6
W71759
ID W71759 standard; peptide; 10 AA.
AC W71759;
DT 08-DEC-1998 (first entry)
DE Mimotope capable of binding to monoclonal antibody C-34 #2.
KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
KW binding site; platelet epitope; neutralise; aggregation; inhibition;
KW von Willebrand factor interaction; adhesion; agglutination.
OS Synthetic.
OS Homo sapiens.
PN US5817748-A.
PD 06-OCT-1998.
PF 17-MAR-1995; 406330.
PR 17-MAR-1995; US-406330.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
PI Lyle VA, Miller JL;
DR WPI; 98-556458/47.
PT Peptides that mimic platelet epitope - and neutralise
PT aggregation-inhibiting antibody
PS Disclosure; Column 4; 26pp; English.
CC The present invention provides peptides which functionally mimic a
CC binding site for a monoclonal antibody, where the monoclonal antibody
CC recognises an epitope within the human glycoprotein Ib/IX complex.
CC Peptides W71752 to W71832 are mimotopes which are capable of binding
CC to monoclonal antibody C-34. The invention also provides an isolated
CC molecule capable of binding the mimotopes, where the molecule can be
CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
CC molecule, or other naturally or chemically synthesised molecules. These
CC molecules are called anti-mimotopes and can act as anti-thrombotic
CC drugs. A method has also been described for modulating the adhesion,
CC aggregation, or agglutination of platelets, where the method comprises
CC selecting platelets and exposing them to an anti-mimotope molecule. The
CC exposure affects von Willebrand factor interaction with platelets
CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
CC aggregation, or agglutination of the platelets. The peptide mimotopes

CC mimic platelet epitopes.
SQ Sequence 10 AA;

Query Match 73.8%; Score 45; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 0.09;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNWRYREYV 9
Db 2 NNWRNKKYV 10

RESULT 7
W32627
ID W32627 standard; peptide; 10 AA.
AC W32627;
DT 30-JAN-1998 (first entry)
DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
KW anti thrombotic drug; ristocetin.
OS Synthetic.
OS Homo sapiens.
PN W09718236-A1.
PD 22-MAY-1997.
PF 08-NOV-1996; U17882.
PR 13-NOV-1995; US-556597.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
PI Lyle VA, Miller JL;
DR WPI; 97-289227/26.
PT Peptide which mimics human platelet glycoprotein Ib/IX complex
PT epitope - also anti-mimotope molecule capable of binding to the
PT peptide and useful to modulate platelet adhesion, aggregation or
PT agglutination
PS Claim 3; Page 96; 115pp; English.
CC The present sequence represents a mimotope which functionally mimics a
CC binding site for a monoclonal antibody (MAB) which recognises an epitope
CC within the human platelet glycoprotein (gp) Ib/IX complex. More
CC specifically the MAB is C-34. The mimotope peptide can be used for
CC raising antibodies, as probes to search for anti-mimotopes and to
CC neutralise the inhibitory activity of those antibodies which recognise
CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
CC to modulate the adhesion, aggregation or agglutination of platelets by
CC affecting von Willebrand factor interaction with the platelets through
CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
CC the ristocetin induced aggregation of platelets.
SQ Sequence 10 AA;

Query Match 62.3%; Score 38; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WRYREYV 9
Db 4 WRYSEYV 10

RESULT 8
W71754
ID W71754 standard; peptide; 10 AA.
AC W71754;
DT 08-DEC-1998 (first entry)
DE Mimotope capable of binding to monoclonal antibody C-34 #4.
KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
KW binding site; platelet epitope; neutralise; aggregation; inhibition;
KW von Willebrand factor interaction; adhesion; agglutination.
OS Synthetic.
OS Homo sapiens.
PN US5817748-A.
PD 06-OCT-1998.


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FT misc_difference 397 /note= "residue 397 is Thr in CP2-PCR2"
FT misc_difference 449 /note= "residue 449 is Arg in CP2"
FT EP-745674-A2.
PD 04-DEC-1996.
PF 30-MAY-1996; 108637.
PR 02-JUN-1995; JP-136564.
PR 05-APR-1996; JP-083512.
PA (WAKP ) WAKO PURE CHEM IND LTD.
PI Hirayasu K, Kawabata T, Sugiyama T, Tanaka T;
DR WPI; 97-013697/02.
DR N-PSDB; T45042.
PT Helicobacter pylori CP2 antigen structural polypeptide(s) - also
PT the corresponding DNA, useful as reagents for detecting H. pylori and in
PT the production of vaccines
PS Claim 1; Page 18-20; 29pp; English.
CC Helicobacter pylori ATCC 43504 CP2-PCR1 antigen (W06482) is useful
CC in the specific and quantitative detection of H. pylori and in
CC vaccine prodn. CP2 antibody titre shows high correlation with the
CC pathology of gastritis. The CP2-PCR1 amino acid sequence was
CC deduced from a DNA clone (T45042) obt'd. by PCR amplification.
CC Slightly different sequences were deduced for CP2 (W06481) from
CC genomic DNA (T45041) and for CP2-PCR2 (W06483) from a PCR fragment
CC (T45043) derived from a clinical isolate. Isolation of the gene
CC sequences allows the mass prodn. of recombinant CP2 in transformed
CC host cells.
SQ Sequence 505 AA;

Query Match 62.3%; Score 38; DB 1; Length 505;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

~QY 1 WNWRYR 6
Db 414 WNWDR 419
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RESULT 11
W06483
ID W06483 standard; Protein; 505 AA.
AC W06483;
DC 24-FEB-1997 (first entry)
DE Helicobacter CP2-PCR2 antigen.
KW CP2; antigen; vaccine; diagnosis; gastritis.
OS Helicobacter pylori.
PH Key Location/Qualifiers
FT misc_difference 130 /note= "residue 130 is Asn in CP2 and CP2-PCR1"
FT misc_difference 160 /note= "residue 160 is His in CP2 and CP2-PCR1"
FT misc_difference 218 /note= "residue 218 is His in CP2 and CP2-PCR1"
FT misc_difference 234 /note= "residue 234 is Val in CP2 and CP2-PCR1"
FT misc_difference 237 /note= "residue 237 is Tyr in CP2 and CP2-PCR1"
FT misc_difference 248 /note= "residue 248 is Asn in CP2 and CP2-PCR1"
FT misc_difference 262 /note= "residue 262 is Val in CP2 and CP2-PCR1"
FT misc_difference 285 /note= "residue 285 is Tyr in CP2 and CP2-PCR1"
FT misc_difference 287 /note= "residue 287 is Gln in CP2 and CP2-PCR1"
FT misc_difference 292 /note= "residue 292 is Met in CP2 and CP2-PCR1"
FT misc_difference 316 /note= "residue 316 is Ser in CP2 and CP2-PCR1"
FT misc_difference 344 /note= "residue 344 is Cys in CP2-PCR1"
FT misc_difference 358
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FT misc_difference 397 /note= "residue 358 is Lys in CP2 and CP2-PCR1"
FT misc_difference 449 /note= "residue 397 is Ala in CP2 and CP2-PCR1"
FT misc_difference 449 /note= "residue 449 is Arg in CP2"
FT EP-745674-A2.
PD 04-DEC-1996.
PF 30-MAY-1996; 108637.
PR 02-JUN-1995; JP-136564.
PR 05-APR-1996; JP-083512.
PA (WAKP ) WAKO PURE CHEM IND LTD.
PI Hirayasu K, Kawabata T, Sugiyama T, Tanaka T;
DR WPI; 97-013697/02.
DR N-PSDB; T45043.
PT Helicobacter pylori CP2 antigen structural polypeptide(s) - also
PT the corresponding DNA, useful as reagents for detecting H. pylori and in
PT the production of vaccines
PS Claim 1; Page 21-23; 29pp; English.
CC Helicobacter pylori CP2-PCR2 antigen (W06483) is useful in the
CC specific and quantitative detection of H. pylori and in vaccine
CC prodn. CP2 antibody titre shows high correlation with the
CC pathology of gastritis. The CP2-PCR2 amino acid sequence was
CC deduced from a DNA clone (T45043) obt'd. by PCR amplification of
CC DNA from H. pylori isolated from a patient with chronic gastritis.
CC Slightly different sequences were deduced for CP2 (W06481-82) from
CC H. pylori ATCC 43504. Isolation of these gene allows the mass
CC prodn. of recombinant CP2 in transformed host cells.
SQ Sequence 505 AA;

Query Match 62.3%; Score 38; DB 1; Length 505;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNWRYR 6
Db 414 WNWDR 419
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RESULT 12
W52810
ID W52810 standard; Protein; 505 AA.
AC W52810;
DC 20-JUL-1998 (first entry)
DE Helicobacter pylori isolate RUI catalase.
KW Treatment; prevention; gastroduodenal disease; detection.
OS Helicobacter pylori.
PN W09806853-A1.
PD 19-FEB-1998.
PF 14-AUG-1997; AU0515.
PR 15-AUG-1996; US-695987.
PA (CSLC-) CSL LTD.
PI (UYNE-) UNIV NEW SOUTH WALES.
PI Doldge CV, Hazell SL, Lee A, Radcliff EJ;
DR WPI; 98-159544/14.
DR N-PSDB; V20910.
PT New isolated Helicobacter catalase nucleic acid - used to develop
PT products for the treatment or prevention of Helicobacter infection,
PT particularly H. pylori gastroduodenal disease
PS Disclosure; Page 33-34; 46pp; English.
CC The Helicobacter pylori catalase is a protein of 58650 Da. The protein,
CC gene sequence and products, such as an immunogenic fragment, can be used
CC for the treatment or prevention of Helicobacter infection, particularly
CC H. pylori infections which cause gastroduodenal disease. They can also
CC be used for the detection and diagnosis of Helicobacter infection.
SQ Sequence 505 AA;

Query Match 62.3%; Score 38; DB 1; Length 505;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNWRYR 6
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Db 414 WNWDR 419
|||||
RESULT 13
W54146
ID W54146 standard; Protein; 505 AA.
AC W54146;
DT 20-JUL-1998 (first entry)
DE Helicobacter pylori isolate 921023 catalase.
KW Treatment; prevention; gastroduodenal disease; detection.
OS Helicobacter pylori.
PN W09808653-A1.
PD 19-FEB-1998.
PR 14-AUG-1997; AU0515.
PR 15-AUG-1996; US-695987.
PA (CSLC-) CSL LTD.
PA (UYNE-) UNIV NEW SOUTH WALES.
PI Doidge CV, Hazell SL, Lee A, Radcliff FJ;
DR WPI; 98-159544/14.
DR N-PSDB; V20911.
PT New isolated Helicobacter catalase nucleic acid - used to develop
PT products for the treatment or prevention of Helicobacter infection,
PT particularly H. pylori gastroduodenal disease
PS Disclosure; Page 37-38; 46pp; English.
CC The Helicobacter pylori catalase is a protein of 58650 Da. The protein,
CC gene sequence and products, such as an immunogenic fragment, can be used
CC for the treatment or prevention of Helicobacter infection, particularly
CC H. pylori infections which cause gastroduodenal disease. They can also
CC be used for the detection and diagnosis of Helicobacter infection.
SQ Sequence 505 AA;

Query Match 62.3%; Score 38; DB 1; Length 505;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WNWDR 6
|||||
Db 414 WNWDR 419

RESULT 14
W98423
ID W98423 standard; Protein; 505 AA.
AC W98423;
DT 31-MAR-1999 (first entry)
DE H. pylori GHP 358 protein.
KW GHP protein; Helicobacter infection; gastroduodenal disease; gastritis;
KW peptic ulcer disease.
OS Helicobacter pylori.
PN W09843478-A1.
PD 08-OCT-1998.
PF 01-APR-1998; U06371.
PR 29-JUL-1997; US-902615.
PR 01-APR-1997; US-833457.
PR 24-JUN-1997; US-881227.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (INNR-) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PI Al-Garawi A, Kleanthous H, Miller C, Oomen RP, Tomb J;
DR WPI; 98-542293/46.
DR N-PSDB; X14142.
PT New isolated Helicobacter polynucleotides - used to develop products
PT for the diagnosis, prevention and treatment of Helicobacter
PT infections and gastrointestinal diseases
PS Claim 8; Page 711-713; 2054pp; English.
CC This sequence represents a Helicobacter pylori GHP protein of the
CC invention. The polypeptides can be used for preventing or treating
CC Helicobacter infections, and gastroduodenal diseases associated with
CC these infections, including acute, chronic, and atrophic gastritis, and
CC peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be
CC used for the production of antibodies. The products can also be used for
CC detection and diagnosis.

SQ Sequence 505 AA;

Query Match 62.3%; Score 38; DB 1; Length 505;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WNWDR 6
|||||
Db 414 WNWDR 419

RESULT 15
W32626
ID W32626 standard; peptide; 10 AA.
AC W32626;
DT 30-JAN-1998 (first entry)
DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
KW anti thrombotic drug; ristocetin.
OS Synthetic.
OS Homo sapiens.
PN W09718236-A1.
PD 22-MAY-1997.
PF 08-NOV-1996; U17882.
PR 13-NOV-1995; US-556597.
PA (UNY ) UNIV NEW YORK STATE RES FOUND.
PI Lyle VA, Miller JL;
DR WPI; 97-289227/26.
PT Peptide which mimics human platelet glycoprotein Ib/IX complex
PT epitope - also anti-mimotope molecule capable of binding to the
PT peptide and useful to modulate platelet adhesion, aggregation or
PT agglutination
PS Claim 3; Page 96; 115pp; English.
CC The present sequence represents a mimotope which functionally mimics a
CC binding site for a monoclonal antibody (Mab) which recognises an epitope
CC within the human platelet glycoprotein (gp) Ib/IX complex. More
CC specifically the Mab is C-34. The mimotope peptide can be used for
CC raising antibodies, as probes to search for anti-mimotopes and to
CC neutralise the inhibitory activity of those antibodies which recognise
CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
CC to modulate the adhesion, aggregation or agglutination of platelets by
CC affecting von Willebrand factor interaction with the platelets through
CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
CC the ristocetin induced aggregation of platelets.
SQ Sequence 10 AA;

Query Match 59.0%; Score 36; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 WRYREYV 9
|||||
Db 4 WRYFEYV 10

Search completed: May 2, 2000, 00:20:02
Job time: 90 sec

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RESULT 2
US-08-556-597-38
; Sequence 38, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timlan, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-38

Query Match 100.0%; Score 61; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYREYV 9
Db 1 WNWRYREYV 9

RESULT 3
US-08-406-330-1
; Sequence 1, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timlan, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-1

Query Match 100.0%; Score 61; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYREYV 9
Db 2 WNWRYREYV 10

RESULT 4
US-08-556-597-1
; Sequence 1, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timlan, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids

;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-1

Query Match 100.0%; Score 61; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00021; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYREYV 9
 |||||
Db 2 WNWRYREYV 10

RESULT 5
US-08-406-330-2
; Sequence 2, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-2

Query Match 73.8%; Score 45; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 0.072; Indels 1; Gaps 0;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WNWRYREYV 9
 |||||
Db 2 WNWRYREYV 10

RESULT 6
US-08-556-597-2
; Sequence 2, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:

;
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-2

Query Match 73.8%; Score 45; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 0.072; Indels 1; Gaps 0;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WNWRYREYV 9
 |||||
Db 2 WNWRYREYV 10

RESULT 7
US-08-406-330-4
; Sequence 4, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-4

Query Match 62.3%; Score 38; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.91;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
Db 4 WRYSEYV 10

RESULT 8
US-08-556-597-4
Sequence 4, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
HUMAN PLATELET GLYCOPROTEIN IB/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-4

Query Match 62.3%; Score 38; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.91;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
Db 4 WRYSEYV 10

RESULT 9
US-08-406-330-3
Sequence 3, Application US/08406330
Patent No. 5817748
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
HUMAN PLATELET GLYCOPROTEIN IB/IX
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-3

Query Match 59.0%; Score 36; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
Db 4 WRYFEYV 10

RESULT 10
US-08-556-597-3
Sequence 3, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
HUMAN PLATELET GLYCOPROTEIN IB/IX
NUMBER OF SEQUENCES: 173

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
;; STREET: Clinton Square, P.O. Box 1051
;; CITY: Rochester
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 14603
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/556,597
;; FILING DATE:
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/406,330
;; FILING DATE: 17-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Timlan, Susan J.
;; REGISTRATION NUMBER: 34,103
;; REFERENCE/DOCKET NUMBER: 20884/101
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (716) 263-1636
;; TELEFAX: (716) 263-1600
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
;; US-08-556-597-3

Query Match 59.0%; Score 36; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYEYV 9
 | | | | |
Db 4 WRYEYV 10

RESULT 11
US-08-592-646A-19
; Sequence 19, Application US/08592646A
; Patent No. 5851535
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
; TITLE OF INVENTION: GONDII AND APPLICATIONS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,646A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024

;;
;; REFERENCE/DOCKET NUMBER: WPB 36923
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703 836-6400
;; TELEFAX: 703 836-2787
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: not relevant
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;;
;; US-08-592-646A-19

Query Match 57.4%; Score 35; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYR 6
 | : | | : |
Db 10 WHWRHR 15

RESULT 12
US-08-592-646A-20
; Sequence 20, Application US/08592646A
; Patent No. 5851535
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
; TITLE OF INVENTION: GONDII AND APPLICATIONS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,646A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36923
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-592-646A-20

Query Match 57.4%; Score 35; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYR 6
 | : | | : |
Db 9 WHWRHR 14

RESULT 13
US-08-592-646A-21
; Sequence 21, Application US/08592646A
; Patent No. 5851535
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
; TITLE OF INVENTION: GONDII AND APPLICATIONS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592.646A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36923
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-592-646A-21

Query Match 57.4%; Score 35; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYR 6
Db 8 WHWRHR 13
I:|:|:|

RESULT 14
US-08-592-646A-22
; Sequence 22, Application US/08592646A
; Patent No. 5851535
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
; TITLE OF INVENTION: GONDII AND APPLICATIONS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592.646A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36923
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-592-646A-22

Query Match 57.4%; Score 35; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYR 6
Db 7 WHWRHR 12
I:|:|:|

RESULT 15
US-08-592-646A-23
; Sequence 23, Application US/08592646A
; Patent No. 5851535
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
; TITLE OF INVENTION: GONDII AND APPLICATIONS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592.646A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36923
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-592-646A-23

Query Match 57.4%; Score 35; DB 2; Length 15;

Best Local Similarity 66.7%; Pred. No. 4;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYR 6
|:|:|:
Db 6 WHRRHR 11

Search completed: May 2, 2000, 00:20:47
Job time: 70 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:19:02 ; Search time 13.62 Seconds
(without alignments)
31.169 Million cell updates/sec

Title: US-09-258-947-38
Perfect score: 61
Sequence: 1 WNWRYREYV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues
Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_62:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	41	67.2	368	2	T06460	anthranilate phosphoribosyltransferase
2	40	65.6	254	2	PD0018	mistletoe lectin I A chain - Viscum album (fragment)
3	40	65.6	642	2	H70331	ATP-dependent heli
4	40	65.6	674	2	A47222	Kallmann syndrome
5	40	65.6	675	2	S36170	Kallmann syndrome
6	40	65.6	676	2	B47222	Kallmann syndrome
7	39	63.9	646	2	JN0473	p-selectin precurs
8	38.5	63.1	462	2	H71228	hypothetical prote
9	38	62.3	300	2	D72331	sugar ABC transpor
10	38	62.3	504	2	A55861	alpha-amylase (EC
11	38	62.3	505	2	C64629	catalase (EC 1.11.
12	38	62.3	505	2	F71885	catalase (EC 1.11.
13	38	62.3	505	2	H71303	hypothetical prote
14	38	62.3	928	1	VBEMC	glycoprotein B pre
15	37	60.7	119	2	B49905	protein secretion
16	37	60.7	388	2	S15591	hypothetical prote
17	37	60.7	388	2	S15592	hypothetical prote
18	37	60.7	388	2	S15593	hypothetical prote
19	37	60.7	404	2	G53318	threonine synthase
20	37	60.7	405	2	A48447	procyclin-associat
21	37	60.7	406	2	G69131	threonine synthase
22	37	60.7	488	2	S26576	hemolysin - Aero
23	37	60.7	489	2	I39672	hemolysin 2 - Aero
24	37	60.7	540	2	S47708	hypothetical 61.2k
25	37	60.7	516	2	C71648	DNA primase (EC 2.
26	37	60.7	968	2	T00322	hypothetical prote
27	36	59.0	169	2	A64396	hypothetical prote
28	36	59.0	189	2	S49958	hypothetical prote
29	36	59.0	243	2	B69951	hypothetical prote
30	36	59.0	371	2	B71104	probable cystathio

31	36	59.0	601	2	H69274	long-chain-fatty-a
32	36	59.0	610	1	I46001	C4b-binding protei
33	36	59.0	783	2	T00782	probable anthranil
34	35.5	58.2	234	2	S46348	vif protein - simi
35	35	57.4	162	2	D69899	conserved hypothet
36	35	57.4	169	2	J01210	replication hypothet
37	35	57.4	185	2	T12772	conserved hypothet
38	35	57.4	194	2	H69438	hypothetical prote
39	35	57.4	258	2	S75950	hypothetical prote
40	35	57.4	279	2	B64972	hypothetical prote
41	35	57.4	305	2	S77033	hypothetical prote
42	35	57.4	327	2	S09566	repB protein - Sta
43	35	57.4	329	1	D71316	conserved hypothet
44	35	57.4	334	2	A24455	repB protein - Bac
45	35	57.4	341	2	I51158	major histocompati

ALIGNMENTS

RESULT 1
T06460
anthranilate phosphoribosyltransferase (EC 2.4.2.18) - garden pea (fragment)
N:Alternate names: phosphoribosylanthranilate transferase
C:Species: Pisum sativum (garden pea)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999
C:Accession: T06460
R:Sato, N.; Kazuno, A.; Ohta, N.; Ohshima, K.
Submitted to the EMBL Data Library, June 1996
A:Description: Isolation of a pea cDNA for phosphoribosylanthranilate transferase.
A:Reference number: Z15694
A:Accession: T06460
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-368 <SAT>
A:Cross-references: EMBL:D86180; NID:d1069881; PID:d1013719
A:Experimental source: var. Alaska
C:Genetics:
A:Gene: PAT1
C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 67.2% ; Score 41; DB 2; Length 368;
Best Local Similarity 83.3% ; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 1;

QY 1 WNWRYR 6
|||||
DB 226 WNWRRR 231

RESULT 2
PD0018
mistletoe lectin I A chain - Viscum album (fragment)
C:Species: Viscum album
C:Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999
C:Accession: PD0018
R:Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W.
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A:Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum a
A:Reference number: PD0018; MUID:98308123
A:Accession: PD0018
A:Molecule type: protein
A:Residues: 1-254 <ESC>
C:Superfamily: ricin; rRNA N-glycosidase homology
F:7-246/Domain: rRNA N-glycosidase homology <RNG>

Query Match 65.6% ; Score 40; DB 2; Length 254;
Best Local Similarity 71.4% ; Pred. No. 10; Mismatches 0; Indels 0; Gaps 0;
Matches 5; Conservative 2;

QY 3 WRYREYV 9

Db 174 WRYQYI 180
|||||:

RESULT 3

H70331

ATP-dependent helicase (DinG family) - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998

C:Accession: H70331

R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666

A:Accession: H70331

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-642 <AQP>

A:Cross-references: GB:AE000685; NID:g2983026; PID:g2983030; GB:AE000657

A:Experimental source: strain VF5

C:Genetics:

A:Gene: ding

Query Match

Best Local Similarity 65.6%; Score 40; DB 2; Length 642;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 WRYEYV 9

|||||:

Db 611 WRYEFV 617

RESULT 4

A47222

Kallmann syndrome protein homolog KAL - quail

C:Species: Phasianidae gen. sp. (quail)

C:Date: 24-Feb-1994 #sequence_revision 25-Apr-1997 #text_change 19-Feb-1999

C:Accession: A47222

R:Legouis, R.; Cohen-Salmon, M.; del Castillo, I.; Levilliers, J.; Capy, L.; Mornow, J.F

Genomics 17, 516-518, 1993

A:Title: Characterization of the chicken and quail homologues of the human gene responsi

A:Reference number: A47222; MUID:94010957

A:Accession: A47222

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-674 <LEG>

A:Cross-references: GB:L13976; NID:g1196807; PID:g1196808

A:Note: sequence extracted from NCBI backbone (NCBIP:137995)

A:Note: the species of quail is not identified

C:Superfamily: antileukoproteinase repeat homology

F:124-170/Domain: antileukoproteinase repeat homology <ALP>

Query Match

Best Local Similarity 65.6%; Score 40; DB 2; Length 674;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRYEYV 9

|||||:

Db 326 WSWYISKYV 334

RESULT 5

S36170

Kallmann syndrome protein homolog - chicken

C:Species: Gallus gallus (chicken)

C:Date: 14-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 07-May-1999

C:Accession: S36170

R:Rugaili, E.I.; Lutz, B.; Kuratani, S.C.; Wawersik, S.; Borsani, G.; Ballabio, A.; Eich

Nature Genet. 4, 19-26, 1993

A:Title: Expression pattern of the Kallmann syndrome gene in the olfactory system sugges

A:Reference number: S36170; MUID:93291868

A:Accession: S36170

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-675 <RUG>

C:Superfamily: antileukoproteinase repeat homology

F:124-170/Domain: antileukoproteinase repeat homology <ALP>

Query Match

Best Local Similarity 65.6%; Score 40; DB 2; Length 675;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRYEYV 9

|||||:

Db 326 WSWYISKYV 334

RESULT 6

B47222

Kallmann syndrome protein homolog KAL - chicken

C:Species: Gallus gallus (chicken)

C:Date: 24-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 19-Feb-1999

C:Accession: B47222; A47394

R:Legouis, R.; Cohen-Salmon, M.; del Castillo, I.; Levilliers, J.; Capy, L.; Mornow,

Genomics 17, 516-518, 1993

A:Title: Characterization of the chicken and quail homologues of the human gene respo

A:Reference number: A47222; MUID:94010957

A:Accession: B47222

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-676 <LEG>

A:Cross-references: GB:L12144; NID:g406510; PID:g406511

A:Note: sequence extracted from NCBI backbone (NCBIP:137996)

R:Legouis, R.; Llievre, C.A.; Leibovici, M.; Lapointe, F.; Petit, C.

Proc. Natl. Acad. Sci. U.S.A. 90, 2461-2465, 1993

A:Title: Expression of the KAL gene in multiple neuronal sites during chicken develop

A:Reference number: A47394; MUID:93211981

A:Accession: A47394

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 81-152, p'154-237 <LE2>

A:Experimental source: embryo, olfactory bulb

A:Note: sequence extracted from NCBI backbone (NCBIN:128286, NCBIP:128287)

C:Superfamily: antileukoproteinase repeat homology

F:125-171/Domain: antileukoproteinase repeat homology <ALP>

Query Match

Best Local Similarity 65.6%; Score 40; DB 2; Length 676;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRYEYV 9

|||||:

Db 327 WSWYISKYV 335

RESULT 7

JN0473

P-selectin precursor - bovine

N:Alternate names: granule membrane protein-140

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999

C:Accession: JN0473

R:Strubel, N.A.; Nguyen, M.; Kansas, G.S.; Tedder, T.F.; Bischoff, J.

Biochem. Biophys. Res. Commun. 192, 338-344, 1993

A:Title: Isolation and characterization of a bovine cDNA encoding a functional homolo

A:Reference number: JN0473; MUID:93249394

A:Accession: JN0473

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-646 <STR>

A:Cross-references: GB:L12041; NID:g304246; PID:g304247

C;Comment: This protein is a Ca2+ dependent receptor for myeloid cells.
 C;Superfamily: EGF homology; complement factor H repeat homology
 C;Keywords: cell adhesion; glycoprotein; phospholipid; phosphoprotein; transmembrane
 F;1-41/Domain: signal sequence #status predicted <SIG>
 F;42-646/Product: P-selectin #status predicted <MAT>
 F;163-194/Domain: EGF homology <EGF>
 F;200-257/Domain: complement factor H repeat homology <FH1>
 F;262-319/Domain: complement factor H repeat homology <FH2>
 F;324-381/Domain: complement factor H repeat homology <FH3>
 F;386-443/Domain: complement factor H repeat homology <FH4>
 F;458-515/Domain: complement factor H repeat homology <FH5>
 F;520-577/Domain: complement factor H repeat homology <FH6>
 F;588-611/Domain: transmembrane #status predicted <TM>
 F;612-646/Domain: intracellular #status predicted <CYT>

Query Match 63.9%; Score 39; DB 2; Length 646;
 Best Local Similarity 55.6%; Pred. No. 39;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
 ||||| : |
 Db 9 WNWRFQRAV 17

RESULT 8

H71228
 hypothetical protein PH0090 - Pyrococcus horikoshii
 C;Species: Pyrococcus horikoshii
 C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 14-Aug-1998
 C;Accession: H71228
 R;Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hailkawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A;Reference number: A71000; MUID:98344137
 A;Accession: H71228

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA

A;Residues: 1-462 <RAW>

A;Cross-references: GB:AF000001; NID:g3236128; PID:d1030102; PID:g3256476

A;Experimental source: strain OT3

A;Note: this accession replaces an interim accession for a sequence replaced by GenBank

C;Genetics:
 A;Gene: PH0090

Query Match 63.1%; Score 38.5; DB 2; Length 462;
 Best Local Similarity 70.0%; Pred. No. 34;
 Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 WNW-RYREYV 9
 ||| | |||
 Db 197 WNWVRREYL 206

RESULT 9

D72331
 sugar ABC transporter, permease protein - Thermotoga maritima (strain MSB8)
 C;Species: Thermotoga maritima
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 26-Aug-1999
 C;Accession: D72331
 R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.

Nature 399, 323-329, 1999

A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A;Reference number: A72200; MUID:99287316

A;Accession: D72331

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-300 <ARN>

A;Cross-references: GB:AE001748; GB:AE000512; NID:g4981332; PID:g4981341; TIGR:TM0811

A;Experimental source: strain MSB8

C;Genetics:

A;Gene: TM0811

C;Superfamily: inner membrane protein ugpa

Query Match 62.3%; Score 38; DB 2; Length 300;
 Best Local Similarity 71.4%; Pred. No. 26;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYRE 7
 |||||
 Db 127 WQWYRE 133

RESULT 10

A55861

alpha-amylase (EC 3.2.1.1) - Natronococcus sp. (strain Ah-36)

C;Species: Natronococcus sp.

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Feb-1998

C;Accession: A55861

R;Kobayashi, T.; Kanai, H.; Aono, R.; Horikoshi, K.; Kudo, T.

J. Bacteriol. 176, 5131-5134, 1994

A;Title: Cloning, expression, and nucleotide sequence of the alpha-amylase gene from
 A;Reference number: A55861; MUID:94327485

A;Accession: A55861

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-504 <ROB>

A;Cross-references: GB:D26510; NID:g517136; PID:d1006060; PID:g517137

C;Keywords: glycosidase; hydrolase

Query Match 62.3%; Score 38; DB 2; Length 504;
 Best Local Similarity 55.6%; Pred. No. 44;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
 ||| : |||
 Db 253 WPMYFQYEV 261

RESULT 11

C64629

catalase (EC 1.11.1.6) - Helicobacter pylori (strain 26695)

C;Species: Helicobacter pylori

C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 18-Jun-1999

C;Accession: C64629

R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodok, A.; Mcke

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey,

Nature 388, 539-547, 1997

A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser,

A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.

A;Reference number: A64520; MUID:97394467

A;Accession: C64629

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-505 <TOM>

A;Cross-references: GB:AE000597; GB:AE000511; NID:g2314007; PIDN:AAD07923.1; PID:g231

C;Superfamily: catalase

C;Keywords: chromoprotein; heme; iron; oxidoreductase

F;56,95,129/Active site: His, Ser, Asn #status predicted

F;339/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match 62.3%; Score 38; DB 2; Length 505;
 Best Local Similarity 83.3%; Pred. No. 44;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNWRYR 6
 |||||
 Db 414 WNWYR 419

```

C;Accession: A41992; A40780; S23220
R;Rapp, M.; Messerle, M.; Buehler, B.; Tannheimer, M.; Keil, G.M.; Koszinowski, U.H.
J. Virol. 66, 4399-4406, 1992
A;Title: Identification of the murine cytomegalovirus glycoprotein B gene and its exp
A;Reference number: A41992; MUID:92292266
A;Accession: A41992
A;Molecule type: mRNA
A;Residues: 1-928 <RAP>
A;Cross-references: GB:M86302
R;Elliott, R.; Clark, C.; Jaquish, D.; Spector, D.H.
Virology 185, 169-186, 1991
A;Title: Transcription analysis and sequence of the putative murine cytomegalovirus D
A;Reference number: A40780; MUID:92024072
A;Accession: A40780
A;Molecule type: DNA
A;Residues: 514-521, 'R', 523-526, 'E', 528-555, 'T', 557-561, 'V', 563-582, 'Q', 584-586, 'K', 5
A;Cross-references: GB:M73549
C;Superfamily: herpesvirus glycoprotein B
C;Keywords: glycoprotein; transmembrane protein
F;1-36/Domain: signal sequence #status predicted <SIG>
F;37-928/Product: glycoprotein B #status predicted <GPB>
F;757-804/Domain: transmembrane #status predicted <TMN>
F;93, 223, 315, 354, 398, 429, 470, 487, 618, 667/Binding site: carbohydrate (Asn) (covalent)

Query Match 62.3%; Score 38; DB 1; Length 928;
Best Local Similarity 71.4%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYRE 7
DB 253 WTWRYTE 259

RESULT 15
B49905
Protein secretion operon exe protein I precursor - Aeromonas hydrophila
C;Species: Aeromonas hydrophila
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Sep-1997
C;Accession: B49905; S22912
R;Howard, S.P.; Critch, J.; Bedi, A.
J. Bacteriol. 175, 6695-6703, 1993
A;Title: Isolation and analysis of eight exe genes and their involvement in extracell
A;Reference number: A49905; MUID:94012544
A;Accession: B49905
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-119 <HOW>
A;Cross-references: GB:X66504; NID:9551420; PID:938830
C;Genetics:
A;Gene: exeI

Query Match 60.7%; Score 37; DB 2; Length 119;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNWRYR 6
DB 79 WYWRYY 84

Search completed: May 2, 2000, 00:20:27
Job time: 85 sec

Catalase (EC 1.11.1.6) - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Jun-1999
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Reference number: A71800; MUID:99120557
A;Accession: F71885
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-505 <ARN>
A;Cross-references: GB:AE001510; GB:AE001439; NID:94155371; PID:9415538
A;Experimental source: strain J99
C;Genetics:
A;Gene: katA
C;Superfamily: catalase
C;Keywords: heme; iron; oxidoreductase
F;56, 95, 129/Active site: His, Ser, Asn #status predicted
F;339/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match 62.3%; Score 38; DB 2; Length 505;
Best Local Similarity 83.3%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNWRYR 6
DB 414 WNWYR 419

RESULT 13
H71303
hypothetical protein TP0598 - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-1999
C;Accession: H71303
R;Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McQu
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770
A;Accession: H71303
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-605 <COL>
A;Cross-references: GB:AE001235; GB:AE000520; NID:93322893; PID:93322902
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0598

Query Match 62.3%; Score 38; DB 2; Length 605;
Best Local Similarity 71.4%; Pred. No. 53;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNWRYRE 7
DB 176 WNWRTKE 182

RESULT 14
VGBEMC
glycoprotein B precursor - murine cytomegalovirus (strain Smith [ATCC VR-194])
C;Species: murine cytomegalovirus, murine herpesvirus 1
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1993 #text_change 09-Sep-1994

```


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:20:07 ; Search time 7.65 seconds
(without alignments)
35.135 Million cell updates/sec

Title: US-09-258-947-38
Perfect score: 61
Sequence: 1 WNWRYREV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 82229

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	65.6	254	MLA_VISAL	P81446 viscum albu
2	40	65.6	676	1 KALM_CHICK	P33005 gallus gall
3	39	63.9	646	1 LEM3_BOVIN	P42201 bos taurus
4	38	62.3	505	1 CATA_HELPY	P77872 helicobacte
5	38	62.3	928	1 VGLB_MCMVS	P27171 murine cyto
6	37	60.7	119	1 GSPI_AERHY	P31737 aeromonas h
7	37	60.7	400	1 HUTI_PSEPU	Q31200 pseudomonas
8	37	60.7	405	1 PAGI_TRYBB	Q01889 trypanosoma
9	37	60.7	488	1 AERA_AERSO	Q06304 aeromonas s
10	37	60.7	489	1 AERA_AERSA	Q08676 aeromonas s
11	37	60.7	540	1 YH1J_ECOLI	P37627 escherichia
12	37	60.7	593	1 PRIM_RICPR	P30103 rickettsia
13	36	59.0	169	1 Y769_METJA	Q58179 methanococc
14	36	59.0	189	1 Y1C4_YEAST	P40543 saccharomyc
15	36	59.0	243	1 YQEF_BACSU	P54451 bacillus su
16	36	59.0	610	1 C4BP_BOVIN	Q28065 bos taurus
17	36	59.0	882	1 ALKS_PSEOL	P17051 pseudomonas
18	35	57.4	89	1 Y4MD_RHISN	P55563 rhizobium s
19	35	57.4	220	1 TRBE_AGTAT6	P54914 agrobacteri
20	35	57.4	235	1 REPE_STAAU	P05061 staphylococ
21	35	57.4	245	1 Y4PL_RHISN	P55617 rhizobium s
22	35	57.4	279	1 WCAA_ECOLI	P77414 escherichia
23	35	57.4	422	1 AURL_SCHPO	Q10142 schizosacch
24	35	57.4	501	1 YFWA_BACSU	P50848 bacillus su
25	35	57.4	639	1 PPO_SPIOI	P43310 spinacia ol
26	35	57.4	678	1 SCOB_EMENI	Q00659 emericella
27	35	57.4	741	1 GUNS_CLOTM	P38686 clostridium
28	35	57.4	760	1 DPP4_MOUSE	P28843 mus musculu
29	35	57.4	766	1 DPP4_HUMAN	P27487 homo sapien
30	35	57.4	767	1 DPP4_RAT	P14740 rattus norv
31	35	57.4	769	1 LEM3_SHEEP	P98109 ovis aries
32	35	57.4	1742	1 GUNA_CALSA	P22534 caldocellum
33	35	57.4	3079	1 IRA2_YEAST	P19158 saccharomyc
34	34	55.7	167	1 OB_MOUSE	P41160 mus musculu

ALIGNMENTS

RESULT 1

ID	MLA_VISAL	STANDARD;	PRT;	254 AA.
AC	P81446;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	BETA-GALACTOSIDE SPECIFIC LECTIN I A CHAIN (MLA) (ML-I A) (RRNA N-GLYCOSIDASE) (EC 3.2.2.22)			
OS	Viscum album (European mistletoe).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Santalales; Viscaceae; Viscum.			
RN	[1]			
RP	SEQUENCE			
RX	MEDLINE; 97134581.			
RA	HUGUET SOLER M., STOEVA S., SCHWABORN C., WILHELM S., STIEFFEL T., VOELTER W.;			
RL	"Complete amino acid sequence of the A chain of mistletoe lectin I.";			
FEBS Lett. 399:153-157(1996).				
CC	-I- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR CELL AGGLUTINATION (LECTIN ACTIVITY).			
CC	-I- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.			
CC	-I- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.			
CC	-I- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA AND NON-GLYCOSYLATED FORM MLA'.			
CC	-I- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING PROTEINS. BELONGS TO TYPE 2 RIP.			
CC	PROSITE; PS00275; SHIGA_RICIN; FALSE_NEG.			
DR	PFAM; PF00161; RIP; 1.			
KW	Hydrolase; Toxin; Repeat; Glycoprotein; Lectin.			
ACT_SITE	165 165			
FT	CARBOHYD 112 112			
FT	VARIANT 15 15			
FT	VARIANT 66 66			
FT	VARIANT 112 112			
FT	VARIANT 116 116			
FT	VARIANT 133 133			
FT	VARIANT 140 140			
FT	VARIANT 144 144			
FT	VARIANT 151 151			
FT	VARIANT 179 179			
FT	VARIANT 184 184			
FT	VARIANT 190 190			
FT	VARIANT 218 218			
FT	VARIANT 223 223			
FT	VARIANT 231 231			
FT	VARIANT 235 235			
SQ	SEQUENCE 254 AA; 28478 MW; 98D4F18B CRC32;			

Query Match 65.6%; Score 40; DB 1; Length 254;

Best Local Similarity 71.4%; Pred. No. 8.7;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 WRYREYV 9
| | | | | : |
Db 174 WRYROYI 180

RESULT 2
KALM_CHICK STANDARD; PRT; 676 AA.
AC P33005;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE KALLMANN SYNDROME PROTEIN HOMOLOG PRECURSOR.
GN KAL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE; 94010957.
RA LEGOUTS R., COHEN-SALMON M., DEL CASTILLO I., LEVILLIERS J.,
RAY L., MORNON J.-P., PETIT C.;
RT "Characterization of the chicken and quail homologues of the human
gene responsible for the X-linked Kallmann syndrome.";
RL Genomics 17:516-518(1993).
CC -1- FUNCTION: THIS PROTEIN MAY BE A SECRETED ADHESION-LIKE MOLECULE
CC WITH ANTI-PROTEASE ACTIVITY.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 1 WAP-TYPE 'FOUR-DISULFIDE CORE' DOMAIN.

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DR EMBL; L12144; AAA51435.1; -;
DR PIR; B47222; B47222.
DR HSSP; P19957; 2REL.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PFAM; PF00041; fn3; 3.
DR PFAM; PF00095; wap; 1.
DR Cell adhesion; Glycoprotein; Serine protease inhibitor; Signal.
KW SIGNAL 1 21
FT CHAIN 22 676
FT DOMAIN 22 115
FT DOMAIN 126 171
FT DOMAIN 176 280
FT DOMAIN 281 397
FT DOMAIN 398 536
FT DOMAIN 537 657
FT CARBOHYD 66 66
FT CARBOHYD 204 204
FT CARBOHYD 295 295
FT CARBOHYD 466 466
FT CARBOHYD 549 549
FT CARBOHYD 560 560
SQ SEQUENCE 676 AA; 76375 MW; 2934E37F CRC32;

Query Match 65.68; Score 40; DB 1; Length 676;
Best Local Similarity 55.68; Pred. No. 23;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
| : | : | : |
Db 327 WSWYYSKXV 335

RESULT 3
LEM3_BOVIN STANDARD; PRT; 646 AA.
AC P42201;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
DE (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
GN SELP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-CAPILLARY ENDOTHELIIUM;
RX MEDLINE; 93249394.
RA STRUBEL N.A., NGUYEN M., KANSAS G.S., TEDDER T.F., BISCHOFF J.;
RT "Isolation and characterization of a bovine cDNA encoding a
functional homolog of human P-selectin.";
RL Biochem. Biophys. Res. Commun. 192:338-344(1993).
CC -1- FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS
CC TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE
CC INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH
CC LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
CC AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
CC ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
CC THE CELL SURFACE.
CC -1- SIMILARITY: TO OTHER SELECTINS/LECAMs.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
CC -1- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS; BOVINE P-LECTIN LACKS
CC THE HUMAN SUSHI-3, -4 AND -7 EQUIVALENTS.

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DR EMBL; L12041; AAA30743.1; -;
DR HSSP; P16109; IFSB.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS00615; C_TYPE_LLECTIN_1; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
DR PFAM; PF00008; EGF; 1.
DR PFAM; PF00059; lectin_c; 1.
DR PFAM; PF00084; sushi; 6.
DR Cell adhesion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
KW Selectin; Signal; Sushi; Repeat.
FT SIGNAL 1 41
FT CHAIN 42 646
FT DOMAIN 42 587
FT TRANSMEM 588 611
FT DOMAIN 612 646
FT DOMAIN 58 158
FT DOMAIN 159 195
FT DOMAIN 199 578
FT REPEAT 199 258
FT REPEAT 261 320
FT REPEAT 323 382
FT REPEAT 385 444
FT REPEAT 457 516
FT REPEAT 519 578
FT DISULFID 60 158
BY SIMILARITY.

FT DISULFID 131 BY SIMILARITY.
 FT DISULFID 163 BY SIMILARITY.
 FT DISULFID 168 BY SIMILARITY.
 FT DISULFID 185 BY SIMILARITY.
 FT DISULFID 200 BY SIMILARITY.
 FT DISULFID 230 BY SIMILARITY.
 FT DISULFID 262 BY SIMILARITY.
 FT DISULFID 292 BY SIMILARITY.
 FT DISULFID 324 BY SIMILARITY.
 FT DISULFID 354 BY SIMILARITY.
 FT DISULFID 386 BY SIMILARITY.
 FT DISULFID 416 BY SIMILARITY.
 FT DISULFID 458 BY SIMILARITY.
 FT DISULFID 488 BY SIMILARITY.
 FT DISULFID 520 BY SIMILARITY.
 FT DISULFID 550 BY SIMILARITY.
 FT CARBOHYD 48 POTENTIAL.
 FT CARBOHYD 54 POTENTIAL.
 FT CARBOHYD 80 POTENTIAL.
 FT CARBOHYD 180 POTENTIAL.
 FT CARBOHYD 212 POTENTIAL.
 FT CARBOHYD 219 POTENTIAL.
 FT CARBOHYD 336 POTENTIAL.
 FT CARBOHYD 481 POTENTIAL.
 FT CARBOHYD 532 POTENTIAL.
 FT CARBOHYD 539 POTENTIAL.
 FT CARBOHYD 557 POTENTIAL.
 FT SITE 634 ENDOCYTOSIS SIGNAL (PROBABLE).
 SQ SEQUENCE 646 AA; 71229 MW; D8B66498 CRC32;

Query Match 63.9%; Score 39; DB 1; Length 646;
 Best Local Similarity 55.6%; Pred. No. 32;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

COY 1 WNNRYREYV 9
 ||||: |
 Db 9 WNNRFQRAV 17

RESULT 4

ID CATA_HELPY STANDARD; PRT; 505 AA.
 AC P77872; P94823;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CATALASE (EC 1.11.1.6).
 GN KATA OR HP0875.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RUI;
 RX MEDLINE; 98207782.
 RA MANOS J., KOLESNIKOW T., HAZELL S.L.;
 RT "An investigation of the molecular basis of the spontaneous
 occurrence of a catalase-negative phenotype in Helicobacter pylori."
 RL Helicobacter 3:28-38(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PI;
 RX MEDLINE; 97113460.
 RA ODBREIT S., WIELAND B., HAAS R.;
 RT "Cloning and genetic characterization of Helicobacter pylori catalase
 and construction of a catalase-deficient mutant strain."
 RL J. Bacteriol. 178:6960-6967(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=26695 / ATCC 700392;
 RX MEDLINE; 97394467.
 RA TOMB J.-F., WHITE O., KERLAVAGE A.R., CLAYTON R.A., SUTTON G.G.,

RA FLEISCHMANN R.D., KETCHUM K.A., KLENK H.-P., GILL S., DOUGHERTY B.A.,
 RA NELSON K., QUACKENBUSH J., ZHOU L., KIRKNESS E.F., PETERSON S.,
 RA LOFTUS B., RICHARDSON D., DODSON R., ADAMS H.G., GLODER A.,
 RA MCKENNEY K., FITZGERALD L.M., LEE N., KHALAK M.D., HICKEY E.K.,
 RA BERG D.E., GOCAYNE J.D., UTTERBACK T.R., PETERSON J.D., KELLEY J.M.,
 RA COTTON M.D., WEIDMAN J.M., FUJII C., BOWMAN C., WATTHEY L., WALLIN E.,
 RA HAYES W.S., BORODOVSKY M., KARP P.D., SMITH H.O., FRASER C.M.,
 RA VENTER J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 pylori."
 RL Nature 388:539-547(1997).
 CC -I- FUNCTION: DECOMPOSES HYDROGEN PEROXIDE IN WATER AND OXYGEN; SERVES
 TO PROTECT CELLS FROM THE TOXIC EFFECTS OF HYDROGEN PEROXIDE.
 CC -I- CATALYTIC ACTIVITY: 2 H(2)O(2) -> O(2) + 2 H(2)O.
 CC -I- COFACTOR: HEME GROUP.
 CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
 CC -I- SIMILARITY: BELONGS TO THE CATALASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; U67458; AAC16068.1; -;
 DR EMBL; Z70679; CAA94567.1; -;
 DR EMBL; AE00597; AAD07923.1; -;
 DR HSSP; P42321; 2CAH.
 DR TIGR; HP0875; -;
 DR PROSITE; PS00437; CATALASE_1; 1.
 DR PROSITE; PS00438; CATALASE_2; 1.
 DR PFAM; PF00199; catalase; 1.
 KW Oxidoreductase; Peroxidase; Iron; Heme; Hydrogen peroxide.
 FT ACT_SITE 56 56 BY SIMILARITY.
 FT BINDING 129 129 BY SIMILARITY.
 FT BINDING 339 339 PROXIMAL HEME LIGAND (BY SIMILARITY).
 FT CONFLICT 82 82 S -> F (IN REF. 1).
 FT CONFLICT 234 234 V -> I (IN REF. 2).
 FT CONFLICT 237 237 Y -> H (IN REF. 2).
 FT CONFLICT 248 248 N -> D (IN REF. 2).
 FT CONFLICT 255 255 F -> Y (IN REF. 2).
 FT CONFLICT 286 286 L -> T (IN REF. 2).
 FT CONFLICT 313 313 A -> V (IN REF. 1).
 FT CONFLICT 316 316 S -> T (IN REF. 2).
 SQ SEQUENCE 505 AA; 58629 MW; DCA0095E CRC32;

Query Match 62.3%; Score 38; DB 1; Length 505;
 Best Local Similarity 83.3%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNNRYR 6
 |||| |
 Db 414 WNNMDYR 419

RESULT 5

ID VGLB_MCMVS STANDARD; PRT; 928 AA.
 AC P27171;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE GLYCOPROTEIN B PRECURSOR.
 GN GB OR UL55.
 OS Murine cytomegalovirus (strain Smith).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Muromegalovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 92292266.

RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: 4-MIDAZOLONE-5-PROPANOATE + H(2)O = N-
CC FORMIMINO-L-GLUTAMATE.
CC -!- PATHWAY: THIRD STEP IN HISTIDINE DEGRADATION.
CC -!- SIMILARITY: BELONGS TO THE HUTI FAMILY.

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CC -----

DR EMBL: AF032970; AAB86968.1; -
KW Hydrolase; Histidine metabolism.
SQ SEQUENCE 400 AA; 43146 MW; 96A39BB7 CRC32;

Query Match 60.7%; Score 37; DB 1; Length 400;
Best Local Similarity 83.3%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WRYREY 8
|||:|
Db 95 WRYRQY 100

RESULT 8
PAGL TRYBB STANDARD; PRT; 405 AA.
AC Q01889;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE PAGL PROTEIN PRECURSOR.
GN PAGL.
OS Trypanosoma brucei brucei.
CC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=427;
RX MEDLINE: 93063044.
RA KOENIG-MARTIN E., YAMAGE M., RODITI I.;
RT "A procyclin-associated gene in trypanosoma brucei encodes a
RT polypeptide related to ESAG 6 and 7 proteins."
RL Mol. Biochem. Parasitol. 55:135-145(1992).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
CC -!- SIMILARITY: TO ESAG6 AND 7 PROTEINS.
CC -----

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DR EMBL: X62148; CAA44074.1; -
DR PIR: A48447; A48447.
DR PIR: S27847; S27847.
KW Glycoprotein; Membrane; GPI-anchor; Signal.
FT SIGNAL 1 50
FT CHAIN 51 396 POTENTIAL.
FT PROPEP 397 405 PAGL PROTEIN.
FT LIPID 396 396 REMOVED IN MATURE FORM (POTENTIAL).
FT CARBOHYD 55 55 GPI-ANCHOR (POTENTIAL).
FT CARBOHYD 104 104 POTENTIAL.
FT CARBOHYD 256 256 POTENTIAL.
FT CARBOHYD 351 351 POTENTIAL.
SQ SEQUENCE 405 AA; 45138 MW; A830B2FE CRC32;

Query Match 60.7%; Score 37; DB 1; Length 405;
Best Local Similarity 44.4%; Pred. No. 41;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
|||:|
Db 335 WNWRYAQAI 343

RESULT 9
AERA_AERSO STANDARD; PRT; 488 AA.
ID AERA_AERSO
AC Q06304;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE AEROLYSIN PRECURSOR (HEMOLYSIN).
GN ASAL.

OS Aeromonas sobria.
CC Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
CC Aeromonas.
CC [1]

RP SEQUENCE FROM N.A.

RC STRAIN=33;
RX MEDLINE: 93254202.
RA HIRONO I., AOKI T., ASAO T., KOZAKI S.;
RT "Nucleotide sequences and characterization of haemolysin genes from
RT Aeromonas hydrophila and Aeromonas sobria."
RL Microb. Pathog. 13:433-446(1992).
CC -!- FUNCTION: AEROLYSIN IS A CYTOLYTIC TOXIN EXPORTED BY THE GRAM
CC NEGATIVE AEROMONAS BACTERIA. THE MATURE TOXIN BINDS TO EUKARYOTIC
CC CELLS AND AGGREGATES TO FORM HOLES APPROXIMATIVELY 3NM IN
CC DIAMETER, LEADING TO DESTRUCTION OF THE MEMBRANE PERMEABILITY
CC BARRIER AND OSMOTIC LYSIS (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER IN SOLUTION; HEPTAMER IN THE MEMBRANE (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED
CC -!- SIMILARITY: SMALL REGIONS OF SIMILARITY WITH ALPHA-TOXIN.

CC -----
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CC -----

DR EMBL: X65046; CAA46182.1; -
DR HSSP: P09167; 1PRE.
DR PROSITE: PS00274; AEROLYSIN; 1.
DR PFAM: PF01117; Aerolysin; 1.
KW Hemolysis; Toxin; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 443 AEROLYSIN.
FT PROPEP 444 488 POTENTIAL.
FT DISULFID 43 99 BY SIMILARITY.
FT DISULFID 183 188 BY SIMILARITY.
FT SIMILAR 246 255 TO S.AUREUS ALPHA-TOXIN.
SQ SEQUENCE 488 AA; 53921 MW; 0769B994 CRC32;

Query Match 60.7%; Score 37; DB 1; Length 488;
Best Local Similarity 62.5%; Pred. No. 49;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNWRYREY 8
|||
Db 396 WNWRTISEY 403

RESULT 10
AERA_AERSA STANDARD; PRT; 489 AA.
ID AERA_AERSA

```
AC Q08676;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE AEROLYSIN PRECURSOR (HEMOLYSIN 3).
GN ASH3.
OS Aeromonas salmonicida.
OC Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
OC Aeromonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-17-2.
RX MEDLINE; 94142497.
RA HIRONO I., AOKI T.;
RT "Cloning and characterization of three hemolysin genes from Aeromonas
salmonicida.";
RL Microb. Pathog. 15:269-282(1993).
CC -1- FUNCTION: AEROLYSIN IS A CYTOLYTIC TOXIN EXPORTED BY THE GRAM
CC NEGATIVE AEROMONAS BACTERIA. THE MATURE TOXIN BINDS TO EUKARYOTIC
CC CELLS AND AGGREGATES TO FORM HOLES APPROXIMATIVELY 3NM IN
CC DIAMETER, LEADING TO DESTRUCTION OF THE MEMBRANE PERMEABILITY
CC BARRIER AND OSMOTIC LYSIS (BY SIMILARITY).
CC -1- SUBUNIT: HOMODIMER IN SOLUTION; HEPTAMER IN THE MEMBRANE (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: SMALL REGIONS OF SIMILARITY WITH ALPHA-TOXIN.
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CC -----
DR EMBL; X65048; CAA46184.1; -.
DR HSPF; P09167; 1PRE.
DR PROSITE; PS00274; AEROLYSIN; 1.
DR PFAM; PF01117; Aerolysin; 1.
KW Hemolysis; Toxin; Signal.
FT SIGNAL 1 24
FT CHAIN 25 444 POTENTIAL.
FT PROPEP 445 489 POTENTIAL.
FT DISULFD 44 100 BY SIMILARITY.
FT DISULFD 184 189 BY SIMILARITY.
FT SIMILAR 247 256 TO S.AUREUS ALPHA-TOXIN.
SQ SEQUENCE 489 AA; 54188 MW; 2D820124 CRC32;

Query Match 60.7%; Score 37; DB 1; Length 489;
Best Local Similarity 62.5%; Pred. No. 50;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WNWRYREY 8
Db 397 WNWITSEY 404
|||||

RESULT 11
YHIJ_ECOLI
ID YHIJ_ECOLI STANDARD; PRT; 540 AA.
AC P37627;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 61.2 KD PROTEIN IN RHB-PIT INTERGENIC REGION (F540).
GN YHIJ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
```

```
RX MEDLINE; 94316500.
RA SOFIA H.J., BURLAND V., DANIELS D.L., PLUNKETT G. III, BLATTNER F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes.";
RL Nucleic Acids Res. 22:2576-2586(1994).
CC -----
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CC -----
DR EMBL; U00039; AAB18464.1; -.
DR EMBL; AE00425; AAC76513.1; -.
DR ECGENE; EG12225; YhiJ.
KW Hypothetical protein.
SQ SEQUENCE 540 AA; 61164 MW; 309B934B CRC32;

Query Match 60.7%; Score 37; DB 1; Length 540;
Best Local Similarity 50.0%; Pred. No. 55;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WNWRYREY 8
Db 157 WNWKISQY 164
|||||

RESULT 12
PRIM_RICPR
ID PRIM_RICPR STANDARD; PRT; 593 AA.
AC P30103;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE DNA PRIMASE (EC 2.7.7.-).
GN DNAG OR RP859.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MADRID E;
RX MEDLINE; 93138420.
RA MARKS G.L., WOOD D.O.;
RT "Characterization of the gene coding for the Rickettsia prowazekii
RT DNA primase analogue.";
RL Gene 123:121-125(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MADRID E;
RX MEDLINE; 99039499.
RA ANDERSSON S.G.E., ZOMORODIPOUR A., ANDERSSON J.O.,
RA SICHERTZ-PONTEN T., ALSMARK U.C.M., PODOWSKI R.M., NAESLUND A.K.,
RA ERIKSSON A.-S., WINKLER H.H., KURLAND C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -1- FUNCTION: DNA PRIMASE IS THE POLYMERASE THAT SYNTHESIZES SMALL
CC RNA PRIMERS FOR THE OKAZAKI FRAGMENTS ON BOTH TEMPLATE STRANDS AT
CC REPLICATION FORKS DURING CHROMOSOMAL DNA SYNTHESIS.
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -----
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CC -----
DR EMBL; U02878; AAB81403.1; -.
DR EMBL; AJ235273; CAA15283.1; ALT_INIT.
DR PIR; JN0534; JN0534.
DR KW Transferrase; DNA replication; DNA-directed RNA polymerase; Primosome;
KW Zinc; Metal-binding. 62
KW ZN_FING 38 CHC2-TYPE (PROBABLE).
FT SEQUENCE 593 AA; 68683 MW; D8125A84 CRC32;
-----
Query Match 60.7%; Score 37; DB 1; Length 593;
Best Local Similarity 50.0%; Pred. No. 60;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYREY 8
   | | | | |
Db 537 WQWLYKKY 544

RESULT 13
YI69_METJA STANDARD; PRT; 169 AA.
ID Y769_METJA
AC Q58179;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL PROTEIN MJ0769.
GN MJ0769.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,
RA SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,
RA KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I.,
RA OVERBECK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,
RA SCOTT J.L., GEOCHANE N.S.M., WETDMAN J.F., FUHRMANN J.L., NGUYEN D.,
RA UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,
RA COTTON M.D., ROBERTS K.M., HURST M.A., KATNE B.P., BORODOVSKY M.,
RA KLENK H.-P., FRASER C.W., SMITH H.O., WOESE C.R., VENTER J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
   jannaschii."
RL Science 273:1058-1073(1996).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; U67522; AAB98774.1; -.
DR TIGR; MJ0769; -.
KW Hypothetical protein.
SQ SEQUENCE 169 AA; 20167 MW; A3725865 CRC32;
-----
Query Match 59.0%; Score 36; DB 1; Length 169;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
   | | | | |
Db 121 WEYREYL 127

RESULT 14
YIC4_YEAST STANDARD; PRT; 189 AA.
ID YIC4_YEAST

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DR EMBL; Z99117; CAB14511.1; -.
DR SUBTILIST; BG11634; YQEF.
DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
DR PFAM; PF00657; Lipase_GDSL; 1.
KW Hypothetical protein; Membrane; Lipoprotein; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 243 HYPOTHETICAL LIPOPROTEIN YQEF.
FT LIPID 17 17 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 243 AA; 27639 MW; 53E0EDCA CRC32;

Query Match 59.0%; Score 36; DB 1; Length 243;
Best Local Similarity 71.4%; Pred. No. 35;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWRYREY 8
|||
Db 37 NWDYRDY 43

Search completed: May 2, 2000, 00:21:31
Job time: 84 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:19:58 ; Search time 14.64 Seconds
(without alignments)
42.623 Million cell updates/sec

Title: US-09-258-947-38
Perfect score: 61
Sequence: 1 WNWRYREYV 9

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	70.5	367	10 Q9XEG0	Q9xeg0 arabidopsis
2	41	67.2	368	10 Q43085	Q43085 pisum sativ
3	40	65.6	505	10 Q22236	Q22236 arabidopsis
4	40	65.6	642	2 O66684	O66684 aquifex aeo
5	40	65.6	674	13 Q90369	Q90369 coturnix co
6	39	63.9	649	6 Q28657	Q28657 oryctolagus
7	39	63.9	2783	5 Q77089	Q77089 panulirus a
8	38.5	63.1	462	1 Q57832	Q57832 pyrococcus
9	38	62.3	104	12 Q83193	Q83193 mouse cytom
10	38	62.3	104	12 Q83198	Q83198 mouse cytom
11	38	62.3	104	12 Q83203	Q83203 mouse cytom
12	38	62.3	104	12 Q83212	Q83212 mouse cytom
13	38	62.3	104	12 Q83216	Q83216 mouse cytom
14	38	62.3	104	12 Q83228	Q83228 mouse cytom
15	38	62.3	104	12 Q83236	Q83236 mouse cytom
16	38	62.3	104	12 Q83241	Q83241 mouse cytom
17	38	62.3	104	12 Q83247	Q83247 mouse cytom
18	38	62.3	237	8 Q9XMS6	Q9xms6 tetrahymena
19	38	62.3	300	2 Q9WZ88	Q9wz88 thermotoga
20	38	62.3	504	1 Q60224	Q60224 natronococc

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21 38 62.3 505 2 Q92KX5
22 38 62.3 605 2 O83607
23 38 62.3 1238 11 O88879
24 38 62.3 1444 10 Q92VJ8
25 37 60.7 406 1 Q29700
26 37 60.7 406 1 O26354
27 37 60.7 566 12 Q36454
28 37 60.7 566 12 Q9YMW9
29 37 60.7 783 12 Q98210
30 37 60.7 968 4 O60289
31 36 59.0 108 10 Q9ZSV6
32 36 59.0 192 12 Q79667
33 36 59.0 318 2 O50561
34 36 59.0 329 2 Q9ZNA6
35 36 59.0 371 1 O58820
36 36 59.0 492 2 P95529
37 36 59.0 587 8 O21309
38 36 59.0 601 1 O30039
39 36 59.0 783 10 O80558
40 36 59.0 930 5 Q09588
41 35.5 58.2 185 8 Q33831
42 35.5 58.2 234 12 O87109
43 35 57.4 162 2 O34377
44 35 57.4 170 2 Q04141
45 35 57.4 185 2 O31999

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ALIGNMENTS

```

RESULT 1
Q9XEG0
ID Q9XEG0 PRELIMINARY; PRT; 367 AA.
AC Q9XEG0;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE SHRUNKEN SEED PROTEIN.
OS SSEL.
GN Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. C24;
RX MEDLINE: 99212146.
RA LIN Y., SUN L., NGUYEN L.V., RACHUBINSKI R.A., GOODMAN H.M.;
RT "The Pex16p homolog SSEL and storage organelle formation in
RT Arabidopsis seeds.";
RL Science 284:328-330(1999).
DR EMBL: AF085354; AAD30661.1; -.
SQ SEQUENCE 367 AA; 41624 MW; D73B4E39 CRC32;

```

Query Match 70.5%; Score 43; DB 10; Length 367;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 WNWRYREYV 9
Db 7 WNWRYREYV 15

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RESULT 2
Q43085
ID Q43085 PRELIMINARY; PRT; 368 AA.
AC Q43085;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TEMBLrel. 12, Last annotation update)
DE PHOSPHORIBOSYLANTHRANILATE TRANSFERASE (EC 2.4.2.18) (ANTHRANILATE

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DE PHOSPHORIBOSYLTRANSFERASE) (PHOSPHORIBOSYL-ANTHRANILATE
DE PYROPHOSPHORYLASE) (FRAGMENT).
GN PAT1.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RC SATO N., KAZUO A., OHTA N., OHSHIMA K.;
RA "Isolation of a pea cDNA for phosphoribosylanthranilate transferase.";
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RL CC -1- CATALYTIC ACTIVITY: ANTHRANILATE + PHOSPHORIBOSYLPHOSPHATE =
CC N-5'-PHOSPHORIBOSYL- ANTHRANILATE + DIPHOSPHATE.
DR EMBL; D86180; BAA13032.1; -.
DR MENDEL; 12557; P1ssa:1757;12557.
KW Transferase; Glycosyltransferase.
FT NON_TER
SQ SEQUENCE 368 AA; 42789 MW; 00DF558A CRC32;

Query Match 67.28; Score 41; DB 10; Length 368;
Best Local Similarity 83.38; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYR 6
Db 226 WNWRF 231
|||||

RESULT 3
O22236 PRELIMINARY; PRT; 505 AA.
ID O22236
AC O22236
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE HYPOTHETICAL 58.5 KD PROTEIN.
GN T32N15.6.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA DE LA BASTIDE M.R., PARNELL L.D., KAPLAN N., GNOJ L., HAMEED A.,
RA SCHUTZ K., HASEGAWA A., GOTTESMAN T., SHOHDY N., GRANAT S., JENSEN K.,
RA JOHNSON A.F., LODHI M., DEDHTA N., MARTIENSSEN R., MCCOMBIE W.R.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002534; AAB70030.1; -.
DR MENDEL; 25136; Arath;3230;25136.
KW Hypothetical protein.
SQ SEQUENCE 505 AA; 58451 MW; 60B6DC03 CRC32;

Query Match 65.68; Score 40; DB 10; Length 505;
Best Local Similarity 62.58; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYREY 8
Db 22 WNWRLHY 29
|||||

RESULT 4
O66684 PRELIMINARY; PRT; 642 AA.
AC O66684
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)

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DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE ATP-DEPENDENT HELICASE (DING FAMILY).
GN DING.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE; 98196666.
RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA GRAHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RA DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
RA GRAHAM D.E., OVERBEER R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
RA FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE000885; AAC06840.1; -.
DR PFAM; PF00270; DEAD; 1.
KW Helicase.
SQ SEQUENCE 642 AA; 75417 MW; 633E4488 CRC32;

Query Match 65.68; Score 40; DB 2; Length 642;
Best Local Similarity 85.78; Pred. No. 74;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WRYREYV 9
Db 611 WRYREYV 617
|||||

RESULT 5
O90369 PRELIMINARY; PRT; 674 AA.
ID O90369
AC Q90369;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE KALLMANN SYNDROME PROTEIN HOMOLOG KAL.
GN KAL.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94010957.
RA LEGOUIS R., COHEN-SALMON M., DEL CASTILLO I., LEVILLIERS J., CAPY L.,
RA MORNOW J.P., PETIT C.;
RT "Characterization of the chicken and quail homologues of the human
RT gene responsible for the x-linked Kallmann syndrome.";
RL Genomics 17:516-518 (1993).
DR EMBL; L13976; AAA88500.1; -.
DR HSPS; P19957; 2REL.
DR PROSITE; PS00317; 4_DISULFIDE_CORE; 1.
DR PFAM; PF00041; fn3; 3.
DR PFAM; PF00095; wap; 1.
DR PRINTS; PR00003; 4DISULPHCORE.
SQ SEQUENCE 674 AA; 76439 MW; 66C20245 CRC32;

Query Match 65.68; Score 40; DB 13; Length 674;
Best Local Similarity 55.68; Pred. No. 78;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
Db 326 WSWTYSKYV 334
|||||

```

RESULT 6
Q28657 Q28657 PRELIMINARY; PRT; 649 AA.
ID AC Q28657;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE P-SELECTIN.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RA VORA D.K., FANG Z., LIVA S.M., PARHAMI F., WATSON A.D., DRAKE T.A.,
RA TERRITO M.C., BERLINER J.A.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA WARDEN C.H.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U39446; AAC81385.1; -;
DR HSSP; P16109; IFSB.
DR PROSITE; PS00615; C-TYPE LECTIN_1; 1.
DR PFAM; PF00008; EGF_1;
DR PFAM; PF00059; lectin_C; 1.
DR PFAM; PF00084; sushi; 6.
DR PRINTS; PR00343; SELECTIN.
KW Lectin; Glycoprotein.
SQ SEQUENCE 649 AA; 71755 MW; 2C34857A CRC32;

Query Match 63.9%; Score 39; DB 6; Length 649;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 WNWRYREYV 9
|||||:
Db 9 WNWRFQAV 17

RESULT 7
O77089 O77089 PRELIMINARY; PRT; 2783 AA.
ID AC O77089;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE INOSITOL 1,4,5-TRISPHOSPHATE RECEPTOR.
GN IP3R.
OS Panulirus argus (Spiny lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Palinura;
OC Palinuridae; Panulirus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OLFACTORY ORGAN;
RA MUNGER S.D., ACHE B.W., GREENBERG R.M.;
RT "Plasma Membrane Localization of an Olfactory Inositol 1,4,5-
RT Trisphosphate Receptor";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF055079; AAC61691.1; -;
DR PFAM; PF01365; RYDR_ITPR; 1.
DR PRINTS; PR00779; INSP3RECEPTR.
SQ SEQUENCE 2783 AA; 316000 MW; 2CCBC21C CRC32;

Query Match 63.9%; Score 39; DB 5; Length 2783;
Best Local Similarity 44.4%; Pred. No. 4.5e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 WNWRYREYV 9

|||||:
Db 624 WDWRFDLYL 632

RESULT 8
O57832 O57832 PRELIMINARY; PRT; 462 AA.
ID AC O57832;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE 462AA LONG HYPOTHETICAL PROTEIN.
GN PH0090.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE; 98344137.
RA KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
RA YAMAMOTO S., SERINE M., BABA S., KOSUGI H., HOSOTAMA A., NAGAI Y.,
RA SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
RA FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
RA AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
RA KIKUCHI H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
DR EMBL; AP000001; BAA29159.1; -;
SQ SEQUENCE 462 AA; 52933 MW; 7A6D3A16 CRC32;

Query Match 63.1%; Score 38.5; DB 1; Length 462;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
Qy 1 WNWRYREYV 9
|||||:
Db 197 WNWVRREYL 206

RESULT 9
Q83193 Q83193 PRELIMINARY; PRT; 104 AA.
ID AC Q83193;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE GLYCOPROTEIN B (FRAGMENT).
GN GB.
OS Mouse cytomegalovirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-G3E;
RX MEDLINE; 96145134.
RA XU J., LYONS P.A., CARTER M.D., BOOTH T.W., DAVIS-POYNTER N.J.,
RA SHELLAM G.R., SCALZO A.A.;
RT "Assessment of antigenicity and genetic variation of glycoprotein B of
RT murine cytomegalovirus";
RL J. Gen. Virol. 77:49-59(1996).
DR EMBL; L39260; AAB01385.1; -;
DR NON_TER 1
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 12287 MW; E88A074A CRC32;

Query Match 62.3%; Score 38; DB 12; Length 104;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 WNWRYREYV 7

```

Db      77 WTWRYTE 83
| ||| |
RESULT 10
Q83198 PRELIMINARY; PRT; 104 AA.
AC Q83198;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE GLYCOPROTEIN B (FRAGMENT).
GN GB.
OS Mouse cytomegalovirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G4;
RA MEDLINE; 92292266.
RA RAPP M., MESSERLE M., BUHLER B., TANNHEIMER M., KEIL G.M.,
RA KOSZINOWSKI U.H.;
RT "Identification of the murine cytomegalovirus glycoprotein B gene and
RT its expression by recombinant vaccinia virus.";
RL J. Virol. 66:4399-4406(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=G4;
RA MEDLINE; 96145134.
RA XU J., LYONS P.A., CARTER M.D., BOOTH T.W., DAVIS-POYNTER N.J.,
RA SHELLAM G.R., SCALZO A.A.;
RT "Assessment of antigenicity and genetic variation of glycoprotein B of
RT murine cytomegalovirus.";
RL J. Gen. Virol. 77:49-59(1996).
DR EMBL; L39258; AAB01389.1; -.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 12287 MW; E88A074A CRC32;

Query Match 62.3%; Score 38; DB 12; Length 104;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WNWRYRE 7
Db 77 WTWRYTE 83
| ||| |
RESULT 11
Q83203 PRELIMINARY; PRT; 104 AA.
AC Q83203;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE GLYCOPROTEIN B (FRAGMENT).
GN GB.
OS Mouse cytomegalovirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=G5;
RA MEDLINE; 92292266.
RA RAPP M., MESSERLE M., BUHLER B., TANNHEIMER M., KEIL G.M.,
RA KOSZINOWSKI U.H.;
RT "Identification of the murine cytomegalovirus glycoprotein B gene and
RT its expression by recombinant vaccinia virus.";
RL J. Virol. 66:4399-4406(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=G5;
RX STRAIN=K17B;
RX MEDLINE; 96145134.

Query Match 62.3%; Score 38; DB 12; Length 104;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WNWRYRE 7
Db 77 WTWRYTE 83
| ||| |
RESULT 12
Q83212 PRELIMINARY; PRT; 104 AA.
AC Q83212;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE GLYCOPROTEIN B (FRAGMENT).
GN GB.
OS Mouse cytomegalovirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K17A;
RA MEDLINE; 96145134.
RA XU J., LYONS P.A., CARTER M.D., BOOTH T.W., DAVIS-POYNTER N.J.,
RA SHELLAM G.R., SCALZO A.A.;
RT "Assessment of antigenicity and genetic variation of glycoprotein B of
RT murine cytomegalovirus.";
RL J. Gen. Virol. 77:49-59(1996).
DR EMBL; L39253; AAB01399.1; -.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 12301 MW; 79C42F18 CRC32;

Query Match 62.3%; Score 38; DB 12; Length 104;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WNWRYRE 7
Db 77 WTWRYTE 83
| ||| |
RESULT 13
Q83216 PRELIMINARY; PRT; 104 AA.
AC Q83216;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE GLYCOPROTEIN B (FRAGMENT).
GN GB.
OS Mouse cytomegalovirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K17B;
RX MEDLINE; 96145134.

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RA XU J., LYONS P.A., CARTER M.D., BOOTH T.W., DAVIS-POYNTER N.J.,
RA SHELLAM G.R., SCALZO A.A.;
RT "Assessment of antigenicity and genetic variation of glycoprotein B of
RT murine cytomegalovirus.";
RL J. Gen. Virol. 77:49-59(1996).
DR EMBL; L39259; AAB01402.1; -
FT NON_TER 1 104
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 12287 MW; E88A074A CRC32;

Query Match 62.3%; Score 38; DB 12; Length 104;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYRE 7
| | | | |
Db 77 WTWRYTE 83

RESULT 14

Q83228 PRELIMINARY; PRT; 104 AA.
AC Q83228;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE GLYCOPROTEIN B (FRAGMENT).
GN GB.
OS Mouse cytomegalovirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
RN [J]
RP SEQUENCE FROM N.A.
RC STRAIN-K181;
RX MEDLINE; 96145134.
RA XU J., LYONS P.A., CARTER M.D., BOOTH T.W., DAVIS-POYNTER N.J.,
RA SHELLAM G.R., SCALZO A.A.;
RT "Assessment of antigenicity and genetic variation of glycoprotein B of
RT murine cytomegalovirus.";
RL J. Gen. Virol. 77:49-59(1996).
DR EMBL; L39252; AAB01408.1; -
FT NON_TER 1 104
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 12301 MW; 79C42F18 CRC32;

Query Match 62.3%; Score 38; DB 12; Length 104;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYRE 7
| | | | |
Db 77 WTWRYTE 83

RESULT 15

Q83236 PRELIMINARY; PRT; 104 AA.
AC Q83236;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE GLYCOPROTEIN B (FRAGMENT).
GN GB.
OS Mouse cytomegalovirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Betaherpesvirinae; Muromegalovirus.
RN [J]
RP SEQUENCE FROM N.A.
RC STRAIN-K4;
RX MEDLINE; 96145134.
RA XU J., LYONS P.A., CARTER M.D., BOOTH T.W., DAVIS-POYNTER N.J.,

RA SHELLAM G.R., SCALZO A.A.;
RT "Assessment of antigenicity and genetic variation of glycoprotein B of
RT murine cytomegalovirus.";
RL J. Gen. Virol. 77:49-59(1996).
DR EMBL; L39254; AAB01414.1; -
FT NON_TER 1 104
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 12301 MW; 79C42F18 CRC32;

Query Match 62.3%; Score 38; DB 12; Length 104;
Best Local Similarity 71.4%; Pred. No. 25;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRYRE 7
| | | | |
Db 77 WTWRYTE 83

Search completed: May 2, 2000, 00:21:13
Job time: 75 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:02:01 ; Search time 32.85 Seconds
(without alignments)
4.326 Million cell updates/sec

Title: US-09-258-947-174
Perfect score: 30
Sequence: 1 WRXKEY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	90.0	10	1 W32627	Human platelet gly
2	27	90.0	10	1 W32628	Human platelet gly
3	27	90.0	10	1 W1754	Mimotope capable o
4	27	90.0	10	1 W1755	Mimotope capable o
5	27	90.0	506	1 W44158	Infectious pancrea
6	26	86.7	9	1 W15299	Human platelet gly
7	26	86.7	9	1 W1758	Mimotope capable o
8	26	86.7	10	1 W32626	Human platelet gly
9	26	86.7	10	1 W32629	Human platelet gly
10	26	86.7	10	1 W32624	Human platelet gly
11	26	86.7	10	1 W1752	Mimotope capable o
12	26	86.7	10	1 W1753	Mimotope capable o
13	26	86.7	10	1 W1756	Mimotope capable o
14	26	86.7	42	1 W59181	Pig CII TMP-2 bind
15	26	86.7	42	1 W59182	Human CII TMP-2 bi
16	26	86.7	370	1 R37016	Type I matrix meta
17	26	86.7	426	1 P40254	Human Igd. Novel i
18	26	86.7	457	1 P3628	Sequence of human
19	26	86.7	469	1 P70611	Sequence encoded b
20	25	83.3	10	1 W32631	Human platelet gly
21	25	83.3	10	1 W1757	Mimotope capable o
22	25	83.3	313	1 W37990	A double-stranded
23	25	83.3	352	1 W39953	Human regulatory m
24	25	83.3	803	1 R60883	P. occultum DNA po
25	25	83.3	803	1 R32523	Pyrodictum occult
26	25	83.3	1289	1 R20067	B.thuringiensis to
27	25	83.3	1289	1 R28890	Toxin 17b. New bac
28	25	83.3	1289	1 R29027	Bacillus thuringie
29	25	83.3	1289	1 R28810	BT toxin 17b. New
30	25	83.3	1289	1 R29517	BT toxin 17b. Nema
31	25	83.3	1289	1 R58632	Bacillus thuringie
32	25	83.3	1289	1 R44202	Bacillus thuringie
33	25	83.3	1289	1 R76113	PSI7b acaride-acti
34	25	83.3	1289	1 W3885	17b toxin. Bacillu

35 24 80.0 16 1 R57946 Randomly generated
36 24 80.0 186 1 R39447 Phase P1 Ref prote
37 24 80.0 202 1 R25117 Non-A, Non-B Hepat
38 24 80.0 250 1 W12845 Pro-alpha(1) chai
39 24 80.0 252 1 W64659 Mistletoe rMLA pro
40 24 80.0 252 1 W64661 Mistletoe rMLA var
41 24 80.0 253 1 W10022 Prepro mistletoe 1
42 24 80.0 253 1 W90125 Mistletoe ML A-cha
43 24 80.0 300 1 W82558 C. elegans glycoge
44 24 80.0 436 1 W37350 PsbA (Wbpa) protei
45 24 80.0 487 1 R88619 Phytase protein. F

ALIGNMENTS

RESULT 1
W32627
ID W32627 standard; peptide; 10 AA.
AC W32627;
DT 30-JAN-1998 (first entry)
DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
KW anti thrombotic drug; ristocetin.
OS Synthetic.
OS Homo sapiens.
PN WO9718236-A1.
PD 22-MAY-1997.
PF 08-NOV-1996; U17882.
PR 13-NOV-1995; US-556397.
PA (UYNV) UNIV NEW YORK STATE RES FOUND.
PI Lyle VA, Miller JL;
DR WPI: 97-289227/26.
PT Peptide which mimics human platelet glycoprotein Ib/IX complex
PT epitope - also anti-mimotope molecule capable of binding to the
PT peptide and useful to modulate platelet adhesion, aggregation or
PT agglutination
PS Claim 3; Page 96; 115pp; English.
CC The present sequence represents a mimotope which functionally mimics a
CC binding site for a monoclonal antibody (MAB) which recognises an epitope
CC within the human platelet glycoprotein (gp) Ib/IX complex. More
CC specifically the MAB is C-34. The mimotope peptide can be used for
CC raising antibodies, as probes to search for anti-mimotopes and to
CC neutralise the inhibitory activity of those antibodies which recognise
CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
CC to modulate the adhesion, aggregation or agglutination of platelets by
CC affecting von Willebrand factor interaction with the platelets through
CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
CC the ristocetin induced aggregation of platelets.
SQ Sequence 10 AA;

Query Match 90.0%; Score 27; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXKEY 6
Db 4 WRYSEY 9

RESULT 2
W32628
ID W32628 standard; peptide; 10 AA.
AC W32628;
DT 30-JAN-1998 (first entry)
DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
KW anti thrombotic drug; ristocetin.

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OS Synthetic.
OS Homo sapiens.
PN WO9718236-A1.
PD 22-MAY-1997.
PR 08-NOV-1996; U17882.
PR 13-NOV-1995; US-556597.
PA (UYNV ) UNIV NEW YORK STATE RES FOUND.
PI Lyle VA, Miller JL;
PI WPI: 97-289227/26.
DR
PT Peptide which mimics human platelet glycoprotein Ib/IX complex
PT epitope - also anti-mimotope molecule capable of binding to the
PT peptide and useful to modulate platelet adhesion, aggregation or
PT agglutination
PS Claim 3; Page 96; 115pp; English.
CC The present sequence represents a mimotope which functionally mimics a
CC binding site for a monoclonal antibody (MAb) which recognises an epitope
CC within the human platelet glycoprotein (gp) Ib/IX complex. More
CC specifically the MAb is C-34. The mimotope peptide can be used for
CC raising antibodies, as probes to search for anti-mimotopes and to
CC neutralise the inhibitory activity of those antibodies which recognise
CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
CC to modulate the adhesion, aggregation or agglutination of platelets by
CC affecting von Willebrand factor interaction with the platelets through
CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
CC the ristocetin induced aggregation of platelets.
CC Sequence 10 AA;

SQ
Query Match          90.0%; Score 27; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
   || ||
Db 4 WRAREY 9

RESULT 3
W1754
ID W1754 standard; peptide: 10 AA.
AC W1754;
DT 08-DEC-1998 (first entry)
DE Mimotope capable of binding to monoclonal antibody C-34 #4.
KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
KW binding site; platelet epitope; neutralise; aggregation; inhibition;
KW von Willebrand factor interaction; adhesion; agglutination.
OS Synthetic.
OS Homo sapiens.
PN US5817748-A.
PD 06-OCT-1998.
PR 17-MAR-1995; US-406330.
PA (UYNV ) UNIV NEW YORK STATE RES FOUND.
PI Lyle VA, Miller JL;
PI WPI: 98-556458/47.
DR
PT Peptides that mimic platelet epitope - and neutralise
PT aggregation-inhibiting antibody
PS Claim 1; Column 47; 26pp; English.
CC The present invention provides peptides which functionally mimic a
CC binding site for a monoclonal antibody, where the monoclonal antibody
CC recognises an epitope within the human glycoprotein Ib/IX complex.
CC Peptides W1752 to W1832 are mimotopes which are capable of binding
CC to monoclonal antibody C-34. The invention also provides an isolated
CC molecule capable of binding the mimotopes, where the molecule can be
CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
CC molecule, or other naturally or chemically synthesised molecules. These
CC molecules are called anti-mimotopes and can act as anti-thrombotic
CC drugs. A method has also been described for modulating the adhesion,
CC aggregation, or agglutination of platelets, where the method comprises
CC selecting platelets and exposing them to an anti-mimotope molecule. The
CC exposure affects von Willebrand factor interaction with platelets
CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
CC aggregation, or agglutination of the platelets. The peptide mimotopes
CC mimic platelet epitopes.
CC Sequence 10 AA;

Query Match          90.0%; Score 27; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
   || ||
Db 4 WRAREY 9

RESULT 5
W44158
ID W44158 standard; Protein; 506 AA.
AC W44158;
DT 14-MAY-1998 (first entry)
DE Infectious pancreatic necrosis virus VP2 protein.
KW Infectious pancreatic necrosis virus; IPNV; VP2; vaccine; fish;
KW immunisation; VR-299; SP serotype; viral A segment.
OS Infectious pancreatic necrosis virus.
PN US5165925-A.
PD 24-NOV-1992.

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PF 02-MAY-1989; 346623.
 PR 02-MAY-1989; US-346623.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 PI Leong JC;
 DR WPI; 92-414903/50.
 DR N-PSDB; V1202.
 PT Vaccine for infectious pancreatic necrosis virus in fish - comprises polypeptide from viral A segment including VP2, produced by bacterial expression
 PT
 PS Claim 1; Fig 15; 28pp; English.
 CC The present sequence represents the VP2 protein from infectious pancreatic necrosis virus (IPNV). A vaccine has been developed for immunising susceptible fish against infection by VR-299 or Sp serotypes of the IPNV. The vaccine comprises an IPNV polypeptide from the viral A segment and includes at least VP2. The vaccine is capable of inducing immunity in the fish to subsequent infection by the VR-299 or Sp serotypes of IPNV. The polypeptide is produced by an expression vector in a compatible bacterial host, where the vector includes an inserted DNA sequence from the A segment of the viral DNA coding for the IPNV polypeptide in the vaccine. Large amounts of the IPNV polypeptide can be produced by the transformed bacteria. The bacterial lysate containing the viral protein can be added directly to water containing the fish to simultaneously immunise large numbers of fish, particularly young fish.
 SQ Sequence 506 AA;

Query Match 90.08; Score 27; DB 1; Length 506;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WRXXEY 6
 II II
 DB 415 WRTBEY 420

RESULT 6
 W15299 ID W15299 standard; peptide; 9 AA.
 AC W15299;
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope consensus.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.
 PF 08-NOV-1996; U17882.
 PR 13-NOV-1995; US-556597.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI; 97-289227/26.
 PT Peptide which mimics human platelet glycoprotein Ib/IX complex epitope - also anti-mimotope molecule capable of binding to the peptide and useful to modulate platelet adhesion, aggregation or agglutination
 PT
 PS Claim 4; Page 98; 115pp; English.
 CC The present sequence represents the consensus sequence for a mimotope which functionally mimics a binding site for a monoclonal antibody (Mab) which recognises an epitope within the human platelet glycoprotein (gp) Ib/IX complex. More specifically the Mab is C-34. The mimotope peptide can be used for raising antibodies, as probes to search for anti-mimotopes and to neutralise the inhibitory activity of those antibodies which recognise the epitope which is mimicked by the peptide. Anti-mimotopes can be used to modulate the adhesion, aggregation or agglutination of platelets by affecting von Willebrand factor or interaction with the platelets through the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits the ristocetin induced aggregation of platelets.
 SQ Sequence 9 AA;

Query Match 86.7%; Score 26; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.5e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WRXXEY 6
 II II
 DB 3 WRYREY 8

RESULT 7
 W171758 ID W171758 standard; peptide; 9 AA.
 AC W171758;
 DT 08-DEC-1998 (first entry)
 DE Minotope capable of binding to monoclonal antibody C-34 #38.
 KW Minotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex; binding site; platelet epitope; neutralise; aggregation; inhibition; von Willebrand factor interaction; adhesion; agglutination.
 KW Synthetic.
 OS Homo sapiens.
 PN US817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI; 98-556458/47.
 PT Peptides that mimic platelet epitope - and neutralise aggregation-inhibiting antibody
 PT
 PS Claim 1; Column 48; 26pp; English.
 CC The present invention provides peptides which functionally mimic a binding site for a monoclonal antibody, where the monoclonal antibody recognises an epitope within the human glycoprotein Ib/IX complex. Peptides W171752 to W171832 are mimotopes which are capable of binding to monoclonal antibody C-34. The invention also provides an isolated molecule capable of binding the mimotopes, where the molecule can be an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA molecule, or other naturally or chemically synthesised molecules. These molecules are called anti-mimotopes and can act as anti-thrombotic drugs. A method has also been described for modulating the adhesion, aggregation, or agglutination of platelets, where the method comprises selecting platelets and exposing them to an anti-mimotope molecule. The exposure affects von Willebrand factor interaction with platelets through the glycoprotein Ib/IX receptor, which modulates the adhesion, aggregation, or agglutination of the platelets. The peptide mimotopes mimic platelet epitopes.
 SQ Sequence 9 AA;

Query Match 86.7%; Score 26; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.5e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 WRXXEY 6
 II II
 DB 3 WRYREY 8

RESULT 8
 W32626 ID W32626 standard; peptide; 10 AA.
 AC W32626;
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.

Query Match 86.7%; Score 26; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 6;

PT aggregation-inhibiting antibody
 PS Claim 1: Column 47: 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 86.7%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
 || ||
 Db 4 WRYREY 9

RESULT 12

ID W71753 standard; peptide; 10 AA.
 AC W71753;
 DT 08-DEC-1998 (first entry)
 DE Mimotope capable of binding to monoclonal antibody C-34 #3.
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 98-556458/47.
 PT Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1: Column 47: 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 86.7%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
 || ||
 Db 4 WRYFEY 9

RESULT 13

ID W71756 standard; peptide; 10 AA.
 AC W71756;
 DT 08-DEC-1998 (first entry)
 DE Mimotope capable of binding to monoclonal antibody C-34 #6.
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 98-556458/47.
 PT Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1: Column 48: 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 86.7%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
 || ||
 Db 1 WRQREY 6

RESULT 14

ID W59181 standard; peptide; 42 AA.
 AC W59181;
 DT 14-AUG-1998 (first entry)
 DE Pig CII TMP-2 binding peptide beta-propeller blade III region.
 KW Gelatinase A; Gela; TIMP-2; matrix metalloprotease; MMP; beta-propeller;
 KW cell surface activation; inhibition; screening; target; treatment;
 KW disease; tissue repair; tissue damage; rheumatoid arthritis; restenosis;
 KW osteoarthritis.
 OS Sus scrofa.
 PN WO9812309-A2.
 PD 26-MAR-1998.
 PF 15-SEP-1997; U16216.
 PR 17-SEP-1996; US-026226.
 PA (UNIW) UNIV WASHINGTON.
 PI Goldberg GI;
 DR WPI: 98-217253/19.

PT Identifying matrix metallo:protease inhibitors - using a target area
PT comprising specific residues of the TIMP-2 binding site of the
PT gelatinase-A C-terminal domain
PS Disclosure: Fig 5; 54pp: English.
CC W59179-W59196 are peptide fragments of beta-propeller blade regions
CC III and IV from C-terminal domains of various matrix metalloprotease
CC family members which are used in a method to study cell surface
CC activation and inhibition. The method involves the interaction of an
CC inhibitor of matrix metalloprotease, TIMP-2 with the enzyme gelatinase A
CC (Gela). A target area for screening matrix metalloprotease (MMP)
CC inhibitors comprises the following residues of the TIMP-2 binding site
CC on the surface of the gelatinase-A (Gela)-C-terminal domain (CTD):
CC Asp656, Gly651, Phe650 and Tyr636. Also claimed is a target area for
CC screening MMP inhibitors comprising the following residues of the
CC TIMP-2 binding site on the surface of the Gela-CTD domain: Asp656,
CC Gly651, Phe650, Tyr636, Asp615, Lys646, Lys579, Arg590, Lys579,
CC Lys604 and Asn611. The target areas can be used for obtaining MMP
CC inhibitors which can be used for the treatment of diseases that involve
CC tissue repair and damage and other diseases in which MMPs are implicated
CC e.g. rheumatoid arthritis, osteoarthritis and restenosis.
SQ Sequence 42 AA;

Query Match 86.7%; Score 26; DB 1; Length 42;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
|| ||
Db 17 WRYDEY 22

RESULT 15

W59182
ID W59182 standard; peptide; 42 AA.
AC W59182;
DT 14-AUG-1998 (first entry)
DE Human CLI TIMP-2 binding peptide beta-propeller blade III region.
KW Gelatinase A; Gela; TIMP-2; matrix metalloprotease; MMP; beta-propeller;
KW cell surface activation; inhibition; screening; target; treatment;
KW disease; tissue repair; tissue damage; rheumatoid arthritis; restenosis;
KW osteoarthritis.
OS Homo sapiens.
PN W09812309-A2.
PD 26-MAR-1998.
PF 15-SEP-1997; U16216.
PR 17-SEP-1996; US-026226.
PA (UNIW) UNIV WASHINGTON.
PI Goldberg GI.
DR WPI: 98-217253/19.
PT Identifying matrix metallo:protease inhibitors - using a target area
PT comprising specific residues of the TIMP-2 binding site of the
PT gelatinase-A C-terminal domain
PS Disclosure: Fig 5; 54pp: English.
CC W59179-W59196 are peptide fragments of beta-propeller blade regions
CC III and IV from C-terminal domains of various matrix metalloprotease
CC family members which are used in a method to study cell surface
CC activation and inhibition. The method involves the interaction of an
CC inhibitor of matrix metalloprotease, TIMP-2 with the enzyme gelatinase A
CC (Gela). A target area for screening matrix metalloprotease (MMP)
CC inhibitors comprises the following residues of the TIMP-2 binding site
CC on the surface of the gelatinase-A (Gela)-C-terminal domain (CTD):
CC Asp656, Gly651, Phe650 and Tyr636. Also claimed is a target area for
CC screening MMP inhibitors comprising the following residues of the
CC TIMP-2 binding site on the surface of the Gela-CTD domain: Asp656,
CC Gly651, Phe650, Tyr636, Asp615, Lys646, Lys579, Arg590, Lys579,
CC Lys604 and Asn611. The target areas can be used for obtaining MMP
CC inhibitors which can be used for the treatment of diseases that involve
CC tissue repair and damage and other diseases in which MMPs are implicated
CC e.g. rheumatoid arthritis, osteoarthritis and restenosis.
SQ Sequence 42 AA;

Query Match 86.7%; Score 26; DB 1; Length 42;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
|| ||
Db 17 WRYDEY 22

Search completed: May 2, 2000, 00:14:45
Job time: 764 sec

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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:03:11 ; Search time 26.35 Seconds
(without alignments)
3.028 Million cell updates/sec

Title: US-09-258-947-174

Perfect score: 30

Sequence: 1 WRXXEY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 133990 seqs, 13297546 residues

Total number of hits satisfying chosen parameters: 133990

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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5: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	90.0	10	2	US-08-406-330-4
2	27	90.0	10	2	US-08-406-330-5
3	27	90.0	10	2	US-08-556-597-4
4	27	90.0	10	2	US-08-556-597-5
5	27	90.0	507	5	5165925-4
6	26	86.7	9	2	US-08-406-330-38
7	26	86.7	9	2	US-08-556-597-38
8	26	86.7	10	2	US-08-406-330-1
9	26	86.7	10	2	US-08-406-330-3
10	26	86.7	10	2	US-08-406-330-6
11	26	86.7	10	2	US-08-556-597-1
12	26	86.7	10	2	US-08-556-597-3
13	26	86.7	10	2	US-08-556-597-6
14	25	83.3	10	2	US-08-406-330-8
15	25	83.3	10	2	US-08-556-597-8
16	25	83.3	72	1	US-08-280-443-11
17	25	83.3	72	1	US-08-280-443-14
18	25	83.3	72	1	US-08-457-459-11
19	25	83.3	72	1	US-08-457-459-14
20	25	83.3	72	1	US-08-555-678-11
21	25	83.3	72	1	US-08-555-678-14
22	25	83.3	72	4	PCr-US95-02275-11
23	25	83.3	72	4	PCr-US95-02275-14
24	25	83.3	298	2	US-08-855-518-3
25	25	83.3	313	2	US-08-855-518-1
26	25	83.3	352	2	US-08-933-750C-46
27	25	83.3	365	2	US-08-855-518-5
28	25	83.3	366	2	US-08-855-518-4
29	25	83.3	803	1	US-08-062-368-4

30	25	83.3	1289	1	US-07-876-280-4	Sequence 4, Appl1
31	25	83.3	1289	1	US-07-675-772-4	Sequence 4, Appl1
32	25	83.3	1289	1	US-08-063-170-4	Sequence 4, Appl1
33	25	83.3	1289	1	US-08-158-232-4	Sequence 4, Appl1
34	25	83.3	1289	1	US-08-304-626-4	Sequence 4, Appl1
35	25	83.3	1289	1	US-08-316-301A-4	Sequence 4, Appl1
36	25	83.3	1289	2	US-08-611-928-4	Sequence 4, Appl1
37	25	83.3	1289	4	PCr-US92-03624-4	Sequence 4, Appl1
38	25	83.3	3200	2	US-08-477-451-8	Sequence 8, Appl1
39	24	80.0	16	1	US-08-077-797A-42	Sequence 42, Appl1
40	24	80.0	16	4	PCr-US94-01238-42	Sequence 42, Appl1
41	24	80.0	110	2	US-08-727-118-3	Sequence 3, Appl1
42	24	80.0	186	5	5229273-2	Patent No. 5229273
43	24	80.0	240	1	US-08-261-822A-69	Sequence 69, Appl1
44	24	80.0	240	1	PCr-US95-07744A-69	Sequence 69, Appl1
45	24	80.0	436	2	US-08-846-762-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-406-330-4
; Sequence 4, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-4

Query Match 90.0%; Score 27; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 WRXXEY 6
DB 4 WRYYSEY 9

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RESULT 2
US-08-406-330-5
; Sequence 5, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-5
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Query Match 90.0%; Score 27; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1 WRXXEY 6
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DB 4 WRAREY 9
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RESULT 3
US-08-556-597-4
; Sequence 4, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-4
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Query Match 90.0%; Score 27; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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OY 1 WRXXEY 6
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DB 4 WRYSEY 9
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RESULT 4
US-08-556-597-5
; Sequence 5, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-5

Query Match 90.0%; Score 27; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 4 WRAREY 9

RESULT 5
5165925-4
; Patent No. 5165925
; APPLICANT: Leong, Jo-ann C.
; TITLE OF INVENTION: VACCINE FOR IMMUNIZING FISH AGAINST
; INFECTIOUS PANCREATIC NECROSIS VIRUS
; NUMBER OF SEQUENCES: 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/346,623
; FILING DATE: 02-MAY-1989
; SEQ ID NO: 4
; LENGTH: 507
5165925-4

Query Match 90.0%; Score 27; DB 5; Length 507;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 416 WRTEEY 421

RESULT 6
US-08-406-330-38
; Sequence 38, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600

; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-38

Query Match 86.7%; Score 26; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 9.9e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 3 WRREY 8

RESULT 7
US-08-556-597-38
; Sequence 38, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-38

Query Match 86.7%; Score 26; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 9.9e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 3 WRREY 8

RESULT 8
US-08-406-330-1
; Sequence 1, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-1

Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|||
Db 4 WRYFEY 9

RESULT 9
US-08-406-330-3
; Sequence 3, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-3

Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|||
Db 4 WRYFEY 9

RESULT 10
US-08-406-330-6
; Sequence 6, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-6

Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 1 WRQREY 6

RESULT 11
US-08-556-597-1
; Sequence 1, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; APPLICATION TYPE: peptide

US-08-556-597-1
Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 4 WRQREY 9

RESULT 12
US-08-556-597-3
; Sequence 3, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.

; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; APPLICATION TYPE: peptide

US-08-556-597-3
Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 4 WRQREY 9

RESULT 13
US-08-556-597-6
; Sequence 6, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:

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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-556-597-6

Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
DB 1 WRQREY 6

RESULT 14
US-08-406-330-8
; Sequence 8, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-406-330-8

Query Match 83.3%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
DB 5 WRNWEY 10

Query Match 83.3%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
DB 5 WRNWEY 10

Search completed: May 2, 2000, 00:15:21
Job time: 730 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:03:11 ; Search time 45.33 Seconds
(without alignments)
6.243 Million cell updates/sec

Title: US-09-258-947-174
Perfect score: 30
Sequence: 1 WRXXEY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 142080

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR62:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	93.3	640	1 A30452	uromodulin precurs
2	28	93.3	642	1 S52111	uromodulin precurs
3	28	93.3	896	2 A36455	bride of sevenless
4	28	93.3	896	2 S26740	gene boss protein
5	27	90.0	168	2 S21041	cytochrome-c oxida
6	27	90.0	258	2 S45682	acetone-cyanhydrin
7	27	90.0	387	2 H72607	hypothetical prote
8	27	90.0	605	2 S25151	invertase, cell-wa
9	27	90.0	676	1 W2V218	I8 protein - vacci
10	27	90.0	676	2 D42511	I8 protein - vacci
11	27	90.0	676	2 F36843	ATP/GTP-binding pr
12	27	90.0	972	1 GNXSIV	genome polyprotein
13	27	90.0	972	2 GNXSIV	genome polyprotein
14	27	90.0	972	2 T09634	genome polyprotein
15	26	86.7	52	2 S72985	glutamate decarbox
16	26	86.7	301	1 A37766	SPC14 protein - ye
17	26	86.7	351	2 S54259	Delta12-desaturase
18	26	86.7	383	1 DHHU	ig delta chain C r
19	26	86.7	403	2 C72546	probable coenzyme
20	26	86.7	405	2 H64482	threonine synthase
21	26	86.7	468	1 KCRBI	interstitial colla
22	26	86.7	469	1 KCHUI	interstitial colla
23	26	86.7	469	1 KCPGI	interstitial colla
24	26	86.7	469	1 KCBGI	interstitial colla
25	26	86.7	509	2 S17597	Ig delta chain (WI
26	26	86.7	769	2 S35458	SNF2 protein homol
27	26	86.7	893	2 A47550	bride of sevenless
28	26	86.7	971	2 S44645	hypothetical prote
29	26	86.7	975	2 S35457	SNF2 protein homol
30	26	86.7	986	2 S49394	HsdRI protein - My

DNA-directed RNA p
hypothetical prote
plexin 3 precursor
genome polyprotein
peptide synthetase
gramicidin S synth
gramicidin S synth
hypothetical prote
RNA-binding protei
trans-activation-r
TAR RNA-binding pr
hypothetical prote
group II decarboxy
probable membrane

ALIGNMENTS

RESULT 1

uromodulin precursor - human
A30452
N:Alternate names: Tamm-Horsfall urinary glycoprotein; uromuroid
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A30452; A30453
R:Pennica, D.; Kohr, W.J.; Kuang, W.J.; Glaister, D.; Aggarwal, B.B.; Chen, E.Y.; Goe
Science 236, 83-88, 1987
A:Title: Identification of human uromodulin as the Tamm-Horsfall urinary glycoprotein
A:Reference number: A30452; MUID:87177970
A:Accession: A30452
A:Molecule type: DNA; mRNA
A:Residues: 1-640 <PEN>
A:Cross-references: GB:M15881; NID:g340163; PIDN:AAA36798.1; PID:g340164
A:Note: parts of this sequence, including the amino end of the mature protein, were d
R:Heslon, C.; Decker, J.M.; Sherblom, A.P.; Kumar, S.; Yue, C.C.; Mattaliano, R.J.; T
Science 237, 1479-1484, 1987
A:Title: Uromodulin (Tamm-Horsfall glycoprotein): A renal ligand for lymphokines.
A:Reference number: A30453; MUID:87319675
A:Accession: A30453
A:Molecule type: mRNA
A:Residues: 1-640 <HES>
A:Cross-references: GB:M17778
A:Note: the authors translated the codon GTC for residue 381 as Asp
A:Note: parts of this sequence, including the amino end of the mature protein, were d
R:Rindler, M.J.; Naik, S.S.; Li, N.; Hoops, T.C.; Peraldi, M.N.
J. Biol. Chem. 265, 20784-20789, 1990
A:Title: Uromodulin (Tamm-Horsfall Glycoprotein/Uromuroid) is a phosphatidylinositol-
A:Reference number: A30454; MUID:91065873
A:Contents: annotation; GPI-anchor
C:Comment: The protein is anchored to the cell membrane by a phosphatidylinositol lin
e membrane-bound form.
C:Genetics:
A:Gene: GDB:UMOD
A:Cross-references: GDB:l33729; OMIM:191845
A:Map position: 16p13.11-16p12.3
A:Introns: 30/1; 289/1; 325/1; 394/3; 444/2; 526/2; 580/3; 608/1; 621/1
A:Note: the first intron occurs before the initiator codon
C:Superfamily: uromodulin; EGF homology; membrane glycoprotein 2 homology; 2P domain
C:Keywords: duplication; glycoprotein; lipoprotein; phosphatidylinositol linkage; pho
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-640/Product: uromodulin #status predicted <MAT>
F:69-106/Domain: EGF homology <EGF>
F:170-639/Domain: membrane glycoprotein 2 homology <MGH>
F:334-583/Domain: 2P domain homology <2PH>
F:625-640/Domain: transmembrane #status predicted <TRM>
F:38,76,80,275,322,513/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:232,396/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 93.3% Score 28; DB 1; Length 640;
Best Local Similarity 66.7%; Pred. No. 49;

```

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
   || ||
Db 184 WRSTY 189

RESULT 2
S52111
uromodulin precursor - mouse
N:Alternate names: Tamm-Horsfall urinary glycoprotein; uromucoid
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S52111
R:Prasadani, K.; Bates, J.; Badgett, A.; Dell, M.; Sukhatme, V.; Yu, H.; Kumar, S.
Biochim. Biophys. Acta 1260, 328-332, 1995
A:Title: Nucleotide sequence and peptide motifs of mouse uromodulin (Tamm-Horsfall prote
A:Reference number: S52111; MUID:95178555
A:Accession: S52111
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-642 <PRA>
C:Superfamily: uromodulin; EGF homology; membrane glycoprotein 2 homology; ZP domain hom
C:Keywords: duplication; glycoprotein; lipoprotein; membrane protein; phosphatidylinosit
F:69-105/Domain: EGF homology <EG1>
F:111-147/Domain: EGF homology <EG2>
F:171-641/Domain: membrane glycoprotein 2 homology <MGH>
F:335-584/Domain: ZP domain homology <ZPH>

Query Match 93.3%; Score 28; DB 1; Length 642;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
   || ||
Db 185 WRSTY 190

RESULT 3
A36455
bride of sevenless (boss) precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 17-Mar-1999
C:Accession: A36455; B47550; S17425
R:Hart, A.C.; Kraemer, H.; Van Vactor Jr., D.L.; Paidhungat, M.; Zipursky, S.L.
Genes Dev. 4, 1835-1847, 1990
A:Title: Induction of cell fate in the Drosophila retina: the bride of sevenless protein
A:Reference number: A36455; MUID:91115074
A:Accession: A36455
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-896 <HAR>
A:Cross-references: GB:X55887
R:Hart, A.C.; Harrison, S.D.; Van Vactor Jr., D.L.; Rubin, G.M.; Zipursky, S.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 5047-5051, 1993
A:Title: The interaction of bride of sevenless with sevenless is conserved between Dros
A:Reference number: A47550; MUID:93281693
A:Accession: B47550
A:Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 4-896 <HA2>
A:Cross-references: GB:L08133
C:Genetics:
A:Gene: FlyBase:boss
A:Cross-references: FlyBase:FBgn0000206
A:Introns: 18/1; 175/1; 325/1; 811/3
C:Keywords: transmembrane protein

Query Match 93.3%; Score 28; DB 2; Length 896;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
   || ||
Db 413 WRTSEY 418

RESULT 4
S26740
gene boss protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Feb-1997
C:Accession: S26740
R:Kramer, H.
submitted to the EMBL Data Library, September 1990
A:Reference number: S26740
A:Accession: S26740
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-896 <KRA>
A:Cross-references: EMBL:X55887
C:Genetics:
A:Gene: FlyBase:boss
A:Cross-references: FlyBase:FBgn0000206
A:Introns: 18/1; 175/1; 325/1; 811/3

Query Match 93.3%; Score 28; DB 2; Length 896;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
   || ||
Db 413 WRTSEY 418

RESULT 5
S21041
cytochrome-c oxidase (EC 1.9.3.1) chain II - Sulfolobus acidocaldarius
C:Species: Sulfolobus acidocaldarius
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Sep-1997
C:Accession: S21041
R:Luebben, M.; Kolmerer, B.; Saraste, M.
EMBO J. 11, 805-812, 1992
A:Title: An archaeobacterial terminal oxidase combines core structures of two mitochon
A:Reference number: S21041; MUID:92192013
A:Accession: S21041
A:Molecule type: DNA
A:Residues: 1-168 <LUE>
A:Cross-references: EMBL:X62643; NID:g46681; PID:g46682
C:Genetics:
A:Gene: soxa
C:Keywords: copper binding; electron transfer; heme; membrane-associated complex; oxi

Query Match 90.0%; Score 27; DB 2; Length 168;
Best Local Similarity 86.7%; Pred. No. 22;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
   || ||
Db 147 WRDAEY 152

RESULT 6
S45682
acetone-cyanhydrin lyase (EC 4.1.2.37) - cassava
N:Alternate names: alpha-hydroxynitrile lyase
C:Species: Manihot esculenta (cassava)
C:Date: 10-Dec-1994 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C:Accession: S45682; S62859
R:Hughes, J.; de Carvalho, F.J.P.; Hughes, M.A.
Arch. Biochem. Biophys. 311, 496-502, 1994
A:Title: Purification, characterization, and cloning of alpha-hydroxynitrile lyase fr

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A:Reference number: S45682; MUID:94263231

A:Accession: S45682

A:Molecule type: mRNA

A:Residues: 1-258 <HUG>

A:Cross-references: EMBL:229091

A:Accession: S62859

A:Molecule type: protein

A:Residues: 2-37;169-192 <HUG>

C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 90.0%; Score 27; DB 2; Length 258;

Best Local Similarity 66.7%; Pred. No. 34;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6

|| ||

Db 128 WRDTEY 133

RESULT 7

Hypothetical protein APE1326 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: H72607

R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr

A:Reference number: A72450; MUID:99310339

A:Accession: H72607

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-387 <RAW>

A:Cross-references: DDBJ:AP000061; NID:g5104821; PIDN:BAA80318.1; PID:d1044104; PID:g510

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE1326

Query Match 90.0%; Score 27; DB 2; Length 387;

Best Local Similarity 66.7%; Pred. No. 51;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6

|| ||

Db 122 WRAIEY 127

RESULT 8

Invertase, cell-wall-bound - garden pea

N:Alternate names: beta-fructosidase

C:Species: Pisum sativum (garden pea)

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995

C:Accession: S25151

R:Wu, L.L.; Mitchell, J.P.; Cohn, N.S.; Kaufman, P.B.

submitted to the EMBL Data Library, July 1992

A:Description: Molecular cloning characterization of Pea invertase cDNA and gibberellin-

A:Reference number: S25151

A:Accession: S25151

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-605 <WUL>

A:Cross-references: EMBL:X67275

Query Match 90.0%; Score 27; DB 2; Length 605;

Best Local Similarity 66.7%; Pred. No. 79;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6

Db 202 WRSNEY 207

|| ||

RESULT 9

WZVZI8

I8 protein - vaccinia virus (strain WR)

C:Species: vaccinia virus

C:Date: 30-Jun-1989 #sequence_revision 30-Sep-1992 #text_change 16-Jul-1999

C:Accession: B38497; H29889

R:Pathi, Z.; Condit, R.C.

Virol. 181, 258-272, 1991

A:Title: Genetic and molecular biological characterization of a vaccinia virus temper

A:Reference number: A38497; MUID:91134999

A:Accession: B38497

A:Molecule type: DNA

A:Residues: 1-676 <PAT>

A:Cross-references: GB:J03399; EMBL:M29901; NID:g335662; PIDN:AAB59810.1; PID:g335670

R:Schmitt, J.F.C.; Stunnenberg, H.G.

J. Virol. 62, 1889-1897, 1988

A:Title: Sequence and transcriptional analysis of the vaccinia virus HindIII I fragme

A:Reference number: A29889; MUID:88215015

A:Accession: H29889

A:Molecule type: DNA

A:Residues: 1-99 <SCH>

A:Cross-references: GB:J03399

A:Note: the authors translated the codons TAC, AGT, GAA, CAC, ATA, and AGC for r

C:Genetics:

A:Gene: I8

C:Superfamily: vaccinia virus I8 protein; DEAD/H box helicase homology

C:Keywords: ATP; P-loop

F:185-498/Domain: DEAD/H box helicase homology <DEAD>

F:185-192/Region: nucleotide-binding motif A (P-loop)

F:292-297/Region: nucleotide-binding motif B

F:296-299/Region: DEXH motif

Query Match 90.0%; Score 27; DB 1; Length 676;

Best Local Similarity 66.7%; Pred. No. 89;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6

|| ||

Db 553 WRTKEY 558

RESULT 10

D42511

I8R protein - vaccinia virus (strain Copenhagen)

C:Species: vaccinia virus

A:Note: host Homo sapiens (man)

C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 22-May-1998

C:Accession: D42511

R:Johnson, G.P.

submitted to GenBank, June 1990

A:Reference number: A33172

A:Accession: D42511

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-676 <JOH>

C:Superfamily: vaccinia virus I8 protein; DEAD/H box helicase homology

C:Keywords: ATP; P-loop

F:185-498/Domain: DEAD/H box helicase homology <DEAD>

F:185-192/Region: nucleotide-binding motif A (P-loop)

F:292-297/Region: nucleotide-binding motif B

F:296-299/Region: DEXH motif

Query Match 90.0%; Score 27; DB 2; Length 676;

Best Local Similarity 66.7%; Pred. No. 89;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6

```

Db 553 WRXKEY 558
|| ||
RESULT 11
F36843
ATP/GTP-binding protein K8R - variola virus
N:Alternate names: K8R protein
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C:Accession: F36843; S33077
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Description: not shown.
A:Reference number: A36859
A:Accession: F36843
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-676 <BLI>
A:Cross-references: GB:X69198; NID:q456758; PIDN:CAA49003.1; PID:g297243
A:Experimental source: strain India-1967, ssp. major, isolate Ind3
R:Shchelkunov, S.N.; Blinov, V.M.; Totmenin, A.V.; Marennikova, S.S.; Kolykhalov, A.A.;
dzaparidze, O.G.; Sandakhchiev, L.S.
Virus Res. 27, 25-35, 1993
A:Title: Nucleotide sequence analysis of variola virus HindIII M, L, I genome fragments.
A:Reference number: S33069; MUID:93190624
A:Accession: S33077
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-676 <SHC>
A:Cross-references: EMBL:X67119; NID:g62330; PIDN:CAA47562.1; PID:g62339
A:Experimental source: strain India-1967, isolate Ind3
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1992
C:Superfamily: vaccinia virus I8 protein; DEAD/H box helicase homology
C:Keywords: ATP; P-loop
F:185-498/Domain: DEAD/H box helicase homology <DEAD>
F:185-192/Region: nucleotide-binding motif A (P-loop)
F:292-297/Region: nucleotide-binding motif B
F:296-299/Region: DEXH motif

Query Match 90.0%; Score 27; DB 2; Length 676;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
|| ||
Db 553 WRXKEY 558

RESULT 12
GNX5IV
genome polyprotein - Infectious pancreatic necrosis virus (strain Jasper)
C:Species: Infectious pancreatic necrosis virus
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 31-Dec-1996
C:Accession: A23599
R:Duncan, R.; Dobos, P.
Nucleic Acids Res. 14, 5934, 1986
A:Title: The nucleotide sequence of infectious pancreatic necrosis virus (IPNV) dsRNA se
A:Reference number: A23599; MUID:86286599
A:Accession: A23599
A:Molecule type: genomic RNA
A:Residues: 1-972 <DUN>
C:Genetics:
A:Map position: segment A
C:Superfamily: birnavirus segment A genome polyprotein
C:Keywords: polyprotein
F:2-570/Product: major structural protein VP2 #status predicted <VP2>
F:571-739/Product: minor structural protein VP3 #status predicted <VP3>

Query Match 90.0%; Score 27; DB 1; Length 972;
Best Local Similarity 66.7%; Pred. No. 89;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
|| ||
Db 553 WRXKEY 558
```

```

Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
|| ||
Db 415 WRTEY 420

RESULT 13
GNXSN1
genome polyprotein - Infectious pancreatic necrosis virus (strain N1)
N:Contains: major structural protein VP2; minor structural protein VP3; nonstructural
C:Species: Infectious pancreatic necrosis virus
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: B34148
R:Havarstein, L.S.; Kalland, K.H.; Christie, K.E.; Endresen, C.
J. Gen. Virol. 71, 299-308, 1990
A:Title: Sequence of the large double-stranded RNA segment of the N1 strain of infect
A:Reference number: A34148; MUID:90171914
A:Accession: B34148
A:Molecule type: genomic RNA
A:Residues: 1-972 <HAV>
A:Cross-references: EMBL:D00701; NID:g221910; PIDN:BAA00609.1; PID:d1001066; PID:g221
A:Note: the precise cleavage sites were not determined
C:Genetics:
A:Map position: segment A
C:Superfamily: birnavirus segment A genome polyprotein
C:Keywords: polyprotein
F:2-570/Product: major structural protein VP2 #status predicted <VP2>
F:571-739/Product: nonstructural protein VP4 #status predicted <VP4>
F:740-972/Product: minor structural protein VP3 #status predicted <VP3>

Query Match 90.0%; Score 27; DB 1; Length 972;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
|| ||
Db 415 WRTEY 420

RESULT 14
T09624
genome polyprotein - Infectious pancreatic necrosis virus (strain Jasper)
C:Species: Infectious pancreatic necrosis virus
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: T09624
R:Duncan, R.; Nagy, E.; Krell, P.J.; Dobos, P.
J. Virol. 61, 3655-3664, 1987
A:Title: Synthesis of the infectious pancreatic necrosis virus
A:Reference number: Z16783; MUID:88062910
A:Accession: T09624
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-972 <DUN>
A:Cross-references: EMBL:M18049; NID:g331311; PID:g331312
C:Keywords: polyprotein

Query Match 90.0%; Score 27; DB 2; Length 972;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
|| ||
Db 415 WRTEY 420

RESULT 15
S72985
glutamate decarboxylase (EC 4.1.1.15) isozyme gadd - Mycobacterium leprae
N:Alternate names: B229_C2_202 protein
```

C:Species: Mycobacterium leprae
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Sep-1997
C:Accession: S72985
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid B229.
A:Reference number: S72580
A:Accession: S72985
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-52 <SMI>
A:Cross-references: EMBL:U00020; NID:g467102; PID:g467117
C:Genetics:
A:Gene: gadD
A:Start codon: GTG
C:Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 86.7%; Score 26; DB 2; Length 52;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 WRXXEY 6
|| ||
Db 31 WRGNEY 36

Search completed: May 2, 2000, 00:16:18
Job time: 787 sec

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Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	28	93.3	640	1	UROM_HUMAN	P07911	homo sapien
2	28	93.3	643	1	UROM_BOVIN	P48733	bos taurus
3	28	93.3	896	1	BOSS_DROME	P22815	drosophila
4	27	90.0	157	1	Y118_NPVAC	P41671	autographa
5	27	90.0	168	1	Q0X2_SULAC	P39479	sulfolobus
6	27	90.0	257	1	HNL_MANES	P53705	manihot esc
7	27	90.0	461	1	USP_MANSE	P54779	manduca sex
8	27	90.0	676	1	V108_VACCC	P20502	vaccinia vi
9	27	90.0	676	1	V108_VACCV	P12927	vaccinia vi
10	27	90.0	676	1	V108_YARV	P33051	variola vir
11	27	90.0	972	1	POLS_IPNVJ	P05844	infectious
12	27	90.0	972	1	POLS_IPNVN	P22495	infectious
13	26	86.7	118	1	YD55_SCHPO	O14181	schizosacch
14	26	86.7	301	1	SC14_KLULA	P24859	kluveromyc
15	26	86.7	351	1	DESA_SPIPL	Q54794	spirulina p
16	26	86.7	383	1	DTG_HUMAN	P01880	homo sapien
17	26	86.7	405	1	THRC_METJA	Q58860	methanococc
18	26	86.7	468	1	COG1_RABIT	P13943	oryctolagus
19	26	86.7	469	1	COG1_BOVIN	P28053	bos taurus
20	26	86.7	469	1	COG1_HUMAN	P03956	homo sapien
21	26	86.7	469	1	COG1_PIG	P21692	sus scrofa
22	26	86.7	882	1	AKLS_PSEOL	P17051	pseudomonas
23	26	86.7	893	1	BOSS_DPROVI	Q24738	drosophila
24	26	86.7	971	1	SN2L_CAEEL	P41877	caenorhabdi
25	26	86.7	976	1	SN21_HUMAN	P28370	homo sapien
26	26	86.7	1203	1	RPX2_YEAST	P22138	saccharomyc
27	26	86.7	1871	1	PLX4_HUMAN	P51805	homo sapien
28	26	86.7	2109	1	RRPL_VSVJH	P13615	vesicular s
29	26	86.7	2109	1	RRPL_VSVJO	P16379	vesicular s
30	26	86.7	2560	1	PSP2_BACSU	P39846	bacillus su
31	26	86.7	4451	1	GRSB_BACBR	P14688	b grammicidi
32	26	86.7	6486	1	TYCC_CAEEL	Q30409	b tyrocidin
33	25	83.3	296	1	YS42_CAEEL	Q09371	caenorhabdi
34	25	83.3	298	1	TRBP_XENLA	Q91836	xenopus lae

```

DR PIR: A30452; A30452.
DR HSP: P07204; LEGT.
DR MIM: 191845; -.
DR PROSITE: PS00682; ZP_DOMAIN: 1.
DR PROSITE: PS00010; ASX_HYDROXYL: 2.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 2.
DR PFAM: PF00008; EGF; 3.
DR PFAM: PF00100; zona_pellucida; 1.
KW Glycoprotein; Signal; Membrane; GPI-anchor; EGF-like domain.
FT SIGNAL 1 24
FT CHAIN 25 640 UROMODULIN.
FT DOMAIN 28 64 EGF-LIKE 1.
FT DOMAIN 65 107 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 108 149 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 334 585 ZP.
FT DISULFID 32 41 BY SIMILARITY.
FT DISULFID 35 50 BY SIMILARITY.
FT DISULFID 52 63 BY SIMILARITY.
FT DISULFID 69 83 BY SIMILARITY.
FT DISULFID 77 92 BY SIMILARITY.
FT DISULFID 94 106 BY SIMILARITY.
FT DISULFID 112 126 BY SIMILARITY.
FT DISULFID 130 135 BY SIMILARITY.
FT DISULFID 137 148 BY SIMILARITY.
FT CARBOHYD 38 38 POTENTIAL.
FT CARBOHYD 76 76 POTENTIAL.
FT CARBOHYD 80 80 POTENTIAL.
FT CARBOHYD 232 232 POTENTIAL.
FT CARBOHYD 275 275 POTENTIAL.
FT CARBOHYD 322 322 POTENTIAL.
FT CARBOHYD 396 396
FT CONFLICT 565 565 H -> D (IN REF. 2).
SQ SEQUENCE 640 AA; 69760 MW; D3F83A88 CRC32;

Query Match 93.3%; Score 28; DB 1; Length 640;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
DB 184 WRSTEY 189

RESULT 2
UROM_BOVIN
ID UROM_BOVIN STANDARD; PRT; 643 AA.
AC P48733;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE UROMODULIN PRECURSOR (TAMM-HORSFALL URINARY GLYCOPROTEIN) (THP).
GN UMOD.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RX MEDLINE; 95143938.
RA YU H., PAPA F., SUKHATME V.P.;
RT "Bovine and rodent tamm-horsfall protein (THP) genes: cloning,
RT structural analysis, and promoter identification.";
RL Gene Expr. 4:63-75(1994).
CC -!- FUNCTION: NOT KNOWN. MAY PLAY A ROLE IN REGULATING THE CIRCULATING
CC ACTIVITY OF CYTOKINES AS IT BINDS TO IL-1, IL-2 AND TNF WITH HIGH
CC AFFINITY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR,
CC THEN CLEAVED TO PRODUCE A SOLUBLE FORM WHICH IS SECRETED IN
CC URINE (BY SIMILARITY).

CC -!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 1 ZP DOMAIN.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S75958; AAB33312.1; -.
CC HSP; P35555; IENO.
DR PROSITE: PS00682; ZP_DOMAIN: 1.
DR PROSITE: PS00010; ASX_HYDROXYL: 2.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; 3.
DR PROSITE: PS01187; EGF_CA; 2.
DR PFAM: PF00008; EGF; 3.
DR PFAM: PF00100; zona_pellucida; 1.
KW Glycoprotein; Signal; Membrane; GPI-anchor; EGF-like domain.
FT SIGNAL 1 26
FT CHAIN 27 643 UROMODULIN.
FT DOMAIN 30 66 EGF-LIKE 1.
FT DOMAIN 67 109 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 110 151 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 336 587 ZP.
FT DISULFID 34 43 BY SIMILARITY.
FT DISULFID 37 52 BY SIMILARITY.
FT DISULFID 54 65 BY SIMILARITY.
FT DISULFID 71 85 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 96 108 BY SIMILARITY.
FT DISULFID 114 128 BY SIMILARITY.
FT DISULFID 122 137 BY SIMILARITY.
FT DISULFID 139 150 BY SIMILARITY.
FT CARBOHYD 40 40 POTENTIAL.
FT CARBOHYD 78 78 POTENTIAL.
FT CARBOHYD 134 134 POTENTIAL.
FT CARBOHYD 234 234 POTENTIAL.
FT CARBOHYD 277 277 POTENTIAL.
FT CARBOHYD 324 324 POTENTIAL.
FT CARBOHYD 398 398 POTENTIAL.
FT CARBOHYD 449 449 POTENTIAL.
FT CARBOHYD 515 515 POTENTIAL.
SQ SEQUENCE 643 AA; 69898 MW; C0729953 CRC32;

Query Match 93.3%; Score 28; DB 1; Length 643;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
DB 186 WRSTEY 191

RESULT 3
BOSS_DROME
ID BOSS_DROME STANDARD; PRT; 896 AA.
AC P22815;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BRIDE OF SEVENLESS PROTEIN PRECURSOR.
GN BOSS.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91115074.

```


RA HART A.C., KRAEMER H., VAN VACTOR D.L. JR., PAIDHUNGAT M.,
 RA ZIPURSKY S.L.;
 RT "Induction of cell fate in the Drosophila retina: the bride of
 RT sevenless protein is predicted to contain a large extracellular
 RT domain and seven transmembrane segments.";
 RL Genes Dev. 4:1835-1847(1990).
 [2]
 RN REVISIONS.
 RA KRAEMER H.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RN FUNCTION.
 RX MEDLINE: 91312442.
 RA KRAEMER H., CAGAN R.L., ZIPURSKY S.L.;
 RT "Interaction of bride of sevenless membrane-bound ligand and the
 RT sevenless tyrosine-kinase receptor.";
 RL Nature 352:207-212(1991).
 CC -!- FUNCTION: ACTS AS A LIGAND FOR SEVENLESS TYROSINE-KINASE RECEPTOR
 CC DURING EYE DEVELOPMENT.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY BY R8 PHOTORECEPTOR
 CC CELLS AND IS INTERNALIZED IN A SEV-DEPENDENT MANNER BY R7 CELLS.

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 DR EMBL: X55887; CAA39373.1; -
 DR PIR: A36455; A36455.
 DR FLYBASE: FBgn000206; boss.
 KW Transmembrane; Glycoprotein; Vision; Signal.
 FT SIGNAL 1 31
 FT CHAIN 32 896
 FT DOMAIN 32 530
 FT TRANSMEM 531 554
 FT TRANSMEM 570 588
 FT TRANSMEM 615 637
 FT TRANSMEM 655 676
 FT TRANSMEM 693 712
 FT TRANSMEM 728 748
 FT TRANSMEM 759 781
 FT DOMAIN 782 896
 FT CARBOHYD 183 183
 FT CARBOHYD 307 307
 FT CARBOHYD 474 474
 FT CARBOHYD 485 485
 FT SEQUENCE 896 AA; 99950 MW; 705C3CF6 CRC32;

 Query Match 93.3%; Score 28; DB 1; Length 896;
 Best Local Similarity 66.7%; Pred No. 48;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WRXKEY 6
 DB 413 WRTSEY 418

 RESULT 4
 Y118.NPVAC
 ID Y118.NPVAC STANDARD; PRT; 157 AA.
 AC P41671.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE HYPOTHETICAL 18.7 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.
 OS Autographa californica nuclear polyhedrosis virus (ACNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.

RN SEQUENCE FROM N.A.
 RP STRAIN=C6;
 RX MEDLINE: 94303173.
 RA AYRES M.D., HOWARD S.C., KUZIO J., LOPEZ-FERBER M., POSSEE R.D.;
 RT "The complete DNA sequence of Autographa californica nuclear
 RT polyhedrosis virus.";
 RL Virology 202:586-605(1994).
 CC -----
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 DR EMBL: L22858; AAA66748.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 157 AA; 18709 MW; 7FB684ED CRC32;

 Query Match 90.0%; Score 27; DB 1; Length 157;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WRXKEY 6
 DB 6 WRMSEY 11

 RESULT 5
 QOX2_SULAC
 ID QOX2_SULAC STANDARD; PRT; 168 AA.
 AC P39479;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE QUINOL OXIDASE POLYPEPTIDE II (EC 1.9.3.-) (CYTOCHROME AA3 SUBUNIT 2)
 DE (OXIDASE AA(3) SUBUNIT 2).
 GN SOXA.
 OS Sulfolobus acidocaldarius.
 OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=DSM 639;
 RX MEDLINE: 92192013.
 RA LUEBBEN M., KOLMERER B., SARASTE M.;
 RT "An archaeobacterial terminal oxidase combines core structures of two
 RT mitochondrial respiratory complexes.";
 RL EMBO J. 11:805-812(1992).
 CC -!- FUNCTION: THE TERMINAL OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CC CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNITS 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX.
 CC -!- FUNCTION: SUBUNIT 2 TRANSFERS THE ELECTRONS FROM CALDARIELLA
 CC QUINOL TO THE BINETALLIC CENTER OF THE CATALYTIC SUBUNIT 1 THAT IS
 CC FORMED BY HEME A3 AND CU(B).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -!- SIMILARITY: SOME, TO MITOCHONDRIAL OR BACTERIAL COX2 SUBUNITS.
 CC BUT LACK HEME-BINDING DOMAIN.

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 DR EMBL: X62643; CAA44509.1; -
 DR PIR: S21041; S21041.
 KW Oxidoreductase; Transmembrane; Respiratory chain; Electron transport.
 FT TRANSMEM 9 31
 FT POTENTIAL.

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SQ SEQUENCE 168 AA: 18874 MW: 19F07DD0 CRC32;
Query Match 90.0%; Score 27; DB 1; Length 168;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 WRXXEY 6
DB 147 WRDAEY 152
II II

RESULT 6
HNL_MANES
ID HNL_MANES STANDARD; PRT; 257 AA.
AC P52705;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ((S)-ACETONE-CYANOHYDRIN LYASE (EC 4.2.1.39) ((S)-HYDROXYNITRILE LYASE)
DE ((S)-HYDROXYNITRILASE).
GN HNL.
OS Manihot esculenta (Cassava) (Manioc).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Malpighiales; Euphorbiaceae;
OC Manihot.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-36 AND 168-191.
RC TISSUE=COTYLEDON;
RX MEDLINE; 9426231.
RT HUGHES J., CARVALHO F.J.P.D.C., HUGHES M.A.;
RT "Purification, characterization, and cloning of alpha-hydroxynitrile
RT lyase from cassava (Manihot esculenta Crantz).";
RL Arch. Biochem. Biophys. 311:496-502(1994).
CC -!- FUNCTION: INVOLVED IN CYANOGENESIS, THE RELEASE OF HCN FROM
CC INURED TISSUES. DECOMPOSES A VARIETIES OF (R) OR (S) CYNOHYDRINS
CC INTO HCN AND THE CORRESPONDING ALDEHYDES AND KETONES. THE NATURAL
CC SUBSTRATE OF THIS ENZYME IS (S)-ACETONE CYANOHYDRIN.
CC -!- CATALYTIC ACTIVITY: (S)-2-HYDROXYISOBUTYRONITRILE - CYANIDE +
CC ACETONE.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SIMILARITY: DISTANT RELATIONSHIP WITH TYPE-B
CC CARBOXYLSTERASE/LIPASE FAMILY.
CC -----
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CC -----
CC EMBL; Z29091; CA482334.1; -
CC DR HSSP; P52704; LYAS.
CC DR PFAM; PF00561; abhydrolase; 1.
CC KW Lyase.
CC INIT MET 0 0
CC ACT_SITE 79 79 BY SIMILARITY.
CC ACT_SITE 207 207 BY SIMILARITY.
CC ACT_SITE 235 235 BY SIMILARITY.
CC SEQUENCE 257 AA: 29240 MW: 42522403 CRC32;
Query Match 90.0%; Score 27; DB 1; Length 257;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 WRXXEY 6
DB 127 WRDTEY 132
II II

SQ SEQUENCE 168 AA: 18874 MW: 19F07DD0 CRC32;
Query Match 90.0%; Score 27; DB 1; Length 168;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 WRXXEY 6
DB 147 WRDAEY 152
II II

RESULT 7
USP_MANSE
ID USP_MANSE STANDARD; PRT; 461 AA.
AC P54779;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE ULTRASPIRACLE PROTEIN HOMOLOG.
GN USP OR NR2B4.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Spingioidea; Spingidae; Sphinginae; Manduca.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=EPIDERMIS;
RA JINDRA M., HUANG J., MALONE F., ASAHINA M., RIDDIFORD L.M.;
RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: RECEPTOR FOR ECDYSONE. MAY BE AN IMPORTANT MODULATOR OF
CC INSECT METAMORPHOSIS (BY SIMILARITY).
CC -!- SUBUNIT: HETERODIMER OF USP AND ECR. ONLY THE HETERODIMER IS
CC CAPABLE OF HIGH-AFFINITY BINDING TO ECDYSONE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN,
CC A DNA-BINDING DOMAIN AND A C-TERMINAL STEROID-BINDING DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
CC NR2 SUBFAMILY.
CC -----
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CC -----
CC EMBL; U48837; AAB64234.1; -
CC DR HSSP; P19793; 2NLL.
CC DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
CC DR PFAM; PF00104; hormone_rec; 1.
CC DR PFAM; PF00105; zf-C4; 1.
CC KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
CC Zinc-finger.
CC FT DOMAIN 1 112 MODULATING (BY SIMILARITY).
CC FT DNA_BIND 113 178 C4-TYPE ZINC FINGERS (TWO).
CC FT ZN_FING 113 133 C4-TYPE.
CC FT ZN_FING 149 173 C4-TYPE.
CC FT DOMAIN 179 192 HINGE.
CC FT DOMAIN 192 461 LIGAND-BINDING (BY SIMILARITY).
CC SEQUENCE 461 AA: 52066 MW: 87F9EF1E CRC32;
Query Match 90.0%; Score 27; DB 1; Length 461;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 WRXXEY 6
DB 294 WRSMEY 299
II II

RESULT 8
VI08_VACCC
ID VI08_VACCC STANDARD; PRT; 676 AA.
AC P20502;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE PUTATIVE RNA HELICASE I8.
GN I8R.
OS Vaccinia virus (strain Copenhagen).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.

```

RN SEQUENCE FROM N.A.
 RP MEDLINE: 91021027.
 RX GOEBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
 RA PAOLETTI E.;
 RT "The complete DNA sequence of vaccinia virus."
 RL Virology 179:247-266(1990).
 RN [2]
 RP COMPLETE GENOME.
 RA GOEBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
 RA PAOLETTI E.;
 RL Virology 179:517-563(1990).
 RN [3]
 RP SIMILARITY TO HELICASES.
 RX MEDLINE: 92341083.
 RA KOONIN E.V., SENKEVICH T.G.;
 RT "vaccinia virus encodes four putative DNA and/or RNA helicases
 RT distinctly related to each other."
 RL J. Gen. Virol. 73:989-993(1992).
 CC - SIMILARITY: TO RNA HELICASES OF THE "DEAD/DEAH" BOX FAMILY. MOST
 CC SIMILAR TO "DEAH" SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: M35027; AAA48064.1; -
 DR PIR: D42511; D42511
 DR PROSITE: PS00690; DEAH_ATP_HELICASE; 1.
 KW Late protein; ATP-binding; Helicase.
 FT NP_BIND 185 192 ATP (BY SIMILARITY).
 FT SITE 296 299 DEVH BOX.
 SQ SEQUENCE 676 AA; 77658 MW; 150C5530 CRC32;

Query Match 90.0%; Score 27; DB 1; Length 676;
 Best Local Similarity 66.7%; Pred. No. 61;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
 DB 553 WRTKEY 558

RESULT 9
 ID V108_VACCV STANDARD; PRT; 676 AA.
 AC P12927;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE PUTATIVE RNA HELICASE 18.
 GN I8R.
 OS Vaccinia virus (strain WR).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 91134989.
 RA FATHI Z., CONDIT R.C.;
 RT "Genetic and molecular biological characterization of a vaccinia
 RT virus temperature-sensitive complementation group affecting a virion
 RT component."
 RL Virology 181:258-272(1991).
 RN [2]
 RP SEQUENCE OF 1-99 FROM N.A.
 RX MEDLINE: 88215015.
 RA SCHMITT J.F.C., STUNNENBERG H.G.;
 RT "Sequence and transcriptional analysis of the vaccinia virus HindIII

RT I fragment."
 RL J. Virol. 62:1889-1897(1988).
 RN [3]
 RP SIMILARITY TO HELICASES.
 RX MEDLINE: 92341083.
 RA KOONIN E.V., SENKEVICH T.G.;
 RT "vaccinia virus encodes four putative DNA and/or RNA helicases
 RT distinctly related to each other."
 RL J. Gen. Virol. 73:989-993(1992).
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 CC -----
 DR EMBL: J03399; AAB59810.1; -
 DR PIR: B38437; WZVZ18.
 DR PROSITE: PS00690; DEAH_ATP_HELICASE; 1.
 KW Late protein; ATP-binding; Helicase.
 FT NP_BIND 185 192 ATP (BY SIMILARITY).
 FT SITE 296 299 DEVH BOX.
 SQ SEQUENCE 676 AA; 77599 MW; AE534F3B CRC32;

Query Match 90.0%; Score 27; DB 1; Length 676;
 Best Local Similarity 66.7%; Pred. No. 61;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
 DB 553 WRTKEY 558

RESULT 10
 ID V108_VARV STANDARD; PRT; 676 AA.
 AC P33051;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE PUTATIVE RNA HELICASE 18.
 GN I8R OR K8R.
 OS Variola virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-INDIA-1967 / ISOLATE IND3;
 RX MEDLINE: 94152154.
 RA SHCHELKUNOV S.N., BLINOV V.M., RESENCHUK S.M., TOTMENIN A.V.,
 RA SANDAKHCHIEV L.S.;
 RT "Analysis of the nucleotide sequence of a 43 kbp segment of the
 RT genome of variola virus India-1967 strain."
 RL Virus Res. 30:239-258(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-INDIA-1967 / ISOLATE IND3;
 RX MEDLINE: 93190624.
 RA SHCHELKUNOV S.N., BLINOV V.M., TOTMENIN A.V., MARENNIKOVA S.S.,
 RA KOLYKHALOV A.A., FROLOV I.V., CHIZHIKOV V.E., GYTOROV V.V.,
 RA GASHIKOV P.V., BELANOV E.F., BELAVIN P.A., RESENCHUK S.M.,
 RA ANDZHAPARDZE O.G., SANDAKHCHIEV L.S.;
 RT "Nucleotide sequence analysis of variola virus HindIII M, L, I genome
 RT fragments."
 RL Virus Res. 27:25-35(1993).
 RN [3]
 RP COMPLETE GENOME.
 RC STRAIN-INDIA-1967 / ISOLATE IND3;
 RA BLINOV V.M.;
 RT Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.

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DR EMBL; X671119; CAA47562.1; -
DR EMBL; X691598; CAA49003.1; -
DR PIR; F36843; F36843.
DR PIR; S33077; S33077.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
KW ATP-BINDING; Helicase.
FT NP_BIND 185 192 ATP (BY SIMILARITY).
FT SITE 296 299 DEVH BOX.
SQ SEQUENCE 676 AA; 77544 MW; 1899E1BC CRC32;

Query Match 90.0%; Score 27; DB 1; Length 676;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
DB 553 WRTKEY 558

RESULT 11
POLSI_IPNVJ STANDARD; PRT; 972 AA.
ID POLSI_IPNVJ AC P22495;
DT 01-NOV-1988 (Rel. 09, Created)
DT 15-DEC-1999 (Rel. 39, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2;
DE NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3].
OS Infectious pancreatic necrosis virus (serotype Jasper) (IPNV).
OC Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86286599.
RA DUNCAN R., DOBOS P.;
RT "The nucleotide sequence of infectious pancreatic necrosis virus
RT (IPNV) dsRNA segment A reveals one large ORF encoding a precursor
RT polyprotein."
RL Nucleic Acids Res. 14:5934-5934(1986).
RN [2]
RP SEQUENCE OF 433-972 FROM N.A., AND REVISIONS TO 566 AND 708.
RC STRAIN-JASPER;
RX MEDLINE; 88062910.
RA DUNCAN R., NAGY E., KRELL P.J., DOBOS P.;
RT "Synthesis of the infectious pancreatic necrosis virus polyprotein,
RT detection of a virus-encoded protease, and fine structure mapping of
RT genome segment A coding regions."
RL J. Virol. 61:3655-3664(1987).
CC -!- FUNCTION: SEGMENT A ENCODES A POLYPROTEIN, THAT IS PROCESSED INTO
CC THE MAJOR STRUCTURAL PROTEINS OF THE VIRION VP2 AND VP3, AND INTO
CC THE PUTATIVE PROTEASE VP4.
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DR EMBL; M18049; AAA89179.1; -
DR PIR; A23599; GNXSIV.
KW Polyprotein; Structural protein; Nonstructural protein; Hydrolase;
Protease.

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FT CHAIN 1 453 MAJOR STRUCTURAL PROTEIN VP2.
FT CHAIN 455 721 NONSTRUCTURAL PROTEIN VP4 (PROTEASE).
FT CHAIN 723 972 MINOR STRUCTURAL PROTEIN VP3.
SQ SEQUENCE 972 AA; 106665 MW; B1BB1FBA CRC32;

Query Match 90.0%; Score 27; DB 1; Length 972;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
DB 415 WRTKEY 420

RESULT 12
POLSI_IPNVN STANDARD; PRT; 972 AA.
ID POLSI_IPNVN AC P22495;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE STRUCTURAL POLYPROTEIN [CONTAINS: MAJOR STRUCTURAL PROTEIN VP2;
DE NONSTRUCTURAL PROTEIN VP4; MINOR STRUCTURAL PROTEIN VP3].
OS Infectious pancreatic necrosis virus (strain NI) (IPNV).
OC Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90171914.
RA HAVARSTEIN L.S., KALLAND K.H., CHRISTIE K.E., ENDRESEN C.;
RT "Sequence of the large double-stranded RNA segment of the NI strain
RT of infectious pancreatic necrosis virus: a comparison with other
RT Birnaviridae."
RL J. Gen. Virol. 71:299-308(1990).
CC -!- FUNCTION: SEGMENT A ENCODES A POLYPROTEIN, THAT IS PROCESSED INTO
CC THE MAJOR STRUCTURAL PROTEINS OF THE VIRION VP2 AND VP3, AND INTO
CC THE PUTATIVE PROTEASE VP4.
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-----
DR EMBL; D00701; BAA00609.1; -
DR PIR; B34148; GNXSNI.
KW Polyprotein; Structural protein; Nonstructural protein; Hydrolase;
KW Protease.
FT CHAIN 1 453 MAJOR STRUCTURAL PROTEIN VP2.
FT CHAIN 455 721 NONSTRUCTURAL PROTEIN VP4 (PROTEASE).
FT CHAIN 723 972 MINOR STRUCTURAL PROTEIN VP3.
SQ SEQUENCE 972 AA; 106669 MW; AF982053 CRC32;

Query Match 90.0%; Score 27; DB 1; Length 972;
Best Local Similarity 66.7%; Pred. No. 87;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
DB 415 WRTKEY 420

RESULT 13
YDS5_SCHPO STANDARD; PRT; 118 AA.
ID YDS5_SCHPO AC O14181;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PUTATIVE 60S RIBOSOMAL PROTEIN C4F8.05C.

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GN SPAC4F8.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA GENTILES S., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YDR462W.
CC
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CC
CC EMBL: 298530; CAB11052.1; -.
KW Hypothetical protein; Ribosomal protein; Mitochondrion.
SQ SEQUENCE 118 AA; 13793 MW; 584D6B941 CRC32;

Query Match 86.7%; Score 26; DB 1; Length 118;
Best Local Similarity 66.7%; Pred. No. 18;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
DB 53 WRKEY 58

RESULT 14
ID SC14_KLULA STANDARD; PRT; 301 AA.
AC P24859;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSITOL/PHOSPHATIDYLCHOLINE
DE TRANSFER PROTEIN) (PI/PC TP).
GN SEC14.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Kluyveromyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90330560.
RA SALAMA S.R., CLEVES A.E., MALEHORN D.E., WHITTERS E.A.,
RA BANKAITIS V.A.;
RT "Cloning and characterization of Kluyveromyces lactis SEC14, a gene
RT whose product stimulates Golgi secretory function in Saccharomyces
RT cerevisiae";
RL J. Bacteriol. 172:4510-4521(1990).
CC -!- FUNCTION: REQUIRED FOR TRANSPORT OF SECRETORY PROTEINS FROM THE
CC GOLGI COMPLEX. CATALYZES THE TRANSFER OF PHOSPHATIDYLINOSITOL AND
CC PHOSPHATIDYLCHOLINE BETWEEN MEMBRANES IN VITRO (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: ASSOCIATED WITH THE GOLGI COMPLEX AS A
CC PERIPHERAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SEC14 CYTOSOLIC FACTOR FAMILY.
DR PIR; A37766; A37766.
DR HSSP; P24280; 1AUA.
DR PFAM; PF00650; CRAL_TRIO; 1.
KW Transport; Protein transport; Golgi stack.
SQ SEQUENCE 301 AA; 34529 MW; B0223578 CRC32;

Query Match 86.7%; Score 26; DB 1; Length 301;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
DB 283 WRKEY 288

RESULT 15
ID DESA_SPIPL STANDARD; PRT; 351 AA.
AC Q54794;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE FATTY ACID DESATURASE (EC 1.14.99.-) (DELTA 12 DESATURASE).
GN DESA.
OS Spirulina platensis.
OC Bacteria; Cyanobacteria; Oscillatoriales; Spirulina.
RN [1]
RP SEQUENCE FROM N.A.
RA MURATA N., DESHNITUM P., TASAKA Y.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CAN INTRODUCE A SECOND CIS DOUBLE BOND AT THE DELTA 12
CC POSITION OF FATTY ACID BOUND TO MEMBRANE GLYCEROLIPIDS. THIS
CC ENZYME IS INVOLVED IN CHILLING TOLERANCE BECAUSE THE PHASE
CC TRANSITION TEMPERATURE OF LIPIDS OF CELLULAR MEMBRANES DEPENDS ON
CC THE DEGREE OF UNSATURATION OF FATTY ACIDS OF THE MEMBRANE LIPIDS.
CC -!- SIMILARITY: TO PLANT'S STEAROYL-ACP DESATURASE.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X86736; CAA60415.1; -.
DR PROSITE; PS00574; FATTY_ACID_DESATUR_2; FALSE_NEG.
DR PFAM; PF00487; FA_desaturase; 1.
KW Oxidoreductase; Fatty acid biosynthesis; Membrane.
FT DOMAIN 89 93 HISTIDINE BOX 1.
FT DOMAIN 125 129 HISTIDINE BOX 2.
FT DOMAIN 286 290 HISTIDINE BOX 3.
SQ SEQUENCE 351 AA; 40928 MW; F6E718C1 CRC32;

Query Match 86.7%; Score 26; DB 1; Length 351;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXKEY 6
DB 144 WRKEY 149

Search completed: May 2, 2000, 00:17:46
Job time: 179 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:14:12 ; Search time 39.35 Seconds
(without alignments)
10.572 Million cell updates/sec

Title: US-09-258-947-174
Perfect score: 30
Sequence: 1 WRXXEY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_l2.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	93.3	520	2 O87814	O87814 alcaligenes
2	28	93.3	642	11 O62285	O62285 mus musculus
3	28	93.3	917	5 Q24265	Q24265 drosophila
4	28	93.3	2236	12 Q9WJ28	Q9WJ28 porcine ent
5	27	90.0	274	2 O87974	O87974 bordetella
6	27	90.0	354	3 O14347	O14347 schizosacch
7	27	90.0	387	1 Q9YCD0	Q9YCD0 aeropyrum p
8	27	90.0	472	5 O76202	O76202 choristoneu
9	27	90.0	539	12 O82746	O82746 infectious
10	27	90.0	556	12 O82743	O82743 infectious
11	27	90.0	562	12 O93076	O93076 marine birn
12	27	90.0	567	3 O94381	O94381 schizosacch
13	27	90.0	584	12 O89208	O89208 variola vir
14	27	90.0	676	12 O57193	O57193 vaccinia vi
15	27	90.0	676	12 O85378	O85378 variola vir
16	27	90.0	972	12 P90205	P90205 infectious
17	27	90.0	972	12 O55651	O55651 yellowtail
18	27	90.0	972	12 P89521	P89521 birnavirus
19	27	90.0	972	12 O82731	O82731 infectious
20	27	90.0	972	12 Q9YJV0	Q9YJV0 infectious

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21 27 90.0 972 12 Q9WLE3
22 27 90.0 4545 2 Q9X4W2
23 26 86.7 31 2 P94213
24 26 86.7 52 2 Q49863
25 26 86.7 192 12 Q80234
26 26 86.7 192 12 Q80235
27 26 86.7 192 12 Q89670
28 26 86.7 251 5 Q20156
29 26 86.7 330 11 Q9WV75
30 26 86.7 367 10 Q9XEG0
31 26 86.7 403 1 Q9YBE2
32 26 86.7 429 3 O13897
33 26 86.7 469 6 Q9XZ25
34 26 86.7 488 5 Q97286
35 26 86.7 538 3 Q9Y700
36 26 86.7 576 3 Q9Y7S4
37 26 86.7 577 3 O59699
38 26 86.7 580 3 O59698
39 26 86.7 862 4 O95985
40 26 86.7 862 11 Q9Z321
41 26 86.7 986 2 Q50357
42 26 86.7 986 2 Q30380
43 26 86.7 1052 4 O60264
44 26 86.7 1234 3 O74633
45 26 86.7 1234 5 O77285

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ALIGNMENTS

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RESULT 1
O87814 ID O87814 PRELIMINARY; PRT; 520 AA.
AC O87814;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE NAD-DEPENDENT FORMATE DEHYDROGENASE BETA SUBUNIT (EC 1.2.1.2).
GN FDSB.
OS Alkaligenes eutrophus.
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Ralstonia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H16;
RX MEDLINE; 98434537.
RA OH J.I., BOWEN B.;
RT "Structural analysis of the fds operon encoding the NAD+-linked
formate dehydrogenase of Ralstonia eutropha.";
RL J. Biol. Chem. 273:26349-26360(1998).
DR EMBL; AJ223295; CAIL1234.1; -.
DR PROSITE; PS00644; COMPLEX1_51K_1; 1.
DR PROSITE; PS00645; COMPLEX1_51K_2; 1.
DR PFAM; PF01512; Complex1_51K; 1.
KW Oxidoreductase.
SQ SEQUENCE 520 AA; 55158 MW; 701AA664 CRC32;

```

Query Match 93.3%; Score 28; DB 2; Length 520;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 WRXXEY 6
    || ||
Db 322 WRAAEY 327

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RESULT 2
Q62285 ID Q62285 PRELIMINARY; PRT; 642 AA.
AC Q62285;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

```

DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE UROMODULIN.

GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE; 95178555.

RA PRASADAN K., BATES J., BADGETT A., DELL M., SUKHATWE V., YU H.,
RA KUMAR S.;

"Nucleotide sequence and peptide motifs of mouse uromodulin (Tamm-
Horsfall protein)--the most abundant protein in mammalian urine.";

RT Biochim. Biophys. Acta 1260:328-332(1995).
RL EMBL; L33406; AAA73896.1; -.

DR HSSP; P35555; IEMO.
DR MGD; MGI:102674; Umod.

DR PROSITE; PS01187; EGF_CA; 2.
DR PROSITE; PS00010; ASX_HYDROXYL; 2.

DR PROSITE; PS00682; ZP_DOMAIN; 1.
DR PFAM; PF00008; EGF; 3.

DR PFAM; PF00100; zona_pellucida; 1.
DR PRINTS; PR00023; ZPELLUCIDA.

KW Glycoprotein; EGF-like domain.
SQ SEQUENCE 642 AA; 70839 MW; FA022F8D CRC32;

Query Match 93.3%; Score 28; DB 11; Length 642;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6

DB 185 WRSTY 190

RESULT 3

Q24265 ID Q24265 PRELIMINARY; PRT; 917 AA.

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)

DE BRIDE OF SEVENLESS PROTEIN.
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE; 93281693.

RA HART A.C., HARRISON S.D., VAN VACTOR D.L. JR., RUBIN G.M.,
RA ZIPURSKY S.L.;

"The interaction of bride of sevenless with sevenless is conserved
between Drosophila virilis and Drosophila melanogaster.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:5047-5051(1993).
DR EMBL; L08133; AAA21141.1; -.

DR FLYBASE; FBgn0000206; Boss.
SQ SEQUENCE 917 AA; 102439 MW; BA2CD34F CRC32;

Query Match 93.3%; Score 28; DB 5; Length 917;

Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6

DB 434 WRTSEY 439

RESULT 4

Q9WJ28 ID Q9WJ28 PRELIMINARY; PRT; 2236 AA.

AC Q9WJ28;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE POLYPROTEIN.
OS porcine enterovirus 1.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-F65;
RA DOHERTY M., TODD D., MCFERRAN N., HOEY E.M.;

"Sequence analysis of a porcine enterovirus serotype 1 isolate;
relationships with other members of the family Picornaviridae.";

RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ011380; CAB40546.1; -.

KW Polyprotein.
FT CHAIN 1 118 L PROTEIN.

FT CHAIN 119 192 VP4 PROTEIN.
FT CHAIN 193 471 VP2 PROTEIN.

FT CHAIN 472 713 VP3 PROTEIN.
FT CHAIN 714 975 VP1 PROTEIN.

FT CHAIN 976 996 2A PROTEIN.
FT CHAIN 997 1142 2B PROTEIN.

FT CHAIN 1143 1463 2C PROTEIN.
FT CHAIN 1464 1554 3A PROTEIN.

FT CHAIN 1555 1579 3B PROTEIN.
FT CHAIN 1580 1784 3C PROTEIN.

FT CHAIN 1785 2236 3D PROTEIN.
SQ SEQUENCE 2236 AA; 250486 MW; 7BEF6057 CRC32;

Query Match 93.3%; Score 28; DB 12; Length 2236;

Best Local Similarity 66.7%; Pred. No. 5.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6

DB 1175 WRTAEY 1180

RESULT 5

O87974 ID O87974 PRELIMINARY; PRT; 274 AA.

AC O87974;

DT 01-NOV-1998 (TReMBLrel. 08, Created)

DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)

DE PUTATIVE FORMYL TRANSFERASE (FRAGMENT).
GN BBLPS1.01.

OS Bordetella bronchiseptica.
OC Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;

OC Bordetella.
RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CN7635E;
RA STEVENS K., CHURCHER C.M., BADCOCK K.L.;

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-CN7635E;
RA PARKHILL J., PRESTON A., MASKELL D.J., BARRELL B.G.;

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ007747; CAA07640.1; -.

DR PFAM; PF00551; formyl_transf; 1.
KW Transferase.

FT NON_TER 1 1
FT NON_TER 274 274

SQ SEQUENCE 274 AA; 29113 MW; A2CEFD68 CRC32;

Query Match 90.0%; Score 27; DB 2; Length 274;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
Db 211 WRAGEY 216

RESULT 6
O14347 PRELIMINARY; PRT; 354 AA.
AC O14347;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PUTATIVE ZUOTIN-LIKE PROTEIN C30D10.01 (FRAGMENT).
GN SPBC30D10.01.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA WOOD V., RAJANDREAM M.A., BARRELL B.G., LAUBER J., HILBERT H.,
RA DUESTERHOEF A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: 2-DNA BINDING PROTEIN. COULD BE INVOLVED IN CHROMOSOME
CC ORGANIZATION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS A DNAJ-LIKE DOMAIN.
DR EMBL; 297992; CAB10796.1; -;
DR HSP; P25685; 1HDJ.
DR PROSITE; PS00636; DNAJ_1; 1.
DR PFAM; PF00226; DnaJ; 1.
KW Hypothetical protein; Chaperone; DNA-binding; Nuclear protein.
FT NON_TER 1 81 DNAJ-LIKE.
FT DOMAIN 217 267 ALA/LYS-RICH.
FT DOMAIN 217 267
SQ SEQUENCE 354 AA; 40290 MW; 465F92F6 CRC32;

Query Match 90.0%; Score 27; DB 3; Length 354;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
Db 141 WRSFEY 146

RESULT 7
Q9YCD0 PRELIMINARY; PRT; 387 AA.
AC Q9YCD0;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE 387AA LONG HYPOTHETICAL PROTEIN.
GN APE1326.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Aeropyrum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE; 99310339.
RA KAWARABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,
RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
RA HOSYOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,
RA TAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,
RA YAMAZAKI J., KUSHIDA N., OGUCHI N., AOKI K., KUBOTA K., NAKAMURA Y.,
RA NOMURA N., SAKO Y., KIKUCHI H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix K1.";

RL DNA Res. 6:83-101(1999).
DR EMBL; AF000061; BAA80318.1; -; BD575803 CRC32;
SQ SEQUENCE 387 AA; 42809 MW;

Query Match 90.0%; Score 27; DB 1; Length 387;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
Db 122 WRAIEY 127

RESULT 8
O76202 PRELIMINARY; PRT; 472 AA.
AC O76202;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE ULTRASPIRACLE.
GN ULTRASPIRACLE.
OS Choristoneura fumiferana (Spruce budworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricidae; Tortricidae; Tortricinae; Choristoneura.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98242389.
RA PERERA S.C., PALLI S.R., LADD T.R., KRELL P.J., RETNAKARAN A.;
RT "The ultraspiracle gene of the spruce budworm, Choristoneura
fumiferana: cloning of cDNA and developmental expression of mRNA.";
RL Dev. Genet. 22:169-179(1998).
CC -1- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
DR EMBL; AF016368; AAC31795.1; -;
DR HSP; P19793; 2NULL.
DR PROSITE; PS00031; NUCLEAR_RECEPTOR; 1.
DR PFAM; PF00104; hormone_rec; 1.
DR PFAM; PF00105; zf-C4; 1.
DR PRINTS; PR00047; STROIDFINGER.
KW Receptor; Transcription regulation; DNA-binding; Nuclear protein;
KW Zinc-finger.
SQ SEQUENCE 472 AA; 53138 MW; 8ED7D18 CRC32;

Query Match 90.0%; Score 27; DB 5; Length 472;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
Db 303 WRSMEY 308

RESULT 9
Q82746 PRELIMINARY; PRT; 539 AA.
AC Q82746;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS Infectious pancreatic necrosis virus.
OC Viruses; dsRNA viruses; Birnaviridae; Aquabirnavirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LWRT 60-1 (VR-299);
RX MEDLINE; 93331748.
RA HEPPPELL J., BERTHAUME L., CORBIN F., TARRAB E., LECOMTE J.,
RA ARELLA M.;
RT "Comparison of amino acid sequences deduced from a cDNA fragment
obtained from infectious pancreatic necrosis virus (IPNV) strains of

```

RT different serotypes.";
RL Virology 195:840-844(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LWRT 60-1 (VR-299);
RX MEDLINE; 95363432.
RA HEPPPELL J., TARRAB E., BERTHAUME L., LECOMTE J., ARELLA M.;
RT "Characterization of the small open reading frame on genome segment A
of infectious pancreatic necrosis virus.";
RL J. Gen. Virol. 76:2091-2096(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=LWRT 60-1 (VR-299);
RX MEDLINE; 96095222.
RA HEPPPELL J., TARRAB E., LECOMTE J., BERTHAUME L., ARELLA M.;
RT "Strain variability and localization of important epitopes on the
major structural protein (VP2) of infectious pancreatic necrosis
virus.";
RL Virology 214:40-49(1995).
DR EMBL; L40584; AAA92631.1; -.
KW Polyprotein.
FT NON_TER 539 539
SQ SEQUENCE 539 AA; 59056 MW; 5CA2FA25 CRC32;

Query Match 90.0%; Score 27; DB 12; Length 539;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
   || ||
DB 415 WRTEY 420

RESULT 10
Q82743 PRELIMINARY; PRT; 556 AA.
AC Q82743;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS Infectious pancreatic necrosis virus.
OC Viruses; GSRNA viruses; Birnaviridae; Aquabirnavirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D'HONNINCTHUN (FR.21);
RX MEDLINE; 93331748.
RA HEPPPELL J., BERTHAUME L., CORBIN F., TARRAB E., LECOMTE J.,
ARELLA M.;
RT "Comparison of amino acid sequences deduced from a cDNA fragment
obtained from infectious pancreatic necrosis virus (IPNV) strains of
different serotypes.";
RL Virology 195:840-844(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D'HONNINCTHUN (FR.21);
RX MEDLINE; 95363432.
RA HEPPPELL J., TARRAB E., BERTHAUME L., LECOMTE J., ARELLA M.;
RT "Characterization of the small open reading frame on genome segment A
of infectious pancreatic necrosis virus.";
RL J. Gen. Virol. 76:2091-2096(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=D'HONNINCTHUN (FR.21);
RX MEDLINE; 96095222.
RA HEPPPELL J., TARRAB E., LECOMTE J., BERTHAUME L., ARELLA M.;
RT "Strain variability and localization of important epitopes on the
major structural protein (VP2) of infectious pancreatic necrosis
virus.";
RL Virology 214:40-49(1995).
DR EMBL; L40582; AAA92628.1; -.
KW Polyprotein.

FT NON_TER 556 556
SQ SEQUENCE 556 AA; 60950 MW; D31BF7A7 CRC32;

Query Match 90.0%; Score 27; DB 12; Length 556;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
   || ||
DB 432 WRTEY 437

RESULT 11
Q93076 PRELIMINARY; PRT; 562 AA.
AC Q93076; Q96646;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TRENBLrel. 10, Last annotation update)
DE POLYPROTEIN (FRAGMENT).
OS marine birnavirus.
OC Viruses; dsRNA viruses; Birnaviridae; Birnavirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y-6;
RA SUZUKI S., KIMURA M., KUSUDA R.;
RT "The complete nucleotide sequence of the polyprotein and VP5 gene of a
marine birnavirus.";
RL Fisheries Sci. 64:428-433(1998).
DR EMBL; D87826; BAA31999.1; -.
KW Polyprotein.
FT NON_TER 562 562
SQ SEQUENCE 562 AA; 61564 MW; 094F4474 CRC32;

Query Match 90.0%; Score 27; DB 12; Length 562;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
   || ||
DB 415 WRTEY 420

RESULT 12
Q94381 PRELIMINARY; PRT; 567 AA.
AC Q94381;
DT 01-MAY-1999 (TRENBLrel. 10, Created)
DT 01-MAY-1999 (TRENBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TRENBLrel. 12, Last annotation update)
DE PUTATIVE SINGLE-STRAND POLYNUCLEOTIDE BINDING PROTEIN.
GN SPBC29A10.02 OR SPBC365.18.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA LYNE M., RAJANDREAM M.A., BARRELL B.G., LELAURE V., GALIBERT F.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA WOOD V., RAJANDREAM M.A., BARRELL B.G., LELAURE V., GALIBERT F.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL034463; CAA22430.1; -.
DR EMBL; AL078627; CAB44770.1; -.
SQ SEQUENCE 567 AA; 62945 MW; 4844657B CRC32;

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Query Match 90.0%; Score 27; DB 3; Length 567;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 478 WRAREY 483

RESULT 13
Q89208 PRELIMINARY; PRT; 584 AA.
ID Q89208;
AC Q89208;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE ORFIR (FRAGMENT).
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GARCIA-1966;
RA SHCHELKUNOV S.N., SOSNOVTSYEV S.V., TOTMENIN A.V., RESENCHUK S.M.,
RA BLINOV V.M., SANDAKHCHIEV L.S.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: X76267; CAAS3387.1; -.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
FT NON_TER 1
SQ SEQUENCE 584 AA; 66922 MW; E9D53C1E CRC32;

Query Match 90.0%; Score 27; DB 12; Length 584;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 455 WRTKEY 460

RESULT 14
Q57193 PRELIMINARY; PRT; 676 AA.
ID Q57193;
AC Q57193;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE NPH-II, HELICASE.
GN MVA069R.
OS Vaccinia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ANKARA.
RA ANTOINE G., SCHEIFLINGER F., FALKNER F.G., DORNER F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U94848; AAB96491.1; -.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
KW Helicase.
SQ SEQUENCE 676 AA; 77600 MW; 0673B4EF CRC32;

Query Match 90.0%; Score 27; DB 12; Length 676;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 553 WRTKEY 558

RESULT 15
Q85378 PRELIMINARY; PRT; 676 AA.
ID Q85378;
AC Q85378;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE HOMOLOG OF VACCINIA VIRUS CDS I8R.
GN K8R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BANGLADESH-1975;
RX MEDLINE; 94088747.
RA MASSUNG R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R.,
RA KNIGHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome."
RL Nature 366:748-751(1993).
DR EMBL: L22579; AAA60810.1; -.
DR PROSITE; PS00690; DEAH_ATP_HELICASE; 1.
SQ SEQUENCE 676 AA; 77574 MW; EDC73E91 CRC32;

Query Match 90.0%; Score 27; DB 12; Length 676;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 553 WRTKEY 558

Search completed: May 2, 2000, 00:17:10
Job time: 178 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:15:22 ; Search time 14.38 seconds
(without alignments)
9.883 Million cell updates/sec

Title: US-09-258-947-174

Perfect score: 30

Sequence: 1 WRXXEY 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 91374

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	27	90.0	10	1 W32627	Human platelet gly
2	27	90.0	10	1 W32628	Human platelet gly
3	27	90.0	10	1 W71754	Mimotope capable o
4	27	90.0	10	1 W71755	Mimotope capable o
5	26	86.7	9	1 W15299	Human platelet gly
6	26	86.7	9	1 W71758	Mimotope capable o
7	26	86.7	10	1 W32626	Human platelet gly
8	26	86.7	10	1 W32629	Human platelet gly
9	26	86.7	10	1 W32624	Human platelet gly
10	26	86.7	10	1 W71752	Mimotope capable o
11	26	86.7	10	1 W71753	Mimotope capable o
12	26	86.7	10	1 W71756	Mimotope capable o
13	25	83.3	10	1 W32631	Human platelet gly
14	25	83.3	10	1 W71757	Mimotope capable o
15	24	80.0	16	1 R57946	Randomly generated
16	22	73.3	10	1 W32625	Human platelet gly
17	22	73.3	10	1 W71759	Mimotope capable o
18	22	73.3	17	1 R51413	Branched peptide C
19	22	73.3	17	1 R51414	Branched peptide C
20	21	70.0	8	1 W94115	VIF-derived HIV pr
21	21	70.0	10	1 W32773	Human platelet gly
22	21	70.0	11	1 P71045	Sequence of peptid
23	21	70.0	11	1 W94114	VIF-derived HIV pr
24	21	70.0	15	1 P90269	Antigenic peptide
25	21	70.0	15	1 W94120	VIF-derived HIV pr
26	21	70.0	20	1 R37689	Synthetic epitope
27	20	66.7	15	1 R38556	Sequence of peptid
28	20	66.7	17	1 R51420	Branched peptide C
29	20	66.7	17	1 W16192	Peptide containing
30	20	66.7	17	1 W58318	IL-1Rt1 binding pe
31	20	66.7	17	1 W68831	Peptide binding in
32	20	66.7	17	1 Y09964	Interleukin-1 type
33	20	66.7	18	1 R47074	Peptide 18A derive
34	20	66.7	18	1 R47075	Peptide 18A derive

35	20	66.7	20	1 W66353	Peptide derived fr
36	20	66.7	20	1 W66354	Peptide derived fr
37	20	66.7	20	1 W66357	Peptide MCF05 deri
38	20	66.7	20	1 W66358	Peptide MCF04 deri
39	19	63.3	8	1 R72201	Hepatitis C Virus
40	19	63.3	8	1 R72202	Hepatitis C Virus
41	19	63.3	8	1 R72203	Hepatitis C Virus
42	19	63.3	9	1 R82877	Human tumor reject
43	19	63.3	9	1 R82878	Human tumor reject
44	19	63.3	9	1 W22082	Tyrosine-derived t
45	19	63.3	9	1 W22089	Tyrosine-derived p
46	19	63.3	9	1 W22091	Tyrosine-derived p
47	19	63.3	9	1 W23045	Tyrosinase peptide
48	19	63.3	9	1 W23044	Tyrosinase peptide
49	19	63.3	9	1 W35515	Tyrosinase protein
50	19	63.3	9	1 W54595	Peptide 5 from tyr
51	19	63.3	9	1 W68379	Human tyrosinase p
52	19	63.3	9	1 W78847	Tyrosinase protein
53	19	63.3	9	1 Y00700	Tumour antigen boo
54	19	63.3	9	1 Y00698	Tumour antigen boo
55	19	63.3	9	1 Y10610	Peptide antigen SE
56	19	63.3	9	1 Y10609	Peptide antigen SE
57	19	63.3	9	1 Y01746	Exemplary antigeni
58	19	63.3	9	1 Y01747	Exemplary antigeni
59	19	63.3	10	1 R79499	Human tumor reject
60	19	63.3	10	1 W21508	HIV, SIV, REV prot
61	19	63.3	10	1 W21509	HIV, SIV, REV prot
62	19	63.3	10	1 W22089	Tyrosine-derived p
63	19	63.3	10	1 Y10608	Peptide antigen SE
64	19	63.3	11	1 W62114	Human MDM2 binding
65	19	63.3	12	1 W61266	BCL1 immunogloblin
66	19	63.3	13	1 R57072	Fasciola hepatica
67	19	63.3	13	1 R71320	Synthetic peptide
68	19	63.3	13	1 R79498	Human tumor reject
69	19	63.3	13	1 W22088	Tyrosine-derived p
70	19	63.3	15	1 R06302	Peptide derived fr
71	19	63.3	15	1 R72156	Hepatitis C Virus
72	19	63.3	15	1 W07991	gpi30 peptide 115
73	19	63.3	15	1 W12279	Synthetic library
74	19	63.3	15	1 W76906	Fusion immunoglob
75	19	63.3	15	1 W76905	Fusion immunoglob
76	19	63.3	16	1 W63064	Human Immunodefici
77	19	63.3	16	1 W68328	MHC binding peptid
78	19	63.3	17	1 R51405	Branched peptide C
79	19	63.3	17	1 R51406	Branched peptide C
80	19	63.3	17	1 R51421	Branched peptide C
81	19	63.3	18	1 R54760	5-HT-1A receptor S
82	19	63.3	18	1 R57842	VnRbeta3-4, bindin
83	19	63.3	19	1 P90815	Non-immunogenic am
84	19	63.3	20	1 R12286	Parvovirus B19 epi
85	19	63.3	20	1 R41190	HCV NS5 protein NS
86	19	63.3	20	1 R41191	HCV NS5 protein NS
87	19	63.3	20	1 R41192	HCV NS5 protein NS
88	19	63.3	20	1 R89347	Cdk2-interacting p
89	19	63.3	20	1 W08050	HIV peptide #35. D
90	19	63.3	20	1 W08051	HIV peptide #36. D
91	19	63.3	20	1 W10148	Hepatitis C virus
92	19	63.3	20	1 W10149	Hepatitis C virus
93	19	63.3	20	1 W23875	HIV-1 strain MN pe
94	19	63.3	20	1 W23876	HIV-1 strain MN pe
95	19	63.3	20	1 W32122	Interaction trap s
96	19	63.3	20	1 W76874	Fusion immunoglob
97	19	63.3	20	1 W76877	Fusion immunoglob
98	18	60.0	6	1 R88698	Allergen Alt a 12
99	18	60.0	9	1 W32485	Strept-tag peptide
100	18	60.0	9	1 W44010	Strept-tag peptide
101	18	60.0	9	1 W59211	Streptavidin tagge
102	18	60.0	9	1 Y06914	Strept-tag sequence
103	18	60.0	10	1 R66446	Streptavidin bindi
104	18	60.0	10	1 R58563	Peptide with high
105	18	60.0	10	1 W32736	Human platelet gly
106	18	60.0	10	1 W50025	Peptide tag for st
107	18	60.0	10	1 Y10273	r cell epitope/MHC

108	18	11	1	1	R52691	PASK46-pl11H encod	181	16	53.3	4	1	W22904	Low density lipopr
109	18	11	1	1	R52693	PASK46-pl1XH encod	182	16	53.3	4	1	W26145	Lactoferrin deriva
110	18	12	1	1	R52696	PASK46-pl11L encod	183	16	53.3	4	1	W15565	20K-cellulase tryp
111	18	12	1	1	R52697	PASK46-pl1XL encod	184	16	53.3	4	1	W19334	Kappa-selective op
112	18	12	1	1	R58561	Peptide with high	185	16	53.3	4	1	W40207	Kappa-selective op
113	18	12	1	1	R81821	Streptavidin bindi	186	16	53.3	4	1	W31938	Kappa-selective op
114	18	12	1	1	R77414	Extension peptide	187	16	53.3	4	1	W31928	Kappa-selective op
115	18	13	1	1	P90243	Antigenic peptide	188	16	53.3	4	1	W31941	Kappa-selective op
116	18	15	1	1	R45658	Human progesterone	189	16	53.3	4	1	W41281	Apoptosis inducer
117	18	16	1	1	R62174	Escherichia coli P	190	16	53.3	4	1	W53216	Lactoferrin hydrol
118	18	18	1	1	R43471	Ro/SSA epitope 330	191	16	53.3	4	1	W53771	Immunisation motif
119	18	18	1	1	R57844	VnRbeta3-8, bindin	192	16	53.3	4	1	W11194	Peptide used in an
120	18	18	1	1	R58559	Peptide with high	193	16	53.3	4	1	W70307	Thrombus formation
121	18	20	1	1	W07921	gp41 peptide 57. D	194	16	53.3	4	1	W99061	Peptide SEQ ID NO:
122	18	20	1	1	W42151	T-cell epitope pep	195	16	53.3	4	1	Y03965	Hepatitis A virus
123	18	20	1	1	W42152	T-cell epitope pep	196	16	53.3	5	1	P71644	Diuretic peptide d
124	17	6	1	1	P30170	Sequence of a cycl	197	16	53.3	5	1	P40591	Somatostatin antag
125	17	6	1	1	W15938	Cyclo(trp-Lys-Orn-	198	16	53.3	5	1	R31350	Antimicrobial pept
126	17	7	1	1	W40895	Leader sequence 14	199	16	53.3	5	1	R42571	Peptide correspond
127	17	8	1	1	R58842	Somatostatin analo	200	16	53.3	5	1	R86330	HIV-1 protease inh
128	17	9	1	1	W40896	Leader sequence 15	201	16	53.3	5	1	W12507	Interleukin-6 anta
129	17	10	1	1	R58557	Peptide with high	202	16	53.3	5	1	W12486	Interleukin-6 anta
130	17	10	1	1	R58562	Peptide with high	203	16	53.3	5	1	W21061	Lipolytic enzyme o
131	17	10	1	1	W32632	Human platelet gly	204	16	53.3	5	1	W21060	Lipolytic enzyme o
132	17	10	1	1	W71761	Mimotope capable o	205	16	53.3	5	1	W22933	Low density lipopr
133	17	12	1	1	R58560	Peptide with high	206	16	53.3	5	1	W20098	Low density lipopr
134	17	12	1	1	W41350	Paecilomyces lilac	207	16	53.3	5	1	W22906	Low density lipopr
135	17	15	1	1	R76371	Bacterial permeabi	208	16	53.3	5	1	W10087	Low density lipopr
136	17	15	1	1	R81212	Anti-fungal BPI pe	209	16	53.3	5	1	W23183	Terminal peptide e
137	17	15	1	1	R87786	BPI.136, BPI domal	210	16	53.3	5	1	W32184	Terminal peptide e
138	17	15	1	1	R81043	BPI protein segmen	211	16	53.3	5	1	W87102	Peptide determined
139	17	15	1	1	R78045	Recombinant BPI pe	212	16	53.3	5	1	W87103	Peptide determined
140	17	15	1	1	W05981	Bactericidal/perme	213	16	53.3	5	1	W87104	Peptide determined
141	17	15	1	1	W63662	Human BPI protein	214	16	53.3	5	1	W87105	Peptide determined
142	17	15	1	1	W63432	Randomly generated	215	16	53.3	5	1	W87106	Peptide determined
143	17	16	1	1	R57931	Mouse anti-human I	216	16	53.3	5	1	W87101	BC loop sequence o
144	17	16	1	1	R77213	Human acetylcholin	217	16	53.3	5	1	W89188	BC loop sequence o
145	17	16	1	1	W12212	Antimicrobial tach	218	16	53.3	5	1	W94148	BC loop sequence o
146	17	17	1	1	R75822	Peptide with high	219	16	53.3	5	1	W94151	BC loop sequence o
147	17	18	1	1	R58558	Glucosyl transfera	220	16	53.3	5	1	W94156	BC loop sequence o
148	17	19	1	1	R20250	A. niger glucosyltr	221	16	53.3	5	1	W94157	BC loop sequence o
149	17	19	1	1	R52018	A. hippocastanum a	222	16	53.3	5	1	W94160	BC loop sequence o
150	17	19	1	1	W19331	Acetylcholin recep	223	16	53.3	5	1	W94144	FG loop sequence o
151	17	20	1	1	W63102	Peptide derived fr	224	16	53.3	5	1	W94177	FG loop sequence o
152	17	20	1	1	R41476	Acetylcholin recep	225	16	53.3	6	1	P61337	Sequence of novel
153	17	20	1	1	W63104	Lactoferrin deriva	226	16	53.3	6	1	P50074	Cyclic peptide wit
154	16	3	1	1	R48523	Bovine lactoferrin	227	16	53.3	6	1	P50103	Cyclic peptide wit
155	16	3	1	1	R84691	Lactoferrin deriva	228	16	53.3	6	1	R20447	Anti-b-endorphin m
156	16	3	1	1	R90601	Peptide for anti-u	229	16	53.3	6	1	R25023	Arg-Arg contg. ant
157	16	3	1	1	R98547	Apoptosis inducer	230	16	53.3	6	1	R25022	Arg-Arg contg. ant
158	16	3	1	1	W41282	Anti-inflammatory	231	16	53.3	6	1	R25028	Arg-Arg contg. ant
159	16	3	1	1	W56219	Motif useful in to	232	16	53.3	6	1	R24508	Antimicrobial olig
160	16	4	1	1	P91630	Melanocyte-stimula	233	16	53.3	6	1	R25000	Arg-Arg contg. ant
161	16	4	1	1	R07103	Antimicrobial pept	234	16	53.3	6	1	R25001	Arg-Arg contg. ant
162	16	4	1	1	R27863	Lactoferrin deriva	235	16	53.3	6	1	R25002	Arg-Arg contg. ant
163	16	4	1	1	R48522	Lactoferrin deriva	236	16	53.3	6	1	R25003	Arg-Arg contg. ant
164	16	4	1	1	R57453	Lactoferrin deriva	237	16	53.3	6	1	R25004	Arg-Arg contg. ant
165	16	4	1	1	R71564	Hepatitis B virus	238	16	53.3	6	1	R25005	Exemplary N-termin
166	16	4	1	1	R79760	Anti-parasitic lac	239	16	53.3	6	1	R30577	Anaphylatoxin anta
167	16	4	1	1	R80463	Artificial male st	240	16	53.3	6	1	R31352	Antimicrobial pept
168	16	4	1	1	R75601	gp120 binding Fab	241	16	53.3	6	1	R31353	Antimicrobial pept
169	16	4	1	1	R75603	HIV principal neut	242	16	53.3	6	1	R31354	Antimicrobial pept
170	16	4	1	1	R93665	C5a C-terminal pep	243	16	53.3	6	1	R29339	Endothelin antagon
171	16	4	1	1	R89743	Class I MHC antige	244	16	53.3	6	1	R39709	Peptide fragment o
172	16	4	1	1	R83083	Bovine lactoferrin	245	16	53.3	6	1	R44175	Snake venom thromb
173	16	4	1	1	R84690	Lactoferrin deriva	246	16	53.3	6	1	R24572	Peptide correspond
174	16	4	1	1	R90600	Lactoferrin deriva	247	16	53.3	6	1	R69132	Endothelin C-termi
175	16	4	1	1	R87614	Lactoferrin-deriva	248	16	53.3	6	1	R66836	Hexapeptide having
176	16	4	1	1	R91847	Lactoferrin-deriva	249	16	53.3	6	1	R83545	Zif268 zinc finger
177	16	4	1	1	R98546	Peptide for anti-u	250	16	53.3	6	1	R89737	C5a peptide analog
178	16	4	1	1	W11946	Dimeric peptide. D	251	16	53.3	6	1	R89492	CryIF class toxin
179	16	4	1	1	W14031	Anti-parasitic pep	252	16	53.3	6	1	R90503	Hybridoma ATCC HB-
180	16	4	1	1	W10094	Low density lipopr	253	16	53.3	6	1	R88547	Varicella zoster g

254	16	53.3	6	1	W05105	C-terminally amide	327	16	53.3	7	1	R25013	C-terminal residue
255	16	53.3	6	1	W03683	Branched chain pol	328	16	53.3	7	1	R25014	C-terminal residue
256	16	53.3	6	1	W03260	Viral integrase in	329	16	53.3	7	1	R25015	C-terminal residue
257	16	53.3	6	1	W09304	Plant acyl-ACP thi	330	16	53.3	7	1	R25016	C-terminal residue
258	16	53.3	6	1	W00917	Acyl-ACP thioester	331	16	53.3	7	1	R25017	C-terminal residue
259	16	53.3	6	1	W21059	Lipolytic enzyme o	332	16	53.3	7	1	R25018	C-terminal residue
260	16	53.3	6	1	W21056	Lipolytic enzyme o	333	16	53.3	7	1	R25019	C-terminal residue
261	16	53.3	6	1	W21070	Lipolytic enzyme o	334	16	53.3	7	1	R25020	C-terminal residue
262	16	53.3	6	1	W24328	New peptide which	335	16	53.3	7	1	R25021	C-terminal residue
263	16	53.3	6	1	R93756	New peptide which	336	16	53.3	7	1	R25022	C-terminal residue
264	16	53.3	6	1	W23182	Terminal peptide e	337	16	53.3	7	1	R25023	Bradykinin antag
265	16	53.3	6	1	W23193	Terminal peptide e	338	16	53.3	7	1	R25024	Mouse NGF peptide
266	16	53.3	6	1	W23179	Terminal peptide e	339	16	53.3	7	1	R25025	Conserved hNAT and
267	16	53.3	6	1	W16566	20K-cellulase try	340	16	53.3	7	1	R25026	Human glycoprotein
268	16	53.3	6	1	W28898	Opioid peptide. Ne	341	16	53.3	7	1	R25027	Protein kinase sub
269	16	53.3	6	1	W30937	Birch pollen aller	342	16	53.3	7	1	R25028	Protein kinase sub
270	16	53.3	6	1	W28967	Opioid peptide. Ne	343	16	53.3	7	1	R25029	Protein kinase sub
271	16	53.3	6	1	W33132	Calmodulin inhibit	344	16	53.3	7	1	R25030	Generic antimicrob
272	16	53.3	6	1	W33133	Calmodulin inhibit	345	16	53.3	7	1	R25031	Mugwort pollen all
273	16	53.3	6	1	W33134	Calmodulin inhibit	346	16	53.3	7	1	R25032	Mugwort pollen all
274	16	53.3	6	1	W33135	Calmodulin inhibit	347	16	53.3	7	1	R25033	Aged band 3 peptid
275	16	53.3	6	1	W33136	Calmodulin inhibit	348	16	53.3	7	1	R25034	Hepatitis C virus
276	16	53.3	6	1	W33137	Calmodulin inhibit	349	16	53.3	7	1	R25035	Human ninjurin pep
277	16	53.3	6	1	W33138	Calmodulin inhibit	350	16	53.3	7	1	R25036	HIV-1 Rev protein
278	16	53.3	6	1	W33139	Calmodulin inhibit	351	16	53.3	7	1	R25037	Tumour homing pept
279	16	53.3	6	1	W33164	Calmodulin inhibit	352	16	53.3	7	1	R25038	Tumour homing pept
280	16	53.3	6	1	W33165	Calmodulin inhibit	353	16	53.3	7	1	R25039	Tumour homing pept
281	16	53.3	6	1	W33166	Calmodulin inhibit	354	16	53.3	7	1	R25040	Carcinoma-associat
282	16	53.3	6	1	W33167	Calmodulin inhibit	355	16	53.3	7	1	R25041	Bactolysin - antim
283	16	53.3	6	1	W33168	Calmodulin inhibit	356	16	53.3	7	1	R25042	Peptide containing
284	16	53.3	6	1	W33169	Calmodulin inhibit	357	16	53.3	7	1	R25043	Cecropin-melittin
285	16	53.3	6	1	W33170	Calmodulin inhibit	358	16	53.3	7	1	R25044	FG loop sequence o
286	16	53.3	6	1	W33171	Calmodulin inhibit	359	16	53.3	7	1	R25045	Peptide used to pr
287	16	53.3	6	1	W24503	Humicollised fluore	360	16	53.3	7	1	R25046	Peptide used to pr
288	16	53.3	6	1	W44268	Cell adhesion inhi	361	16	53.3	7	1	R25047	Human breast cance
289	16	53.3	6	1	W45861	Protein tyrosine p	362	16	53.3	7	1	R25048	Human breast cance
290	16	53.3	6	1	W43021	ENOS binding pepti	363	16	53.3	7	1	R25049	Human breast cance
291	16	53.3	6	1	W40395	Peptide derivative	364	16	53.3	7	1	R25050	Neurokinin A pepti
292	16	53.3	6	1	W50755	Peptide derivative	365	16	53.3	7	1	R25051	Hepatitis C virus
293	16	53.3	6	1	W50756	Peptide derivative	366	16	53.3	7	1	R25052	Hepatitis C virus
294	16	53.3	6	1	W50757	Peptide derivative	367	16	53.3	7	1	R25053	Hepatitis C virus
295	16	53.3	6	1	W48583	Integrin receptor	368	16	53.3	7	1	R25054	Hepatitis C virus
296	16	53.3	6	1	W62477	Antibiotic peptide	369	16	53.3	7	1	R25055	Hepatitis C virus
297	16	53.3	6	1	W66070	Peptide useful as	370	16	53.3	7	1	R25056	Hepatitis C virus
298	16	53.3	6	1	W66582	Peptide component	371	16	53.3	7	1	R25057	Hepatitis C virus
299	16	53.3	6	1	W66588	Peptide component	372	16	53.3	7	1	R25058	Hepatitis C virus
300	16	53.3	6	1	W79200	Conserved region o	373	16	53.3	7	1	R25059	Hepatitis C virus
301	16	53.3	6	1	W83752	Peptide specific a	374	16	53.3	7	1	R25060	Hepatitis C virus
302	16	53.3	6	1	W83740	Peptide specific a	375	16	53.3	7	1	R25061	Hepatitis C virus
303	16	53.3	6	1	W52726	Peptide inhibitor	376	16	53.3	7	1	R25062	Hepatitis C virus
304	16	53.3	6	1	W52727	Peptide inhibitor	377	16	53.3	7	1	R25063	Noggin conserved p
305	16	53.3	6	1	W52728	Peptide inhibitor	378	16	53.3	7	1	R25064	Noggin conserved p
306	16	53.3	6	1	W52729	Peptide inhibitor	379	16	53.3	7	1	R25065	Hepatitis C virus
307	16	53.3	6	1	W52730	Peptide inhibitor	380	16	53.3	7	1	R25066	Hepatitis C virus
308	16	53.3	6	1	W52731	Peptide inhibitor	381	16	53.3	7	1	R25067	Hepatitis C virus
309	16	53.3	6	1	W52732	Peptide inhibitor	382	16	53.3	7	1	R25068	CTOP mu-opioid rec
310	16	53.3	6	1	W52733	Peptide inhibitor	383	16	53.3	7	1	R25069	CTAP mu-opioid rec
311	16	53.3	6	1	W84444	HIV-1 nucleic acid	384	16	53.3	7	1	R25070	Corresp. to human
312	16	53.3	6	1	Y02019	Peptide used to pr	385	16	53.3	7	1	R25071	Conserved region o
313	16	53.3	6	1	W98152	Acyl ACP thioester	386	16	53.3	7	1	R25072	2if268 mutagenised
314	16	53.3	6	1	P80650	Transforming growt	387	16	53.3	7	1	R25073	Lipolytic enzyme o
315	16	53.3	6	1	R08138	Neurokinin A pepti	388	16	53.3	7	1	R25074	Lipolytic enzyme o
316	16	53.3	7	1	R08141	Neurokinin A pepti	389	16	53.3	7	1	R25075	Lipolytic enzyme o
317	16	53.3	7	1	R21674	Cyclic Neurokinin	390	16	53.3	7	1	R25076	Terminal peptide e
318	16	53.3	7	1	R25025	Arg-Arg contg. ant	391	16	53.3	7	1	R25077	Terminal peptide e
319	16	53.3	7	1	R25026	Arg-Arg contg. ant	392	16	53.3	7	1	R25078	Terminal peptide e
320	16	53.3	7	1	R25006	N-terminal residue	393	16	53.3	7	1	R25079	Protein kinase C r
321	16	53.3	7	1	R25007	N-terminal residue	394	16	53.3	7	1	R25080	Protein kinase C r
322	16	53.3	7	1	R25008	N-terminal residue	395	16	53.3	7	1	R25081	Kidney homing pept
323	16	53.3	7	1	R25009	N-terminal residue	396	16	53.3	7	1	R25082	Neurexophilin recep
324	16	53.3	7	1	R25010	N-terminal residue	397	16	53.3	7	1	R25083	Somatostatin analo
325	16	53.3	7	1	R25011	N-terminal residue	398	16	53.3	7	1	R25084	Molecular mimetic
326	16	53.3	7	1	R25012	N-terminal residue	399	16	53.3	7	1	R25085	Molecular mimetic

400	16	53.3	8	1	W53177	Amino terminal seq	473	16	53.3	10	1	R06348	Antigenic peptide
401	16	53.3	8	1	W5829	Mouse mast cell pr	474	16	53.3	10	1	P70520	Antigenic oligopep
402	16	53.3	8	1	W63546	Beta (1 -> 4)-N-ac	475	16	53.3	10	1	R11842	Example of peptide
403	16	53.3	8	1	W84388	Finger 3 binding s	476	16	53.3	10	1	R11846	Example of peptide
404	16	53.3	8	1	W94113	VIF-derived HIV pr	477	16	53.3	10	1	P61443	Luteinising hormon
405	16	53.3	8	1	W32144	Human cytochrome P	478	16	53.3	10	1	P61448	Luteinising hormon
406	16	53.3	8	1	W93241	Human cytochrome P	479	16	53.3	10	1	R49057	Infectious pancrea
407	16	53.3	8	1	W03899	Predicted binding	480	16	53.3	10	1	R49440	HLA-A2 position 10
408	16	53.3	8	1	W96284	Conserved sequence	481	16	53.3	10	1	R57073	Fasciola hepatica
409	16	53.3	9	1	P80622	Peptide to induce	482	16	53.3	10	1	R77850	ID-Ala 28, D-Trp 3
410	16	53.3	9	1	P81298	Peptide to induce	483	16	53.3	10	1	R69771	Thrombospondin pep
411	16	53.3	9	1	R42573	Peptide correspond	484	16	53.3	10	1	R90155	Cys-Bounded LBP-(9
412	16	53.3	9	1	R1689	HLA-A2.1 algorith	485	16	53.3	10	1	R21151	Melanoma-specific
413	16	53.3	9	1	R77851	Des-Asn 29 (D-trp	486	16	53.3	10	1	R93550	Random 10-mer pept
414	16	53.3	9	1	R80017	Cytotoxic Epstein-	487	16	53.3	10	1	R87711	Peptide #10 in nov
415	16	53.3	9	1	R84804	Modified MART-1 me	488	16	53.3	10	1	R92566	VLA-4 binding pept
416	16	53.3	9	1	R84898	Epstein-Barr virus	489	16	53.3	10	1	R92567	VLA-4 binding pept
417	16	53.3	9	1	R90707	T cell epitope mot	490	16	53.3	10	1	R88340	Varicella zoster g
418	16	53.3	9	1	R90706	T cell epitope mot	491	16	53.3	10	1	W04661	Bradykinin antagon
419	16	53.3	9	1	W05103	N-terminally acyla	492	16	53.3	10	1	W09560	Thrombopoietin rec
420	16	53.3	9	1	W05104	N-terminally acety	493	16	53.3	10	1	W19397	Tissue factor pept
421	16	53.3	9	1	W03684	Branched chain pol	494	16	53.3	10	1	W10089	Low density lipopr
422	16	53.3	9	1	W10405	Antiphospholipid a	495	16	53.3	10	1	W10802	Polyclonal anti-HB
423	16	53.3	9	1	W08112	Collagen extracell	496	16	53.3	10	1	W12881	Antimicrobial cati
424	16	53.3	9	1	W30806	Tyrosinase related	497	16	53.3	10	1	W24171	Peanut allergen Ar
425	16	53.3	9	1	W49655	Human leucocyte an	498	16	53.3	10	1	W24172	Human platelet gly
426	16	53.3	9	1	W49656	Human leucocyte an	499	16	53.3	10	1	W32767	Human platelet gly
427	16	53.3	9	1	W49659	Human leucocyte an	500	16	53.3	10	1	W32770	Human platelet gly
428	16	53.3	9	1	W49640	Human leucocyte an	501	16	53.3	10	1	W32780	Human platelet gly
429	16	53.3	9	1	W49641	Human leucocyte an	502	16	53.3	10	1	W32755	Human platelet gly
430	16	53.3	9	1	W49635	Human leucocyte an	503	16	53.3	10	1	W32761	Human platelet gly
431	16	53.3	9	1	W49610	Human leucocyte an	504	16	53.3	10	1	W32762	Human platelet gly
432	16	53.3	9	1	W49611	Human leucocyte an	505	16	53.3	10	1	W32763	Human platelet gly
433	16	53.3	9	1	W49578	Human leucocyte an	506	16	53.3	10	1	W32630	Human platelet gly
434	16	53.3	9	1	W49584	Human leucocyte an	507	16	53.3	10	1	W32833	Human platelet gly
435	16	53.3	9	1	W49587	Human leucocyte an	508	16	53.3	10	1	W32834	Human platelet gly
436	16	53.3	9	1	W49541	Human leucocyte an	509	16	53.3	10	1	W32735	Human platelet gly
437	16	53.3	9	1	W49532	Human leucocyte an	510	16	53.3	10	1	W32749	Human platelet gly
438	16	53.3	9	1	W49533	Human leucocyte an	511	16	53.3	10	1	W32729	Human platelet gly
439	16	53.3	9	1	W49536	Human leucocyte an	512	16	53.3	10	1	W32730	Human platelet gly
440	16	53.3	9	1	W49538	Human leucocyte an	513	16	53.3	10	1	W32732	Human platelet gly
441	16	53.3	9	1	W49539	Human leucocyte an	514	16	53.3	10	1	W32703	Human platelet gly
442	16	53.3	9	1	W49509	Human leucocyte an	515	16	53.3	10	1	W32709	Human platelet gly
443	16	53.3	9	1	W49510	Human leucocyte an	516	16	53.3	10	1	W32712	Human platelet gly
444	16	53.3	9	1	W49521	Human leucocyte an	517	16	53.3	10	1	W17922	Human platelet gly
445	16	53.3	9	1	W49470	Human leucocyte an	518	16	53.3	10	1	W09933	Peptide from clone
446	16	53.3	9	1	W49471	Human leucocyte an	519	16	53.3	10	1	W09941	Peptide from clone
447	16	53.3	9	1	W49321	Human leucocyte an	520	16	53.3	10	1	W36711	Thrombopoietin rec
448	16	53.3	9	1	W49239	Human leucocyte an	521	16	53.3	10	1	R49107	Sequence of peptid
449	16	53.3	9	1	W49406	Human leucocyte an	522	16	53.3	10	1	W22691	BSW17 peptide mime
450	16	53.3	9	1	W49405	Human leucocyte an	523	16	53.3	10	1	W41879	Peptide used in ra
451	16	53.3	9	1	W45672	MAGE-2 66 peptide	524	16	53.3	10	1	W57502	Molecular mimetic
452	16	53.3	9	1	W40872	Cytotoxic Epstein-	525	16	53.3	10	1	W57563	Molecular mimetic
453	16	53.3	9	1	W40874	Cytotoxic Epstein-	526	16	53.3	10	1	W60207	Peptide NFF3, a su
454	16	53.3	9	1	W40854	Cytotoxic Epstein-	527	16	53.3	10	1	W71162	Peptide used in an
455	16	53.3	9	1	W40828	Cytotoxic Epstein-	528	16	53.3	10	1	W70022	Melanoma-associate
456	16	53.3	9	1	W48276	Cytotoxic Epstein-	529	16	53.3	10	1	W71178	Peptide used in an
457	16	53.3	9	1	W52487	Cyclic peptide of	530	16	53.3	10	1	W71760	Mimotope capable o
458	16	53.3	9	1	W50230	Tumour-related sug	531	16	53.3	10	1	W71762	Mimotope capable o
459	16	53.3	9	1	W59479	HIV-1 Rev protein	532	16	53.3	10	1	W71763	Mimotope capable o
460	16	53.3	9	1	W54657	Peptide from EBNA	533	16	53.3	10	1	W66381	Indolicidin analog
461	16	53.3	9	1	W67130	Antibody ACA-6501	534	16	53.3	10	1	W66367	Indolicidin analog
462	16	53.3	9	1	W72461	Dengue virus type-	535	16	53.3	10	1	W82819	Cytomodulating lip
463	16	53.3	9	1	W72466	Dengue virus type-	536	16	53.3	10	1	W81137	Collagen-binding d
464	16	53.3	9	1	W66382	Indolicidin analog	537	16	53.3	10	1	W97258	Cytotoxic T-cell e
465	16	53.3	9	1	W66369	Indolicidin analog	538	16	53.3	10	1	Y10312	T cell epitope/MHC
466	16	53.3	9	1	W84202	Peptide comprising	539	16	53.3	10	1	Y02061	Peptide used to pr
467	16	53.3	9	1	W97290	Cytotoxic T-cell e	540	16	53.3	10	1	Y02065	HLA binding peptid
468	16	53.3	9	1	Y10127	T cell epitope/MHC	541	16	53.3	10	1	Y07164	HLA binding peptid
469	16	53.3	9	1	Y10124	T cell epitope/MHC	542	16	53.3	11	1	P93501	Peptide isolated f
470	16	53.3	9	1	Y01010	Bacterial immunoge	543	16	53.3	11	1	P82047	"Peptide 2" consis
471	16	53.3	10	1	P81576	LHRH analogue no.	544	16	53.3	11	1	R14569	Blood platelet agg
472	16	53.3	10	1	P83019	Example of gonadol	545	16	53.3	11	1		

546	16	53.3	11	1	R14573	Blood platelet agg	619	16	53.3	12	1	R78803	HIV RT residues 67
547	16	53.3	11	1	R26038	Oligopeptide P24-3	620	16	53.3	12	1	R78458	Indolicidin analog
548	16	53.3	11	1	R26330	Murine GM-CSF P24-	621	16	53.3	12	1	R83387	Kbml-binding random
549	16	53.3	11	1	R31357	Antimicrobial pep	622	16	53.3	12	1	R83323	Kb-binding random
550	16	53.3	11	1	R31358	Antimicrobial pep	623	16	53.3	12	1	R83336	Anti-ELAM-1 bindin
551	16	53.3	11	1	R27769	BSA-binding disulp	624	16	53.3	12	1	R86227	Anti-ELAM-1 bindin
552	16	53.3	11	1	R44843	Lactoferrin-relate	625	16	53.3	12	1	R86030	Anti-ELAM-1 bindin
553	16	53.3	11	1	R55114	Peptide P240 from	626	16	53.3	12	1	R86111	Anti-ELAM-1 bindin
554	16	53.3	11	1	R48537	Lactoferrin derive	627	16	53.3	12	1	R90316	IL-8 epitope 8-13.
555	16	53.3	11	1	R49825	Gnt-III peptide fr	628	16	53.3	12	1	R90354	Macrophage-colony
556	16	53.3	11	1	R57464	Lactoferrin derive	629	16	53.3	12	1	R90711	Active peptide #2
557	16	53.3	11	1	R67123	Factor VIII derive	630	16	53.3	12	1	R91456	D32.39 monoclonal
558	16	53.3	11	1	R68912	Factor-VII-derive	631	16	53.3	12	1	W05075	Proline-rich SH3 b
559	16	53.3	11	1	R67865	Factor-VII multi-prot	632	16	53.3	12	1	W12734	Alpha-conotoxin pe
560	16	53.3	11	1	R70293	Subpeptide 7N1 of	633	16	53.3	12	1	W07879	(D)-Src SH3 domain
561	16	53.3	11	1	R74040	Lysozyme peptide H	634	16	53.3	12	1	W07880	(D)-Src SH3 domain
562	16	53.3	11	1	R80266	Anti-parasitic lac	635	16	53.3	12	1	W16172	Peptide containing
563	16	53.3	11	1	R84701	Bovine lactoferrin	636	16	53.3	12	1	W16060	Peptide containing
564	16	53.3	11	1	R84084	Bovine lactoferrin	637	16	53.3	12	1	W15983	Interleukin-1 type
565	16	53.3	11	1	R87611	Lactoferrin-derive	638	16	53.3	12	1	W09447	Alpha-conotoxin pe
566	16	53.3	11	1	R88135	Listeriolysin O ha	639	16	53.3	12	1	W24006	Hepatitis C virus
567	16	53.3	11	1	R91854	Lactoferrin-derive	640	16	53.3	12	1	W24879	Predatory cone sna
568	16	53.3	11	1	R95754	Alpha-4Beta-1 inte	641	16	53.3	12	1	W25320	Peptide clone Laci
569	16	53.3	11	1	W08485	Hen-Egg Lysozyme p	642	16	53.3	12	1	W25238	Antibody D32.39 ep
570	16	53.3	11	1	W14038	Anti-parasitic pep	643	16	53.3	12	1	W26927	ELAM-1 binding pep
571	16	53.3	11	1	W15581	Platelet aggregati	644	16	53.3	12	1	W26850	ELAM-1 binding pep
572	16	53.3	11	1	W15577	Platelet aggregati	645	16	53.3	12	1	W12877	Antimicrobial cati
573	16	53.3	11	1	W21471	Collagenase (fibro	646	16	53.3	12	1	W12890	Antimicrobial cati
574	16	53.3	11	1	W16113	Peptide containing	647	16	53.3	12	1	W32659	Human platelet gly
575	16	53.3	11	1	W26152	Lactoferrin deriva	648	16	53.3	12	1	W32673	Human platelet gly
576	16	53.3	11	1	W13805	Antimicrobial cati	649	16	53.3	12	1	W32650	Human platelet gly
577	16	53.3	11	1	W38765	Delivery peptide u	650	16	53.3	12	1	W32657	Human platelet gly
578	16	53.3	11	1	W41292	Apoptosis inducer	651	16	53.3	12	1	W32693	Human platelet gly
579	16	53.3	11	1	W49731	Human leucocyte an	652	16	53.3	12	1	W32694	Human platelet gly
580	16	53.3	11	1	W52456	Antigenic peptide	653	16	53.3	12	1	W32695	Human platelet gly
581	16	53.3	11	1	W52457	Cyclic peptide of	654	16	53.3	12	1	W32697	Human platelet gly
582	16	53.3	11	1	W52457	Cyclic peptide of	655	16	53.3	12	1	W32697	Human platelet gly
583	16	53.3	11	1	W52459	Cyclic peptide of	656	16	53.3	12	1	W32697	Human platelet gly
584	16	53.3	11	1	W52462	Cyclic peptide of	657	16	53.3	12	1	W32697	Human platelet gly
585	16	53.3	11	1	W53227	Cyclic peptide of	658	16	53.3	12	1	W32694	Human platelet gly
586	16	53.3	11	1	W40396	ENOS binding pep	659	16	53.3	12	1	W49568	Human leucocyte an
587	16	53.3	11	1	W58240	IL-1RTI binding pe	660	16	53.3	12	1	W49569	Human leucocyte an
588	16	53.3	11	1	W62129	Haemophilus influe	661	16	53.3	12	1	W49570	Human leucocyte an
589	16	53.3	11	1	W62089	Human cytomagalovi	662	16	53.3	12	1	W58097	Peptide SEQ ID NO:
590	16	53.3	11	1	W63098	VHD derived peptid	663	16	53.3	12	1	W58177	IL-1RTI binding pe
591	16	53.3	11	1	W68753	Peptide binding in	664	16	53.3	12	1	W58299	IL-1RTI binding pe
592	16	53.3	11	1	W70312	Thrombus formation	665	16	53.3	12	1	W57902	Conotoxin peptide
593	16	53.3	11	1	Y09884	Interleukin-1 type	666	16	53.3	12	1	W62128	Haemophilus influe
594	16	53.3	11	1	Y02853	Fragment of human	667	16	53.3	12	1	W68812	Peptide binding in
595	16	53.3	12	1	R05950	Somatic immunoglob	668	16	53.3	12	1	W68698	Peptide binding in
596	16	53.3	12	1	R12501	Peptide II which b	669	16	53.3	12	1	W68622	Random peptide seq
597	16	53.3	12	1	R35240	D32.39 antibody is	670	16	53.3	12	1	W64046	ELAM-1 peptide mim
598	16	53.3	12	1	R49075	Infectious pancrea	671	16	53.3	12	1	W63921	ELAM-1 peptide mim
599	16	53.3	12	1	R49085	Infectious pancrea	672	16	53.3	12	1	W63854	ELAM-1 peptide mim
600	16	53.3	12	1	R56708	Random peptide #24	673	16	53.3	12	1	W71803	Mimotope capable o
601	16	53.3	12	1	R72141	Endothelium leukoc	674	16	53.3	12	1	W71823	Mimotope capable o
602	16	53.3	12	1	R63302	Peptide fragment o	675	16	53.3	12	1	W71824	Mimotope capable o
603	16	53.3	12	1	R75272	A-lineage conotoxin	676	16	53.3	12	1	W71825	Mimotope capable o
604	16	53.3	12	1	R76049	Netrin peptide p78	677	16	53.3	12	1	W71828	Mimotope capable o
605	16	53.3	12	1	R80712	CXC intercrine fam	678	16	53.3	12	1	W71787	Mimotope capable o
606	16	53.3	12	1	R78819	HIV RT mutant Gly7	679	16	53.3	12	1	W71789	Mimotope capable o
607	16	53.3	12	1	R78821	HIV RT mutant Leu7	680	16	53.3	12	1	W71780	Mimotope capable o
608	16	53.3	12	1	R78815	HIV RT mutant Ile6	681	16	53.3	12	1	W66380	Cationic peptide o
609	16	53.3	12	1	R78817	HIV RT mutant Arg7	682	16	53.3	12	1	W66364	Indolicidin analog
610	16	53.3	12	1	R78818	HIV RT mutant Val7	683	16	53.3	12	1	W66361	Indolicidin analog
611	16	53.3	12	1	R78808	HIV RT mutant Ile7	684	16	53.3	12	1	W94413	Cancer protease-se
612	16	53.3	12	1	R78809	HIV RT mutant Leu7	685	16	53.3	12	1	W94439	Mutant proproctin
613	16	53.3	12	1	R78810	HIV RT mutant'Asn7	686	16	53.3	12	1	Y09945	Interleukin-1 type
614	16	53.3	12	1	R78811	HIV RT mutant Thr6	687	16	53.3	12	1	W94812	Peptide tested for
615	16	53.3	12	1	R78805	HIV RT mutant Tyr7	688	16	53.3	12	1	Y09823	Interleukin-1 type
616	16	53.3	12	1	R78806	HIV RT mutant Gly6	689	16	53.3	12	1	Y09745	Interleukin-1 type
617	16	53.3	12	1	R78807	HIV RT mutant Asn6	690	16	53.3	12	1	W82913	Antipathogenic pep
618	16	53.3	12	1	R78804	HIV RT mutant Gly7	691	16	53.3	12	1	Y02066	Peptide used to pr

692	16	53.3	12	1	Y02062	Peptide used to pr	765	16	53.3	14	1	W30166	Peptide library #3
693	16	53.3	13	1	P81289	Atrial natriuretic	766	16	53.3	14	1	W30169	Interleukin-5 rece
694	16	53.3	13	1	R30370	Broad spectrum ant	767	16	53.3	14	1	W30172	Interleukin-5 rece
695	16	53.3	13	1	R49295	Pseudo HLA-A2 posi	768	16	53.3	14	1	W34421	Fixed library #1 f
696	16	53.3	13	1	R49499	Pseudo HLA-A2 posi	769	16	53.3	14	1	W34427	IL-5 receptor bind
697	16	53.3	13	1	R49500	Pseudo HLA-A2 posi	770	16	53.3	14	1	W34430	IL-5 receptor bind
698	16	53.3	13	1	R71639	Chimeric influenza	771	16	53.3	14	1	W35985	Fixed-sliding libr
699	16	53.3	13	1	R78459	Indolicidin analog	772	16	53.3	14	1	W38038	WW domain binding
700	16	53.3	13	1	R78454	Indolicidin analog	773	16	53.3	14	1	W46652	Biorecognition pep
701	16	53.3	13	1	R78457	Indolicidin analog	774	16	53.3	14	1	W46891	Cyclic peptide wit
702	16	53.3	13	1	R86122	Anti-ELAM-1 bindin	775	16	53.3	14	1	W52538	Cyclic peptide of
703	16	53.3	13	1	W14817	myc oncogene prote	776	16	53.3	14	1	W63082	Human immunodefici
704	16	53.3	13	1	W24442	Nucleic acid (NA)	777	16	53.3	14	1	W63939	ELAM-1 peptide mim
705	16	53.3	13	1	W26064	M28 derivative of	778	16	53.3	14	1	W68346	MHC binding peptid
706	16	53.3	13	1	W26824	ELAM-1 binding pep	779	16	53.3	14	1	W68366	Indolicidin analog
707	16	53.3	13	1	W12873	Antimicrobial cati	780	16	53.3	14	1	W66362	Indolicidin analog
708	16	53.3	13	1	W13807	Antimicrobial cati	781	16	53.3	14	1	W89590	Sequence ID #650 f
709	16	53.3	13	1	W12892	Antimicrobial cati	782	16	53.3	14	1	W89714	Interleukin 5 rece
710	16	53.3	13	1	W12893	Antimicrobial cati	783	16	53.3	14	1	W85699	Interleukin 5 rece
711	16	53.3	13	1	W12895	Antimicrobial cati	784	16	53.3	14	1	Y00964	CRCA-1 protein seq
712	16	53.3	13	1	W12896	Antimicrobial cati	785	16	53.3	15	1	P90211	Antigenic peptide
713	16	53.3	13	1	W12897	Antimicrobial cati	786	16	53.3	15	1	R03179	Receptor fragment
714	16	53.3	13	1	W36395	Antimicrobial prot	787	16	53.3	15	1	P70354	Sequence of new bo
715	16	53.3	13	1	W29516	Immobilised fluore	788	16	53.3	15	1	P60676	HTIV III peptide f
716	16	53.3	13	1	W38112	Dystrophin WW doma	789	16	53.3	15	1	P40385	Sequence of synthe
717	16	53.3	13	1	W63932	ELAM-1 peptide mim	790	16	53.3	15	1	R03898	HIV-antibody react
718	16	53.3	13	1	W66441	Cationic peptide 1	791	16	53.3	15	1	R39541	Calmodulin inhibit
719	16	53.3	13	1	W66365	Indolicidin analog	792	16	53.3	15	1	R39544	Calmodulin inhibit
720	16	53.3	13	1	W66370	Indolicidin analog	793	16	53.3	15	1	R47669	HIV epitope #2. Ne
721	16	53.3	13	1	W66371	Indolicidin analog	794	16	53.3	15	1	R47672	HIV epitope #5. Ne
722	16	53.3	13	1	W66375	Cationic peptide o	795	16	53.3	15	1	R47677	HIV epitope #10. N
723	16	53.3	13	1	W66377	Cationic peptide o	796	16	53.3	15	1	R47686	HIV epitope #19. N
724	16	53.3	13	1	W66378	Cationic peptide o	797	16	53.3	15	1	R47695	HIV epitope #28. N
725	16	53.3	13	1	W66379	Cationic peptide o	798	16	53.3	15	1	R47720	HIV epitope #53. N
726	16	53.3	13	1	W71690	Cationic peptide M	799	16	53.3	15	1	R47778	HIV epitope #111.
727	16	53.3	13	1	W89715	Interleukin 5 rece	800	16	53.3	15	1	R47788	HIV epitope #121.
728	16	53.3	13	1	W89698	Interleukin 5 rece	801	16	53.3	15	1	R49292	Pseudo HLA-A2 posi
729	16	53.3	13	1	W87609	Antimicrobial pept	802	16	53.3	15	1	R53053	Human cathepsin-G
730	16	53.3	14	1	P91877	Peptide sequence o	803	16	53.3	15	1	R63711	BPI derived peptid
731	16	53.3	14	1	P61314	trp Promoter leade	804	16	53.3	15	1	R65053	Random biotinylati
732	16	53.3	14	1	P70883	Sequence encoded b	805	16	53.3	15	1	R65058	Random biotinylati
733	16	53.3	14	1	R10183	Glucosylase/proch	806	16	53.3	15	1	R65064	Random biotinylati
734	16	53.3	14	1	P61005	Discodermine bacte	807	16	53.3	15	1	R76454	Bacterial permeabi
735	16	53.3	14	1	P61006	Discodermine bacte	808	16	53.3	15	1	R76313	Bacterial permeabi
736	16	53.3	14	1	P15705	Rev HIV-lbru 37-50	809	16	53.3	15	1	R87875	BPI-278 for use in
737	16	53.3	14	1	R32980	Tripl encoded by pk	810	16	53.3	15	1	R81157	Anti-fungal BPI pe
738	16	53.3	14	1	R40009	Mastoparan analogu	811	16	53.3	15	1	R86526	BPI-77 for use in
739	16	53.3	14	1	R47801	HIV epitope #132.	812	16	53.3	15	1	R81305	Anti-fungal BPI pe
740	16	53.3	14	1	R49293	Pseudo HLA-A2 posi	813	16	53.3	15	1	R93656	HIV principal neut
741	16	53.3	14	1	R49294	Pseudo HLA-A2 posi	814	16	53.3	15	1	R81038	BPI-77, BPI domain
742	16	53.3	14	1	R49498	Pseudo HLA-A2 posi	815	16	53.3	15	1	R82376	Bactericidal/perme
743	16	53.3	14	1	R60750	Lolium perenne pro	816	16	53.3	15	1	R89152	CAEV env gene TM3
744	16	53.3	14	1	R60751	Lolium perenne pro	817	16	53.3	15	1	R78135	Bacterial permeabi
745	16	53.3	14	1	R60752	Lolium perenne pro	818	16	53.3	15	1	R77986	BPI protein segmen
746	16	53.3	14	1	R60753	Lolium perenne pro	819	16	53.3	15	1	R94731	SPNE 19b-1009-7. N
747	16	53.3	14	1	R60754	Lolium perenne pro	820	16	53.3	15	1	R94742	SPNE 19b-40-715. N
748	16	53.3	14	1	R62082	Forcine PIV analog	821	16	53.3	15	1	W05067	Proline-rich SH3 b
749	16	53.3	14	1	R67407	Biotin-binding pep	822	16	53.3	15	1	W05923	Recombinant BPI pe
750	16	53.3	14	1	R71640	Chimeric influenza	823	16	53.3	15	1	W06070	Recombinant BPI pe
751	16	53.3	14	1	R65049	Random biotinylati	824	16	53.3	15	1	R97574	Tumour rejection a
752	16	53.3	14	1	R93453	GST-PI3K SH3 prote	825	16	53.3	15	1	W10062	Peptide #3 inhibit
753	16	53.3	14	1	R86129	Anti-ELAM-1 bindin	826	16	53.3	15	1	W12201	Tolerogenic peptid
754	16	53.3	14	1	W01066	Anion transporter	827	16	53.3	15	1	W12284	Synthetic library
755	16	53.3	14	1	W16475	Streptococcal inhi	828	16	53.3	15	1	W12276	Synthetic library
756	16	53.3	14	1	W07889	Concanavalin A int	829	16	53.3	15	1	W12277	Synthetic library
757	16	53.3	14	1	W07665	HIV Rev residues 3	830	16	53.3	15	1	W15390	N-alpha-Ac-[Phe27,
758	16	53.3	14	1	W07669	HIV RRE IIB argini	831	16	53.3	15	1	W16151	Peptide containing
759	16	53.3	14	1	W10585	J-C junction regio	832	16	53.3	15	1	W18020	Human alpha-N-acet
760	16	53.3	14	1	W24967	C3/C4/C5-derived c	833	16	53.3	15	1	W22911	Low density lipopr
761	16	53.3	14	1	W26941	ELAM-1 binding pep	834	16	53.3	15	1	W12878	Antimicrobial cati
762	16	53.3	14	1	W12875	Antimicrobial cati	835	16	53.3	15	1	W12879	Antimicrobial cati
763	16	53.3	14	1	W12876	Antimicrobial cati	836	16	53.3	15	1	W12885	Antimicrobial cati
764	16	53.3	14	1	W13806	Antimicrobial cati	837	16	53.3	15	1	W13801	Antimicrobial cati

838	16	53.3	15	1	W13802	Antimicrobial cati	911	16	53.3	16	1	R57907	Randomly generated
839	16	53.3	15	1	W35607	Antimicrobial pept	912	16	53.3	16	1	R58527	Heavy chain CDR3 f
840	16	53.3	15	1	W35587	Antimicrobial pept	913	16	53.3	16	1	R58526	Heavy chain CDR3 f
841	16	53.3	15	1	W36230	Antimicrobial prot	914	16	53.3	16	1	R87908	Bovine lactoferrin
842	16	53.3	15	1	W36231	Antimicrobial prot	915	16	53.3	16	1	R83068	HLA-A2 CTL modul
843	16	53.3	15	1	W36232	Antimicrobial prot	916	16	53.3	16	1	R86123	Anti-ELAM-1 blind
844	16	53.3	15	1	W36233	Antimicrobial prot	917	16	53.3	16	1	R95577	HIV rev protein ep
845	16	53.3	15	1	W36401	Antimicrobial prot	918	16	53.3	16	1	R95299	Heavy chain CDR3 o
846	16	53.3	15	1	W36402	Antimicrobial prot	919	16	53.3	16	1	R95300	Heavy chain CDR3 o
847	16	53.3	15	1	W36412	Antimicrobial prot	920	16	53.3	16	1	R95163	bcl-x(L)/bcl-2 ass
848	16	53.3	15	1	W36398	Antimicrobial prot	921	16	53.3	16	1	W07912	gpi20 peptide 466
849	16	53.3	15	1	W36399	Antimicrobial prot	922	16	53.3	16	1	W06603	Bait peptide used
850	16	53.3	15	1	W18840	Human immunoglobul	923	16	53.3	16	1	W03658	Yama 12-kDa subun
851	16	53.3	15	1	W38928	Peptide resembling	924	16	53.3	16	1	W12213	Human acetylcholin
852	16	53.3	15	1	W42264	Biotinylated cross	925	16	53.3	16	1	W09609	Thrombopoietin rec
853	16	53.3	15	1	W43702	Bactericidal/perme	926	16	53.3	16	1	W23270	Tumour necrosis fa
854	16	53.3	15	1	W43628	Bactericidal/perme	927	16	53.3	16	1	W26932	ELAM-1 binding pep
855	16	53.3	15	1	W49199	Human leucocyte an	928	16	53.3	16	1	W12874	Antimicrobial cati
856	16	53.3	15	1	W49161	Human leucocyte an	929	16	53.3	16	1	W12882	Antimicrobial cati
857	16	53.3	15	1	W46656	Biotinylation pept	930	16	53.3	16	1	W12886	Antimicrobial cati
858	16	53.3	15	1	W46661	Biotinylation pept	931	16	53.3	16	1	W12899	Antimicrobial cati
859	16	53.3	15	1	W46667	Biotinylation pept	932	16	53.3	16	1	W32456	Mycobacterium tube
860	16	53.3	15	1	W52463	Cyclic peptide of	933	16	53.3	16	1	W35604	Antimicrobial pept
861	16	53.3	15	1	W52464	Cyclic peptide of	934	16	53.3	16	1	W36270	Antimicrobial prot
862	16	53.3	15	1	W52547	Cyclic peptide of	935	16	53.3	16	1	W36421	Antimicrobial prot
863	16	53.3	15	1	W52466	Cyclic peptide of	936	16	53.3	16	1	W36408	Antimicrobial prot
864	16	53.3	15	1	W43036	Cyclic peptide of	937	16	53.3	16	1	W36414	Antimicrobial prot
865	16	53.3	15	1	W52548	Cyclic peptide of	938	16	53.3	16	1	W36393	Antimicrobial prot
866	16	53.3	15	1	W52549	Cyclic peptide of	939	16	53.3	16	1	W33414	Arg analogue of pe
867	16	53.3	15	1	W52529	Cyclic peptide of	940	16	53.3	16	1	W33415	Trp Arg analogue o
868	16	53.3	15	1	W52533	Cyclic peptide of	941	16	53.3	16	1	W36760	Thrombopoietin rec
869	16	53.3	15	1	W52534	Cyclic peptide of	942	16	53.3	16	1	W25373	Src SH3 domain bin
870	16	53.3	15	1	W41711	Antigenic peptide	943	16	53.3	16	1	W23319	Human prostate pro
871	16	53.3	15	1	W58278	IL-1RT1 binding pe	944	16	53.3	16	1	W45130	Human cartilage gl
872	16	53.3	15	1	W60152	M. vaccae antigen	945	16	53.3	16	1	W45131	Human cartilage gl
873	16	53.3	15	1	W62175	Escherichia coli p	946	16	53.3	16	1	W47296	Human c-Myc amino
874	16	53.3	15	1	W62154	Agrobacterium faec	947	16	53.3	16	1	W46021	Peptide #53. New n
875	16	53.3	15	1	W62155	Agrobacterium faec	948	16	53.3	16	1	W63933	ELAM-1 peptide mim
876	16	53.3	15	1	W62166	Agrobacterium faec	949	16	53.3	16	1	W60679	Transcription fact
877	16	53.3	15	1	W63521	Human BPI protein	950	16	53.3	16	1	W79495	Peptide inhibitor
878	16	53.3	15	1	W63374	Human BPI protein	951	16	53.3	16	1	W75252	Fragment of human
879	16	53.3	15	1	W68791	Peptide binding in	952	16	53.3	16	1	W81694	M. tuberculosis im
880	16	53.3	15	1	W65548	Peptide YY analogu	953	16	53.3	16	1	W76904	Fusion immunoglob
881	16	53.3	15	1	W71334	A glycolipid sugar	954	16	53.3	16	1	W88510	Collagen binding d
882	16	53.3	15	1	W66360	Indolicidin analog	955	16	53.3	16	1	W88511	Collagen binding d
883	16	53.3	15	1	W68574	P. carinii serine	956	16	53.3	16	1	W89718	Interleukin 5 rece
884	16	53.3	15	1	W85445	Helper T-cell clas	957	16	53.3	16	1	W89710	Interleukin 5 rece
885	16	53.3	15	1	W85442	Helper T-cell clas	958	16	53.3	16	1	W73938	Beta-tubulin isofo
886	16	53.3	15	1	W85341	Helper T-cell clas	959	16	53.3	16	1	W03710	M. tuberculosis LH
887	16	53.3	15	1	W85700	Interleukin 5 rece	960	16	53.3	17	1	P90644	Signal peptide NOS
888	16	53.3	15	1	W89713	Interleukin 5 rece	961	16	53.3	17	1	R38622	Sequence of peptid
889	16	53.3	15	1	W94110	VIF-derived HIV pr	962	16	53.3	17	1	R54389	Pseudo HLA-A2 pos1
890	16	53.3	15	1	W94701	Lipoteichoic acid	963	16	53.3	17	1	R49351	RAE 29.1-2. Isol
891	16	53.3	15	1	W94702	Lipoteichoic acid	964	16	53.3	17	1	R43761	5-HT-1A receptor S
892	16	53.3	15	1	Y09924	Interleukin-1 type	965	16	53.3	17	1	R57339	Peptide fragment o
893	16	53.3	15	1	W94854	Sequence of human	966	16	53.3	17	1	R58464	TSAR binding domai
894	16	53.3	15	1	W95145	Phage peptide K1 b	967	16	53.3	17	1	R67560	Antagonist (11) of
895	16	53.3	15	1	W95124	Peptide K1 express	968	16	53.3	17	1	R67707	HIV-1 Rev protein
896	16	53.3	15	1	Y02067	Peptide used to pr	969	16	53.3	17	1	R68753	Cytotoxic T lympho
897	16	53.3	15	1	Y02063	Peptide used to pr	970	16	53.3	17	1	R66559	uPAR-binding pept1
898	16	53.3	15	1	Y05390	Mouse GCR9 protein	971	16	53.3	17	1	R69772	Thrombospondin pep
899	16	53.3	16	1	P80907	Sequence of a pept	972	16	53.3	17	1	R36557	HIV principal neut
900	16	53.3	16	1	R12502	Peptide III which	973	16	53.3	17	1	R58449	Human factor V res
901	16	53.3	16	1	R15707	Rev HIV-2rod 34-49	974	16	53.3	17	1	R96888	Human cartilage l1
902	16	53.3	16	1	R15708	Rev HIV-2rod 34-49	975	16	53.3	17	1	W02473	RAE 29.1-2 compris
903	16	53.3	16	1	R41218	Peptide fragment'o	976	16	53.3	17	1	R95157	bcl-x(L)/bcl-2 ass
904	16	53.3	16	1	R44568	Encoded by human E	977	16	53.3	17	1	W15542	Anti-TGF beta-1 sc
905	16	53.3	16	1	R47802	HIV epitope #133.	978	16	53.3	17	1	W15543	Anti-TGF beta-1 sc
906	16	53.3	16	1	R48257	Nucleolar retentio	979	16	53.3	17	1	W15544	Anti-TGF beta-1 sc
907	16	53.3	16	1	R49551	NANBHV antigen #1.	980	16	53.3	17	1	W15546	Anti-TGF beta-1 sc
908	16	53.3	16	1	R49352	Pseudo HLA-A2 pos1	981	16	53.3	17	1	W15548	Anti-TGF beta-1 sc
909	16	53.3	16	1	R57953	Randomly generated	982	16	53.3	17	1	W15550	Anti-TGF beta-1 sc
910	16	53.3	16	1	R57919	Randomly generated	983	16	53.3	17	1	W15555	Anti-TGF beta-1 sc

984 16 53.3 17 1 W15558 Anti-TGF beta-1 sc
 985 16 53.3 17 1 W15568 20K-cellulase tryp
 986 16 53.3 17 1 W35590 Antimicrobial pept
 987 16 53.3 17 1 W36337 Antimicrobial prot
 988 16 53.3 17 1 W36340 Antimicrobial prot
 989 16 53.3 17 1 W36341 Antimicrobial prot
 990 16 53.3 17 1 W36015 Human hair epithel
 991 16 53.3 17 1 W37571 Synergistic HIV en
 992 16 53.3 17 1 W58401 Human erythropoiet
 993 16 53.3 17 1 W69102 Neuronal NOS bindi
 994 16 53.3 17 1 W79832 Peptide sequence o
 995 16 53.3 17 1 W79783 Tyrosine aminoacyl
 996 16 53.3 17 1 W85985 CD4-variant genera
 997 16 53.3 17 1 W85986 CD4-variant genera
 998 16 53.3 17 1 W85988 CD4-variant genera
 999 16 53.3 17 1 W85989 CD4-variant genera
 1000 16 53.3 17 1 W85966 CD4-variant genera

ALIGNMENTS

RESULT 1
 W32627 32627 standard; peptide; 10 AA.
 AC W32627;
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.
 PF 08-NOV-1996; U17882.
 PR 13-NOV-1995; US-556597.
 PA (UUNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 97-289227/26.
 PT Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination
 PS Claim 3; Page 96; 115pp; English.
 CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (Mab) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the Mab is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 90.0%; Score 27; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.7;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WRXXEY 6
 DB 4 WRXSEY 9
 RESULT 2
 W32628
 ID W32628 standard; peptide; 10 AA.
 AC W32628;

DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.
 PF 08-NOV-1996; U17882.
 PR 13-NOV-1995; US-556597.
 PA (UUNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 97-289227/26.
 PT Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination
 PS Claim 3; Page 96; 115pp; English.
 CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (Mab) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the Mab is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 90.0%; Score 27; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.7;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WRXXEY 6
 DB 4 WRXSEY 9
 RESULT 3
 W71754
 ID W71754 standard; peptide; 10 AA.
 AC W71754;
 DT 08-DEC-1998 (first entry)
 DE Mimotope capable of binding to monoclonal antibody C-34 #4.
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UUNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 98-558458/47.
 PT Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1; Column 47; 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W7152 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic

CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 90.0%; Score 27; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.7;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
 || ||
 Db 4 WRYSEY 9

RESULT 4

W17155
 ID W17155 standard; peptide; 10 AA.
 AC 08-DEC-1998 (first entry)
 DE Minotope capable of binding to monoclonal antibody C-34 #5.
 KW Minotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UNYNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 98-556458/47.
 PT Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1; Column 48; 26pp; English.

The present invention provides peptides which functionally mimic a
 binding site for a monoclonal antibody, where the monoclonal antibody
 recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W17152 to W17182 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 90.0%; Score 27; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3.7;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
 || ||
 Db 4 WRAREY 9

RESULT 5

W15299
 ID W15299 standard; peptide; 9 AA.
 AC W15299;
 DT 30-JAN-1998 (first entry)

DE Human platelet glycoprotein Ib/IX complex epitope mimotope consensus.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.
 PF 08-NOV-1996; U17882.
 PR 13-NOV-1995; US-556597.
 PA (UNYNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 97-389227/26.
 PT Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination
 PS Claim 4; Page 98; 115pp; English.
 CC The present sequence represents the consensus sequence for a mimotope
 CC which functionally mimics a binding site for a monoclonal antibody (MAb)
 CC which recognises an epitope within the human platelet glycoprotein (gp)
 CC Ib/IX complex. More specifically the MAb is C-34. The mimotope peptide
 CC can be used for raising antibodies, as probes to search for anti-
 CC minotopes and to neutralise the inhibitory activity of those antibodies
 CC which recognise the epitope which is mimicked by the peptide. Anti-
 CC minotopes can be used to modulate the adhesion, aggregation or
 CC agglutination of platelets by affecting von Willebrand factor
 CC interaction with the platelets through the gp Ib/IX receptor, e.g. as an
 CC anti-thrombotic drug which inhibits the ristocetin induced aggregation
 CC of platelets.
 SQ Sequence 9 AA;

Query Match 86.7%; Score 26; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.5e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
 || ||
 Db 3 WRYREY 8

RESULT 6

W17158
 ID W17158 standard; peptide; 9 AA.
 AC W17158;
 DT 08-DEC-1998 (first entry)
 DE Minotope capable of binding to monoclonal antibody C-34 #38.
 KW Minotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UNYNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 98-556458/47.
 PT Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1; Column 48; 26pp; English.

The present invention provides peptides which functionally mimic a
 binding site for a monoclonal antibody, where the monoclonal antibody
 recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W17152 to W17182 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic

CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 9 AA;

Query Match 86.7%; Score 26; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.5e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 || ||
 Db 3 WRYREY 8

RESULT 7

W32626
 ID W32626 standard; peptide: 10 AA.

DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.

OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.

PF 08-NOV-1996; U17882.

PR 13-NOV-1995; US-556597.

PA (UUNY) UNIV NEW YORK STATE RES FOUND.

PI Lyle VA, Miller JL;

DR WPI: 97-289227/26.

PT Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination

PS Claim 3; Page 96; 115pp; English.

CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (MAB) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the MAB is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 86.7%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 || ||
 Db 4 WRYFEY 9

RESULT 8

W32629
 ID W32629 standard; peptide: 10 AA.

AC W32629;

DT 30-JAN-1998 (first entry)

DE Human platelet glycoprotein Ib/IX complex epitope mimotope.

KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;

KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.

OS Synthetic.
 OS Homo sapiens.

PN WO9718236-A1.
 PD 22-MAY-1997.

PF 08-NOV-1996; U17882.

PR 13-NOV-1995; US-556597.

PA (UUNY) UNIV NEW YORK STATE RES FOUND.

PI Lyle VA, Miller JL;

DR WPI: 97-289227/26.

PT Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination

PS Claim 3; Page 96; 115pp; English.

CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (MAB) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the MAB is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 86.7%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 || ||
 Db 1 WRQREY 6

RESULT 9

W32624
 ID W32624 standard; peptide: 10 AA.

AC W32624;

DT 30-JAN-1998 (first entry)

DE Human platelet glycoprotein Ib/IX complex epitope mimotope.

KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;

KW monoclonal antibody C-34; anti mimotope; binding site; antibody;

KW platelet adhesion; aggregation; agglutination; von Willebrand factor;

KW anti thrombotic drug; ristocetin.

OS Synthetic.

OS Homo sapiens.

PN WO9718236-A1.

PD 22-MAY-1997.

PF 08-NOV-1996; U17882.

PR 13-NOV-1995; US-556597.

PA (UUNY) UNIV NEW YORK STATE RES FOUND.

PI Lyle VA, Miller JL;

DR WPI: 97-289227/26.

PT Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination

PS Claim 3; Page 96; 115pp; English.

CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (MAB) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the MAB is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through

CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 86.7%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 II II
 Db 4 WRVREY 9

RESULT 10

W71752 ID W71752 standard; peptide; 10 AA.

AC W71752; AC W71752; DE Mimotope capable of binding to monoclonal antibody C-34 #1.
 DE Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR (UYNV) UNIV NEW YORK STATE RES FOUND.
 PA Lyle VA, Miller JL;
 PI WPI; 98-556458/47.
 DR Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1; Column 47; 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 86.7%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 II II
 Db 4 WRVREY 9

RESULT 11

W71753 ID W71753 standard; peptide; 10 AA.

AC W71753; AC W71753; DE Mimotope capable of binding to monoclonal antibody C-34 #3.
 DE Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.

OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR (UYNV) UNIV NEW YORK STATE RES FOUND.
 PA Lyle VA, Miller JL;
 PI WPI; 98-556458/47.
 DR Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1; Column 47; 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 86.7%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 II II
 Db 4 WRVREY 9

RESULT 12

W71756

ID W71756 standard; peptide; 10 AA.
 AC W71756; AC W71756; DE Mimotope capable of binding to monoclonal antibody C-34 #6.
 DE Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.

OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR (UYNV) UNIV NEW YORK STATE RES FOUND.

PA Lyle VA, Miller JL;
 PI WPI; 98-556458/47.
 DR Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1; Column 48; 26pp; English.

CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets

CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 86.7%; Score 26; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 || ||
 Db 1 WRQREY 6

RESULT 13

W32631
 ID W32631 standard; peptide; 10 AA.
 AC W32631;

DT 30-JAN-1998 (first entry)

DE Human platelet glycoprotein Ib/IX complex epitope mimotope.

KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;

KW monoclonal antibody C-34; anti mimotope; binding site; antibody;

KW platelet adhesion; aggregation; agglutination; von Willebrand factor;

KW anti thrombotic drug, ristocetin.

OS Synthetic.

OS Homo sapiens.

PN W09718236-A1.

PD 22-MAY-1997.

PF 08-NOV-1996; U17882.

PR 13-NOV-1995; US-556597.

PA (UUNY) UNIV NEW YORK STATE RES FOUND.

PI Lyle VA, Miller JL;

DR WPI; 97-289227/26.

PT Peptide which mimics human platelet glycoprotein Ib/IX complex

PT epitope - also anti-mimotope molecule capable of binding to the

PT peptide and useful to modulate platelet adhesion, aggregation or

PT agglutination

PS Claim 3; Page 96; 115pp; English.

CC The present sequence represents a mimotope which functionally mimics a

CC binding site for a monoclonal antibody (Mab) which recognises an epitope

CC within the human platelet glycoprotein (gp) Ib/IX complex. More

CC specifically the Mab is C-34, the mimotope peptide can be used for

CC raising antibodies, as probes to search for anti-mimotopes and to

CC neutralise the inhibitory activity of those antibodies which recognise

CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used

CC to modulate the adhesion, aggregation or agglutination of platelets by

CC affecting von Willebrand factor interaction with the platelets through

CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits

CC the ristocetin induced aggregation of platelets.

CC Sequence 10 AA;

Query Match 83.3%; Score 25; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 9.6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 || ||
 Db 5 WRNWEY 10

RESULT 14

W71757
 ID W71757 standard; peptide; 10 AA.
 AC W71757;

DT 08-DEC-1998 (first entry)

DE Mimotope capable of binding to monoclonal antibody C-34 #8.

KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;

KW binding site; platelet epitope; neutralise; aggregation; inhibition;

KW von Willebrand factor interaction; adhesion; agglutination.

OS Synthetic.

OS Homo sapiens.

PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UUNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI; 98-556458/47.
 PT Reptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1; Column 48; 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets. The
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 83.3%; Score 25; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 9.6;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 || ||
 Db 5 WRNWEY 10

RESULT 15

R57946

ID R57946 standard; peptide; 16 AA.

AC R57946;

DT 28-MAR-1995 (first entry)

DE Randomly generated iron (III) chloride-binding site Fe-1.

KW Metal cation binding site; iron (III) chloride; immunoglobulin;

KW CDR3; complementarity determining region; mutagenesis;

KW metalloantibody; phagemid display library; magnetic antibody.

OS Synthetic.

PN W09418220-A.

PD 18-AUG-1994.

PF 02-FEB-1994; U01238.

PR 02-FEB-1993; US-012566.

PR 14-JUN-1993; US-077797.

PA (SCRI) SCRIPPS RES INST.

PI Barbas CF, Lerner RA, Rosenblum J;

DR WPI; 94-279674/34.

PT Methods using oligo-nucleotide primers in prodn of metal binding

PT sites in CDR regions of immunoglobulin heavy or light-chains -

PT for use therapeutically, diagnostically or as metal ion chelators

PS Claim 26; Page 26; 141pp; English.

CC A human monoclonal antibody capable of immunoreacting with

CC iron (III) chloride has one of the heavy chain variable region

CC amino acid sequences R57946-R57953. The binding sequences were

CC generated by mutagenic PCR on the Ig heavy chain gene and were

CC identified by expression on phagemid display proteins.

CC Sequence 16 AA;

Query Match 80.0%; Score 24; DB 1; Length 16;
 Best Local Similarity 50.0%; Pred. No. 24;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6

Db 11 WRTMDY 16

Search completed: May 2, 2000, 00:18:22
Job time: 180 sec

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OM protein - protein search, using sw model

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(*without alignments)
7.548 Million cell updates/sec

Title: US-09-258-947-174

Perfect score: 30

Sequence: 1 WXXXXY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 133990 seqs, 13297546 residues

Total number of hits satisfying chosen parameters: 72966

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : Issued Patents_AA.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	27	90.0	10	2	US-08-556-597-4
4	27	90.0	10	2	US-08-556-597-5
5	26	86.7	9	2	US-08-406-330-38
6	26	86.7	9	2	US-08-556-597-38
7	26	86.7	10	2	US-08-406-330-1
8	26	86.7	10	2	US-08-406-330-3
9	26	86.7	10	2	US-08-406-330-6
10	26	86.7	10	2	US-08-556-597-1
11	26	86.7	10	2	US-08-556-597-3
12	26	86.7	10	2	US-08-556-597-6
13	25	83.3	10	2	US-08-406-330-8
14	25	83.3	10	2	US-08-556-597-8
15	24	80.0	16	1	US-08-077-797A-42
16	24	80.0	16	4	PCT-US94-01238-42
17	23	76.7	8	2	US-08-350-260A-464
18	22	73.3	10	2	US-08-406-330-2
19	22	73.3	10	2	US-08-556-597-2
20	22	73.3	17	2	US-08-310-912A-24
21	22	73.3	17	4	PCT-US95-04570-24
22	22	73.3	17	4	PCT-US95-04589-24
23	21	70.0	10	2	US-08-556-597-162
24	20	66.7	17	1	US-08-190-788A-231
25	20	66.7	17	1	US-08-383-748B-234
26	20	66.7	17	1	US-08-465-391A-231
27	20	66.7	17	2	US-08-464-538B-231
28	20	66.7	17	2	US-08-463-076E-285
29	20	66.7	18	1	US-08-351-423-2
30	20	66.7	18	1	US-08-406-330-4
31	19	63.3	19	1	US-08-014-979-81
32	19	63.3	19	1	US-08-233-305-8
33	19	63.3	19	1	US-08-233-305-9
34	19	63.3	19	1	US-08-587-391-7
35	19	63.3	19	1	US-08-587-391-8
36	19	63.3	19	1	US-08-587-391-10
37	19	63.3	19	1	US-08-587-391-12
38	19	63.3	19	1	US-08-796-883-3
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58	19	63.3	19	2	US-08-592-646A-51
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61	19	63.3	19	2	US-08-637-759B-316
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105	17	56.7	15	2	US-08-485-445A-132	Sequence 132, App	178	16	53.3	6	2	US-08-482-228-146	Sequence 146, App
106	17	56.7	15	4	PCT-US95-0049A-132	Sequence 132, App	179	16	53.3	6	2	US-08-962-190-25	Sequence 25, Appl
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118	16	53.3	3	1	US-08-256-771-17	Sequence 17, Appl	191	16	53.3	7	1	US-08-253-854-66	Sequence 66, Appl
119	16	53.3	3	1	US-08-381-984-17	Sequence 17, Appl	192	16	53.3	7	1	US-08-253-854-67	Sequence 67, Appl
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124	16	53.3	4	1	US-08-215-137-11	Sequence 11, Appl	197	16	53.3	7	1	US-08-253-854-72	Sequence 72, Appl
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146	16	53.3	6	1	US-08-253-854-61	Sequence 61, Appl	219	16	53.3	8	1	US-08-594-447-72	Sequence 72, Appl
147	16	53.3	6	1	US-08-253-854-62	Sequence 62, Appl	220	16	53.3	8	1	US-08-594-447-73	Sequence 73, Appl
148	16	53.3	6	1	US-08-253-854-78	Sequence 78, Appl	221	16	53.3	8	1	US-08-541-964-71	Sequence 71, Appl
149	16	53.3	6	1	US-08-253-854-79	Sequence 79, Appl	222	16	53.3	8	1	US-08-541-964-72	Sequence 72, Appl
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154	16	53.3	6	1	US-08-487-006-28	Sequence 28, Appl	227	16	53.3	8	2	US-08-583-569-3	Sequence 3, Appl1
155	16	53.3	6	1	US-08-487-006-97	Sequence 97, Appl	228	16	53.3	8	2	US-08-194-981E-40	Sequence 40, Appl
156	16	53.3	6	1	US-08-291-368-25	Sequence 25, Appl	229	16	53.3	8	2	US-08-194-981E-43	Sequence 43, Appl
157	16	53.3	6	2	US-08-660-747-18	Sequence 18, Appl	230	16	53.3	8	2	US-08-665-647-86	Sequence 86, Appl
158	16	53.3	6	2	US-08-660-747-20	Sequence 20, Appl	231	16	53.3	8	2	US-08-665-647-87	Sequence 87, Appl
159	16	53.3	6	2	US-08-660-747-21	Sequence 21, Appl	232	16	53.3	8	2	US-09-016-366A-53	Sequence 53, Appl
160	16	53.3	6	2	US-08-660-747-24	Sequence 24, Appl	233	16	53.3	8	2	US-08-350-260A-433	Sequence 433, App
161	16	53.3	6	2	US-08-660-747-25	Sequence 25, Appl	234	16	53.3	8	4	PCT-US93-08325-6	Sequence 6, Appl1
162	16	53.3	6	2	US-08-660-747-26	Sequence 26, Appl	235	16	53.3	8	4	PCT-US93-08326-6	Sequence 6, Appl1
163	16	53.3	6	2	US-08-660-747-27	Sequence 27, Appl	236	16	53.3	9	5	5190919-29	Patent No. 5190919
164	16	53.3	6	2	US-08-660-747-48	Sequence 48, Appl	237	16	53.3	9	1	US-08-470-837-20	Sequence 20, Appl
165	16	53.3	6	2	US-08-660-747-49	Sequence 49, Appl	238	16	53.3	9	2	US-08-599-603-20	Sequence 20, Appl
166	16	53.3	6	2	US-08-660-747-50	Sequence 50, Appl	239	16	53.3	9	2	US-08-417-174-71	Sequence 71, Appl
167	16	53.3	6	2	US-08-660-747-51	Sequence 51, Appl	240	16	53.3	9	2	US-08-704-655-11	Sequence 11, Appl
168	16	53.3	6	2	US-08-660-747-52	Sequence 52, Appl	241	16	53.3	9	2	US-08-482-651-43	Sequence 43, Appl
169	16	53.3	6	2	US-08-660-747-53	Sequence 53, Appl	242	16	53.3	9	2	US-08-146-028-416	Sequence 416, App
170	16	53.3	6	2	US-08-660-747-54	Sequence 54, Appl	243	16	53.3	9	2	US-08-146-028-417	Sequence 417, App
171	16	53.3	6	2	US-08-660-747-55	Sequence 55, Appl	244	16	53.3	9	2	US-08-146-028-418	Sequence 418, App
172	16	53.3	6	2	US-08-637-759B-179	Sequence 179, App	245	16	53.3	9	2	US-08-146-028-419	Sequence 419, App
173	16	53.3	6	2	US-08-871-163-12	Sequence 12, Appl	246	16	53.3	9	2	US-08-685-589A-136	Sequence 136, App
174	16	53.3	6	2	US-08-488-659A-28	Sequence 28, Appl	247	16	53.3	9	2	US-08-350-260A-352	Sequence 352, App
175	16	53.3	6	2	US-08-488-659A-97	Sequence 97, Appl	248	16	53.3	9	2	US-08-350-260A-394	Sequence 394, App

249	16	53.3	9	2	US-08-350-260A-432	Sequence 432, App	322	16	53.3	11	2	US-08-733-505A-34	Sequence 34, Appl
250	16	53.3	9	2	US-08-751-767A-65	Sequence 65, Appl	323	16	53.3	11	2	US-08-464-538B-153	Sequence 153, App
251	16	53.3	9	4	PCT-US94-01321-56	Sequence 56, Appl	324	16	53.3	11	2	US-08-637-759B-308	Sequence 308, App
252	16	53.3	9	4	PCT-US94-07644A-5	Sequence 5, Appl	325	16	53.3	11	2	US-08-463-076E-205	Sequence 205, App
253	16	53.3	10	1	US-07-841-997A-31	Sequence 31, Appl	326	16	53.3	11	2	US-08-685-589A-105	Sequence 105, App
254	16	53.3	10	1	US-08-290-448A-18	Sequence 18, Appl	327	16	53.3	11	2	US-08-685-589A-106	Sequence 106, App
255	16	53.3	10	1	US-08-469-582-24	Sequence 24, Appl	328	16	53.3	11	2	US-08-685-589A-108	Sequence 108, App
256	16	53.3	10	1	US-08-469-582-25	Sequence 25, Appl	329	16	53.3	11	2	US-08-685-589A-111	Sequence 111, App
257	16	53.3	10	1	US-08-290-448A-18	Sequence 18, Appl	330	16	53.3	11	2	US-08-968-676-7	Sequence 7, Appl
258	16	53.3	10	1	US-08-485-132-2	Sequence 2, Appl	331	16	53.3	11	2	US-08-934-222-116	Sequence 116, App
259	16	53.3	10	1	US-08-175-069A-18	Sequence 18, Appl	332	16	53.3	11	2	US-08-933-402-116	Sequence 116, App
260	16	53.3	10	1	US-08-290-301-31	Sequence 31, Appl	333	16	53.3	11	2	US-09-207-621-116	Sequence 116, App
261	16	53.3	10	2	US-08-406-330-7	Sequence 7, Appl	334	16	53.3	11	2	US-08-706-741B-69	Sequence 69, Appl
262	16	53.3	10	2	US-08-406-330-10	Sequence 10, Appl	335	16	53.3	11	2	US-08-532-818-116	Sequence 116, App
263	16	53.3	10	2	US-08-406-330-11	Sequence 11, Appl	336	16	53.3	11	2	US-08-924-695A-69	Sequence 69, Appl
264	16	53.3	10	2	US-08-480-190-150	Sequence 150, App	337	16	53.3	11	3	US-08-817-926-6	Sequence 6, Appl
265	16	53.3	10	2	US-08-479-223-3	Sequence 3, Appl	338	16	53.3	11	4	PCT-US91-06950-46	Sequence 46, Appl
266	16	53.3	10	2	US-08-764-640-116	Sequence 116, App	339	16	53.3	11	4	PCT-US95-08091-1	Sequence 1, Appl
267	16	53.3	10	2	US-08-637-759B-176	Sequence 176, App	340	16	53.3	11	5	5185431-14	Patent No. 5185431
268	16	53.3	10	2	US-08-556-597-7	Sequence 7, Appl	341	16	53.3	11	5	5190919-30	Patent No. 5190919
269	16	53.3	10	2	US-08-556-597-10	Sequence 10, Appl	342	16	53.3	12	1	US-07-778-233B-14	Sequence 14, Appl
270	16	53.3	10	2	US-08-556-597-11	Sequence 11, Appl	343	16	53.3	12	1	US-07-963-321-14	Sequence 14, Appl
271	16	53.3	10	2	US-08-556-597-83	Sequence 83, Appl	344	16	53.3	12	1	US-08-290-641-14	Sequence 14, Appl
272	16	53.3	10	2	US-08-556-597-89	Sequence 89, Appl	345	16	53.3	12	1	US-08-137-800-12	Sequence 12, Appl
273	16	53.3	10	2	US-08-556-597-92	Sequence 92, Appl	346	16	53.3	12	1	US-08-230-047-36	Sequence 36, Appl
274	16	53.3	10	2	US-08-556-597-94	Sequence 94, Appl	347	16	53.3	12	1	US-08-197-203-6	Sequence 6, Appl
275	16	53.3	10	2	US-08-556-597-95	Sequence 95, Appl	348	16	53.3	12	1	US-08-477-383-12	Sequence 12, Appl
276	16	53.3	10	2	US-08-556-597-99	Sequence 99, Appl	349	16	53.3	12	1	US-08-487-174-12	Sequence 12, Appl
277	16	53.3	10	2	US-08-556-597-104	Sequence 104, App	350	16	53.3	12	1	US-08-190-788A-22	Sequence 22, Appl
278	16	53.3	10	2	US-08-556-597-124	Sequence 124, App	351	16	53.3	12	1	US-08-190-788A-98	Sequence 98, Appl
279	16	53.3	10	2	US-08-556-597-125	Sequence 125, App	352	16	53.3	12	1	US-08-190-788A-212	Sequence 212, App
280	16	53.3	10	2	US-08-556-597-127	Sequence 127, App	353	16	53.3	12	1	US-08-480-750-12	Sequence 12, Appl
281	16	53.3	10	2	US-08-556-597-130	Sequence 130, App	354	16	53.3	12	1	US-08-260-582-18	Sequence 18, Appl
282	16	53.3	10	2	US-08-556-597-144	Sequence 144, App	355	16	53.3	12	1	US-08-260-582-58	Sequence 58, Appl
283	16	53.3	10	2	US-08-556-597-150	Sequence 150, App	356	16	53.3	12	1	US-08-241-054-10	Sequence 10, Appl
284	16	53.3	10	2	US-08-556-597-156	Sequence 156, App	357	16	53.3	12	1	US-08-241-054-96	Sequence 96, Appl
285	16	53.3	10	2	US-08-556-597-159	Sequence 159, App	358	16	53.3	12	1	US-08-390-158A-86	Sequence 86, Appl
286	16	53.3	10	2	US-08-556-597-169	Sequence 169, App	359	16	53.3	12	1	US-08-390-158A-99	Sequence 99, Appl
287	16	53.3	10	2	US-08-488-379-150	Sequence 150, App	360	16	53.3	12	1	US-08-439-817-76	Sequence 9, Appl
288	16	53.3	10	2	US-08-617-929-24	Sequence 24, Appl	361	16	53.3	12	1	US-08-439-817-76	Sequence 76, Appl
289	16	53.3	10	2	US-08-327-451E-26	Sequence 26, Appl	362	16	53.3	12	1	US-08-548-540-14	Sequence 14, Appl
290	16	53.3	10	2	US-08-902-623-51	Sequence 51, Appl	363	16	53.3	12	1	US-08-548-540-158	Sequence 158, App
291	16	53.3	10	2	US-08-902-623-56	Sequence 56, Appl	364	16	53.3	12	1	US-08-383-474B-27	Sequence 27, Appl
292	16	53.3	10	2	US-08-735-253-8	Sequence 8, Appl	365	16	53.3	12	1	US-08-383-474B-103	Sequence 103, App
293	16	53.3	10	2	US-08-735-253-13	Sequence 13, Appl	366	16	53.3	12	1	US-08-627-497-13	Sequence 13, App
294	16	53.3	10	2	US-08-726-308A-127	Sequence 127, App	367	16	53.3	12	1	US-08-627-497-14	Sequence 14, Appl
295	16	53.3	10	2	US-08-458-109-26	Sequence 26, Appl	368	16	53.3	12	1	US-08-485-508-10	Sequence 10, Appl
296	16	53.3	10	2	US-08-986-234-5	Sequence 5, Appl	369	16	53.3	12	1	US-08-485-508-96	Sequence 96, Appl
297	16	53.3	10	3	US-08-467-580-33	Sequence 33, Appl	370	16	53.3	12	1	US-08-465-391A-22	Sequence 22, Appl
298	16	53.3	10	3	PCT-US93-07545-150	Sequence 34, Appl	371	16	53.3	12	1	US-08-465-391A-98	Sequence 98, Appl
299	16	53.3	10	4	PCT-US93-08516-33	Sequence 33, Appl	372	16	53.3	12	1	US-08-465-391A-212	Sequence 212, App
300	16	53.3	10	4	PCT-US95-08516-34	Sequence 34, Appl	373	16	53.3	12	1	US-08-406-330-37	Sequence 37, Appl
301	16	53.3	10	4	PCT-US95-08516-34	Sequence 34, Appl	374	16	53.3	12	2	US-08-406-330-35	Sequence 35, Appl
302	16	53.3	11	1	US-08-029-333-21	Sequence 21, Appl	375	16	53.3	12	2	US-08-406-330-35	Sequence 35, Appl
303	16	53.3	11	1	US-08-029-333-45	Sequence 45, Appl	376	16	53.3	12	2	US-08-406-330-74	Sequence 74, Appl
304	16	53.3	11	1	US-07-851-941-11	Sequence 11, Appl	377	16	53.3	12	2	US-08-406-330-77	Sequence 77, Appl
305	16	53.3	11	1	US-07-851-941-12	Sequence 12, Appl	378	16	53.3	12	2	US-08-464-538B-22	Sequence 22, Appl
306	16	53.3	11	1	US-07-851-941-18	Sequence 18, Appl	379	16	53.3	12	2	US-08-464-538B-98	Sequence 98, Appl
307	16	53.3	11	1	US-08-271-830-51	Sequence 51, Appl	380	16	53.3	12	2	US-08-464-538B-212	Sequence 212, App
308	16	53.3	11	1	US-08-145-939-13	Sequence 13, Appl	381	16	53.3	12	2	US-08-482-651-58	Sequence 58, Appl
309	16	53.3	11	1	US-08-343-267-13	Sequence 13, Appl	382	16	53.3	12	2	US-08-637-759B-156	Sequence 156, App
310	16	53.3	11	1	US-08-190-788A-153	Sequence 153, App	383	16	53.3	12	2	US-08-556-597-28	Sequence 28, Appl
311	16	53.3	11	1	US-08-344-636-16	Sequence 16, App	384	16	53.3	12	2	US-08-556-597-35	Sequence 35, Appl
312	16	53.3	11	1	US-08-256-771-27	Sequence 27, App	385	16	53.3	12	2	US-08-556-597-37	Sequence 37, Appl
313	16	53.3	11	1	US-08-445-745-6	Sequence 6, Appl	386	16	53.3	12	2	US-08-556-597-52	Sequence 52, App
314	16	53.3	11	1	US-08-445-745-10	Sequence 10, Appl	387	16	53.3	12	2	US-08-556-597-72	Sequence 72, App
315	16	53.3	11	1	US-08-451-947-46	Sequence 46, Appl	388	16	53.3	12	2	US-08-556-597-72	Sequence 72, App
316	16	53.3	11	1	US-08-484-009-1	Sequence 1, Appl	389	16	53.3	12	2	US-08-556-597-73	Sequence 73, Appl
317	16	53.3	11	1	US-08-383-474B-156	Sequence 156, App	390	16	53.3	12	2		
318	16	53.3	11	1	US-08-627-497-19	Sequence 19, App	391	16	53.3	12	2		
319	16	53.3	11	1	US-08-465-391A-153	Sequence 153, App	392	16	53.3	12	2		
320	16	53.3	11	1	US-08-381-984-31	Sequence 31, Appl	393	16	53.3	12	2		
321	16	53.3	11	2	US-08-424-826A-46	Sequence 46, Appl	394	16	53.3	12	2		

395	16	53.3	12	2	US-08-556-597-74	Sequence 74, Appl	468	16	53.3	14	2	US-08-685-589A-192	Sequence 192, App
396	16	53.3	12	2	US-08-556-597-77	Sequence 77, Appl	469	16	53.3	14	2	US-08-959-512-31	Sequence 31, Appl
397	16	53.3	12	2	US-08-463-076E-66	Sequence 66, Appl	470	16	53.3	14	2	US-08-955-471-9	Sequence 9, Appl1
398	16	53.3	12	2	US-08-463-076E-144	Sequence 144, App	471	16	53.3	14	2	US-08-484-905-55	Sequence 55, Appl
399	16	53.3	12	2	US-08-463-076E-266	Sequence 266, App	472	16	53.3	14	2	US-08-310-912A-80	Sequence 80, Appl
400	16	53.3	12	2	US-08-666-561-53	Sequence 53, Appl	473	16	53.3	14	2	US-08-481-985B-55	Sequence 55, Appl
401	16	53.3	12	2	US-08-602-723-5	Sequence 53, Appl1	474	16	53.3	14	3	PCT-US92-10242-9	Sequence 9, Appl1
402	16	53.3	12	2	US-08-310-912A-45	Sequence 9, Appl1	475	16	53.3	14	4	PCT-US93-06751-144	Sequence 144, App
403	16	53.3	12	3	US-08-293-728-9	Sequence 9, Appl1	476	16	53.3	14	4	PCT-US93-07545-3	Sequence 3, Appl1
404	16	53.3	12	4	PCT-US93-12245-53	Sequence 53, Appl	477	16	53.3	14	4	PCT-US93-07545-4	Sequence 4, Appl1
405	16	53.3	12	4	PCT-US95-04570-45	Sequence 45, Appl	478	16	53.3	14	4	PCT-US93-07545-208	Sequence 208, App
406	16	53.3	12	4	PCT-US95-04589-45	Sequence 45, Appl	479	16	53.3	14	4	PCT-US95-04570-80	Sequence 80, Appl
407	16	53.3	12	4	PCT-US95-05471-18	Sequence 18, Appl	480	16	53.3	14	4	PCT-US95-04589-80	Sequence 80, Appl
408	16	53.3	12	4	PCT-US95-05471-58	Sequence 58, Appl	481	16	53.3	14	4	PCT-US96-03180-10	Sequence 10, Appl
409	16	53.3	12	4	PCT-US96-07962-9	Sequence 9, Appl1	482	16	53.3	14	5	5258287-51	Patent No. 5258287
410	16	53.3	12	4	PCT-US96-09809-14	Sequence 14, Appl	483	16	53.3	15	1	US-07-859-291C-31	Sequence 31, Appl
411	16	53.3	12	4	PCT-US96-09809-158	Sequence 158, App	484	16	53.3	15	1	US-08-311-611A-72	Sequence 72, Appl
412	16	53.3	12	5	5489533-16	Patent No. 5489533	485	16	53.3	15	1	US-08-311-611A-223	Sequence 223, App
413	16	53.3	12	5	5512660-16	Patent No. 5512660	486	16	53.3	15	1	US-08-230-047-28	Sequence 28, Appl
414	16	53.3	13	1	US-07-715-271-1	Sequence 1, Appl1	487	16	53.3	15	1	US-08-318-200-2	Sequence 2, Appl1
415	16	53.3	13	1	US-07-831-137-1	Sequence 1, Appl1	488	16	53.3	15	1	US-08-372-783-72	Sequence 72, Appl
416	16	53.3	13	1	US-08-287-021-1	Sequence 1, Appl1	489	16	53.3	15	1	US-08-372-783-223	Sequence 223, App
417	16	53.3	13	1	US-08-197-205-1	Sequence 1, Appl1	490	16	53.3	15	1	US-08-268-251-6	Sequence 6, Appl
418	16	53.3	13	1	US-08-197-205-2	Sequence 2, Appl1	491	16	53.3	15	1	US-08-268-251-12	Sequence 12, Appl
419	16	53.3	13	1	US-08-197-205-5	Sequence 5, Appl1	492	16	53.3	15	1	US-08-190-788A-191	Sequence 191, App
420	16	53.3	13	1	US-08-197-205-7	Sequence 7, Appl1	493	16	53.3	15	1	US-08-372-105-72	Sequence 72, Appl
421	16	53.3	13	1	US-08-241-054-107	Sequence 107, App	494	16	53.3	15	1	US-08-372-105-223	Sequence 223, App
422	16	53.3	13	1	US-08-390-156A-83	Sequence 83, Appl	495	16	53.3	15	1	US-07-834-539A-54	Sequence 54, Appl
423	16	53.3	13	1	US-08-170-596-10	Sequence 10, Appl	496	16	53.3	15	1	US-08-370-648-12	Sequence 12, Appl
424	16	53.3	13	1	US-08-439-817-87	Sequence 87, Appl	497	16	53.3	15	1	US-08-306-473A-72	Sequence 72, Appl
425	16	53.3	13	1	US-08-485-508-107	Sequence 107, App	498	16	53.3	15	1	US-08-306-473A-223	Sequence 223, App
426	16	53.3	13	2	US-08-480-190-5	Sequence 5, Appl1	499	16	53.3	15	1	US-08-053-131-62	Sequence 62, Appl
427	16	53.3	13	2	US-08-480-190-209	Sequence 209, App	500	16	53.3	15	1	US-08-645-641-62	Sequence 62, Appl
428	16	53.3	13	2	US-08-480-190-210	Sequence 210, App	501	16	53.3	15	1	US-08-383-753-35	Sequence 35, Appl
429	16	53.3	13	2	US-08-488-379-5	Sequence 5, Appl1	502	16	53.3	15	1	US-08-383-753-40	Sequence 40, Appl
430	16	53.3	13	2	US-08-488-379-209	Sequence 209, App	503	16	53.3	15	1	US-08-383-753-46	Sequence 46, Appl
431	16	53.3	13	2	US-08-488-379-210	Sequence 210, App	504	16	53.3	15	1	US-08-209-762-72	Sequence 72, Appl
432	16	53.3	13	2	US-08-310-912A-68	Sequence 68, Appl	505	16	53.3	15	1	US-08-473-344-72	Sequence 72, Appl
433	16	53.3	13	2	US-08-460-890A-26	Sequence 26, Appl	506	16	53.3	15	1	US-08-625-691-13	Sequence 13, Appl1
434	16	53.3	13	2	US-08-460-890A-40	Sequence 40, Appl	507	16	53.3	15	1	US-08-625-691-13	Sequence 13, Appl
435	16	53.3	13	2	US-08-752-852A-196	Sequence 196, App	508	16	53.3	15	1	US-08-383-474B-194	Sequence 194, App
436	16	53.3	13	3	US-08-630-916A-68	Sequence 68, Appl	509	16	53.3	15	1	US-08-665-220-26	Sequence 26, Appl
437	16	53.3	13	4	PCT-US93-07545-5	Sequence 5, Appl1	510	16	53.3	15	1	US-08-665-220-36	Sequence 36, Appl
438	16	53.3	13	4	PCT-US93-07545-209	Sequence 209, App	511	16	53.3	15	1	US-08-665-220-41	Sequence 41, Appl
439	16	53.3	13	4	PCT-US93-07545-210	Sequence 210, App	512	16	53.3	15	1	US-08-665-220-46	Sequence 46, Appl
440	16	53.3	13	4	PCT-US95-04570-68	Sequence 68, Appl	513	16	53.3	15	1	US-08-665-220-51	Sequence 51, Appl
441	16	53.3	13	4	PCT-US95-04589-68	Sequence 68, Appl	514	16	53.3	15	1	US-08-665-220-56	Sequence 56, Appl
442	16	53.3	14	1	US-08-232-453A-43	Sequence 43, Appl	515	16	53.3	15	1	US-08-465-391A-191	Sequence 191, App
443	16	53.3	14	1	US-08-390-158A-104	Sequence 104, App	516	16	53.3	15	1	US-07-853-408B-62	Sequence 62, Appl
444	16	53.3	14	1	US-08-478-312-23	Sequence 23, Appl	517	16	53.3	15	2	US-08-096-762-62	Sequence 62, Appl
445	16	53.3	14	1	US-08-478-312-29	Sequence 29, App	518	16	53.3	15	2	US-08-480-190-2	Sequence 2, Appl1
446	16	53.3	14	1	US-08-478-312-32	Sequence 32, Appl	519	16	53.3	15	2	US-08-632-514C-15	Sequence 15, Appl
447	16	53.3	14	1	US-08-485-302-23	Sequence 23, Appl	520	16	53.3	15	2	US-08-592-646A-19	Sequence 19, Appl
448	16	53.3	14	1	US-08-485-302-29	Sequence 29, Appl	521	16	53.3	15	2	US-08-592-646A-20	Sequence 20, Appl
449	16	53.3	14	1	US-08-485-302-32	Sequence 32, Appl	522	16	53.3	15	2	US-08-592-646A-21	Sequence 21, Appl
450	16	53.3	14	1	US-08-476-169-19	Sequence 19, Appl	523	16	53.3	15	2	US-08-592-646A-22	Sequence 22, Appl
451	16	53.3	14	1	US-08-295-411-9	Sequence 9, Appl1	524	16	53.3	15	2	US-08-592-646A-23	Sequence 23, Appl
452	16	53.3	14	1	US-08-484-083-19	Sequence 19, Appl	525	16	53.3	15	2	US-08-592-646A-24	Sequence 24, Appl
453	16	53.3	14	1	US-08-383-753-31	Sequence 31, Appl	526	16	53.3	15	2	US-08-592-646A-25	Sequence 25, Appl
454	16	53.3	14	1	US-08-439-817-94	Sequence 94, Appl	527	16	53.3	15	2	US-08-592-646A-26	Sequence 26, Appl
455	16	53.3	14	1	US-08-627-497-5	Sequence 5, Appl1	528	16	53.3	15	2	US-08-592-646A-27	Sequence 27, Appl
456	16	53.3	14	1	US-08-627-497-12	Sequence 12, Appl	529	16	53.3	15	2	US-08-592-646A-28	Sequence 28, Appl
457	16	53.3	14	2	US-08-480-190-3	Sequence 3, Appl1	530	16	53.3	15	2	US-08-592-646A-29	Sequence 29, Appl
458	16	53.3	14	2	US-08-480-190-4	Sequence 4, Appl1	531	16	53.3	15	2	US-08-592-646A-30	Sequence 30, Appl
459	16	53.3	14	2	US-08-480-190-208	Sequence 208, App	532	16	53.3	15	2	US-08-592-646A-48	Sequence 48, Appl
460	16	53.3	14	2	US-08-442-461D-1	Sequence 1, Appl1	533	16	53.3	15	2	US-08-592-646A-49	Sequence 49, Appl
461	16	53.3	14	2	US-08-442-461D-3	Sequence 3, Appl1	534	16	53.3	15	2	US-08-592-646A-56	Sequence 56, Appl
462	16	53.3	14	2	US-08-248-839C-93	Sequence 93, Appl	535	16	53.3	15	2	US-08-621-803-72	Sequence 72, Appl
463	16	53.3	14	2	US-08-392-816-12	Sequence 12, Appl	536	16	53.3	15	2	US-08-621-803-146	Sequence 146, App
464	16	53.3	14	2	US-08-586-772-31	Sequence 31, Appl	537	16	53.3	15	2	US-08-618-408B-26	Sequence 26, Appl
465	16	53.3	14	2	US-08-488-379-3	Sequence 3, Appl1	538	16	53.3	15	2	US-08-618-408B-36	Sequence 36, Appl
466	16	53.3	14	2	US-08-488-379-4	Sequence 4, Appl1	539	16	53.3	15	2	US-08-618-408B-41	Sequence 41, Appl
467	16	53.3	14	2	US-08-488-379-208	Sequence 208, App	540	16	53.3	15	2	US-08-618-408B-46	Sequence 46, Appl

541	16	53.3	15	2	US-08-618-408B-51	Sequence 51, Appl	614	16	53.3	16	1	US-08-652-972A-5	Sequence 5, Appl
542	16	53.3	15	2	US-08-618-408B-56	Sequence 56, Appl	615	16	53.3	16	1	US-08-439-817-88	Sequence 88, Appl
543	16	53.3	15	2	US-08-485-445A-72	Sequence 72, Appl	616	16	53.3	16	1	US-08-485-508-108	Sequence 108, Appl
544	16	53.3	15	2	US-08-485-445A-223	Sequence 223, Appl	617	16	53.3	16	2	US-08-661-479-26	Sequence 26, Appl
545	16	53.3	15	2	US-08-531-662B-12	Sequence 12, Appl	618	16	53.3	16	2	US-08-373-190-26	Sequence 26, Appl
546	16	53.3	15	2	US-08-464-538B-191	Sequence 191, Appl	619	16	53.3	16	2	US-08-764-640-165	Sequence 165, Appl
547	16	53.3	15	2	US-08-583-569-2	Sequence 2, Appl	620	16	53.3	16	2	US-08-903-623-6	Sequence 6, Appl
548	16	53.3	15	2	US-08-586-772-35	Sequence 35, Appl	621	16	53.3	16	2	US-08-595-868C-21	Sequence 21, Appl
549	16	53.3	15	2	US-08-586-772-40	Sequence 40, Appl	622	16	53.3	16	2	US-08-438-190A-26	Sequence 26, Appl
550	16	53.3	15	2	US-08-586-772-46	Sequence 46, Appl	623	16	53.3	16	2	US-08-343-443B-88	Sequence 88, Appl
551	16	53.3	15	2	US-08-800-353-54	Sequence 54, Appl	624	16	53.3	16	2	US-08-343-443B-90	Sequence 90, Appl
552	16	53.3	15	2	US-08-308-865-62	Sequence 62, Appl	625	16	53.3	16	2	US-08-312-202B-3	Sequence 3, Appl
553	16	53.3	15	2	US-08-463-076E-245	Sequence 245, Appl	626	16	53.3	16	2	US-08-752-852A-71	Sequence 71, Appl
554	16	53.3	15	2	US-08-488-379-2	Sequence 2, Appl	627	16	53.3	16	2	US-08-752-852A-194	Sequence 194, Appl
555	16	53.3	15	2	US-08-685-589A-112	Sequence 112, Appl	628	16	53.3	16	2	US-08-752-852A-209	Sequence 209, Appl
556	16	53.3	15	2	US-08-685-589A-113	Sequence 113, Appl	629	16	53.3	16	2	US-08-752-852A-215	Sequence 215, Appl
557	16	53.3	15	2	US-08-685-589A-115	Sequence 115, Appl	630	16	53.3	16	2	US-08-752-852A-222	Sequence 222, Appl
558	16	53.3	15	2	US-08-685-589A-183	Sequence 183, Appl	631	16	53.3	16	4	PCT-US93-06751-145	Sequence 145, Appl
559	16	53.3	15	2	US-08-685-589A-187	Sequence 187, Appl	632	16	53.3	16	4	PCT-US94-01238-3	Sequence 3, Appl
560	16	53.3	15	2	US-08-685-589A-188	Sequence 188, Appl	633	16	53.3	16	4	PCT-US94-01238-15	Sequence 15, Appl
561	16	53.3	15	2	US-08-685-589A-201	Sequence 201, Appl	634	16	53.3	16	4	PCT-US94-01238-49	Sequence 49, Appl
562	16	53.3	15	2	US-08-685-589A-202	Sequence 202, Appl	635	16	53.3	16	4	PCT-US94-01258-43	Sequence 43, Appl
563	16	53.3	15	2	US-08-685-589A-203	Sequence 203, Appl	636	16	53.3	16	4	PCT-US94-01258-44	Sequence 44, Appl
564	16	53.3	15	2	US-08-685-589A-241	Sequence 241, Appl	637	16	53.3	16	4	PCT-US95-11235-43	Sequence 43, Appl
565	16	53.3	15	2	US-08-959-512-35	Sequence 35, Appl	638	16	53.3	16	4	PCT-US95-11235-44	Sequence 44, Appl
566	16	53.3	15	2	US-08-959-512-40	Sequence 40, Appl	639	16	53.3	16	4	PCT-US95-12433-3	Sequence 3, Appl
567	16	53.3	15	2	US-08-959-512-46	Sequence 46, Appl	640	16	53.3	16	4	PCT-US96-06X31A-5	Sequence 5, Appl
568	16	53.3	15	2	US-08-769-745-34	Sequence 34, Appl	641	16	53.3	17	1	US-08-176-500-91	Sequence 91, Appl
569	16	53.3	15	2	US-08-997-080-139	Sequence 139, Appl	642	16	53.3	17	1	US-07-856-036B-17	Sequence 17, Appl
570	16	53.3	15	2	US-08-997-362-139	Sequence 139, Appl	643	16	53.3	17	1	US-08-333-565-20	Sequence 20, Appl
571	16	53.3	15	2	US-08-752-852A-31	Sequence 31, Appl	644	16	53.3	17	1	US-08-471-052A-91	Sequence 91, Appl
572	16	53.3	15	2	US-08-752-852A-32	Sequence 32, Appl	645	16	53.3	17	1	US-08-071-811A-1	Sequence 1, Appl
573	16	53.3	15	2	US-08-752-852A-33	Sequence 33, Appl	646	16	53.3	17	1	US-08-071-811A-3	Sequence 3, Appl
574	16	53.3	15	2	US-08-752-852A-34	Sequence 34, Appl	647	16	53.3	17	1	US-08-071-811A-5	Sequence 5, Appl
575	16	53.3	15	2	US-08-752-852A-199	Sequence 199, Appl	648	16	53.3	17	1	US-08-071-811A-4	Sequence 4, Appl
576	16	53.3	15	2	US-08-752-852A-200	Sequence 200, Appl	649	16	53.3	17	1	US-08-370-567-11	Sequence 11, Appl
577	16	53.3	15	2	US-08-752-852A-202	Sequence 202, Appl	650	16	53.3	17	1	US-08-438-759-11	Sequence 11, Appl
578	16	53.3	15	2	US-08-752-852A-203	Sequence 203, Appl	651	16	53.3	17	1	US-08-213-124-9	Sequence 9, Appl
579	16	53.3	15	2	US-08-752-852A-213	Sequence 213, Appl	652	16	53.3	17	1	US-08-183-331-91	Sequence 91, Appl
580	16	53.3	15	4	PCT-US92-06185-54	Sequence 54, Appl	653	16	53.3	17	1	US-08-538-911-17	Sequence 17, Appl
581	16	53.3	15	4	PCT-US92-10983-62	Sequence 62, Appl	654	16	53.3	17	2	US-08-480-190-62	Sequence 62, Appl
582	16	53.3	15	4	PCT-US93-01112-6	Sequence 6, Appl	655	16	53.3	17	2	US-08-661-479-20	Sequence 20, Appl
583	16	53.3	15	4	PCT-US93-01112-12	Sequence 12, Appl	656	16	53.3	17	2	US-08-471-939-91	Sequence 91, Appl
584	16	53.3	15	4	PCT-US93-06751-2	Sequence 2, Appl	657	16	53.3	17	2	US-08-471-800-91	Sequence 91, Appl
585	16	53.3	15	4	PCT-US93-06751-5	Sequence 5, Appl	658	16	53.3	17	2	US-08-518-967-5	Sequence 5, Appl
586	16	53.3	15	4	PCT-US93-06751-10	Sequence 10, Appl	659	16	53.3	17	2	US-08-488-379-62	Sequence 62, Appl
587	16	53.3	15	4	PCT-US93-06751-19	Sequence 19, Appl	660	16	53.3	17	2	US-08-471-068-91	Sequence 91, Appl
588	16	53.3	15	4	PCT-US93-06751-28	Sequence 28, Appl	661	16	53.3	17	2	US-08-595-868C-25	Sequence 25, Appl
589	16	53.3	15	4	PCT-US93-06751-53	Sequence 53, Appl	662	16	53.3	17	2	US-08-985-234-2	Sequence 2, Appl
590	16	53.3	15	4	PCT-US93-06751-111	Sequence 111, Appl	663	16	53.3	17	2	US-08-310-912A-77	Sequence 77, Appl
591	16	53.3	15	4	PCT-US93-06751-121	Sequence 121, Appl	664	16	53.3	17	2	US-08-752-852A-138	Sequence 138, Appl
592	16	53.3	15	4	PCT-US93-07545-2	Sequence 2, Appl	665	16	53.3	17	2	US-08-752-852A-141	Sequence 141, Appl
593	16	53.3	15	4	PCT-US94-02465-72	Sequence 72, Appl	666	16	53.3	17	2	US-08-752-852A-142	Sequence 142, Appl
594	16	53.3	15	4	PCT-US94-04361-4	Sequence 4, Appl	667	16	53.3	17	4	PCT-US92-10770-22	Sequence 22, Appl
595	16	53.3	15	4	PCT-US95-00498-72	Sequence 72, Appl	668	16	53.3	17	4	PCT-US93-07545-62	Sequence 62, Appl
596	16	53.3	15	4	PCT-US95-00498-223	Sequence 223, Appl	669	16	53.3	17	4	PCT-US94-05591-17	Sequence 17, Appl
597	16	53.3	15	4	PCT-US95-00656-72	Sequence 72, Appl	670	16	53.3	17	4	PCT-US94-05884-11	Sequence 11, Appl
598	16	53.3	15	4	PCT-US95-00656-223	Sequence 223, Appl	671	16	53.3	17	4	PCT-US94-06192-1	Sequence 1, Appl
599	16	53.3	15	5	5227466-4	Patent No. 5227466	672	16	53.3	17	4	PCT-US95-04570-77	Sequence 77, Appl
600	16	53.3	15	5	5460961-9	Patent No. 5460961	673	16	53.3	17	4	PCT-US95-04589-77	Sequence 77, Appl
601	16	53.3	16	1	US-08-218-025A-4	Sequence 4, Appl	674	16	53.3	18	1	US-07-876-883-11	Sequence 11, Appl
602	16	53.3	16	1	US-08-318-200-14	Sequence 14, Appl	675	16	53.3	18	1	US-07-876-883-12	Sequence 12, Appl
603	16	53.3	16	1	US-08-433-454-5	Sequence 5, Appl	676	16	53.3	18	1	US-07-876-883-13	Sequence 13, Appl
604	16	53.3	16	1	US-08-333-565-26	Sequence 26, Appl	677	16	53.3	18	1	US-08-204-487-4	Sequence 4, Appl
605	16	53.3	16	1	US-08-432-694-20	Sequence 20, Appl	678	16	53.3	18	1	US-07-856-036B-18	Sequence 18, Appl
606	16	53.3	16	1	US-08-241-054-108	Sequence 108, Appl	679	16	53.3	18	1	US-08-478-312-12	Sequence 12, Appl
607	16	53.3	16	1	US-08-390-156A-91	Sequence 91, Appl	680	16	53.3	18	1	US-08-478-312-34	Sequence 34, Appl
608	16	53.3	16	1	US-08-300-386A-43	Sequence 43, Appl	681	16	53.3	18	1	US-08-478-312-36	Sequence 36, Appl
609	16	53.3	16	1	US-08-300-386A-44	Sequence 44, Appl	682	16	53.3	18	1	US-08-478-312-40	Sequence 40, Appl
610	16	53.3	16	1	US-08-077-797A-3	Sequence 3, Appl	683	16	53.3	18	1	US-08-478-312-48	Sequence 48, Appl
611	16	53.3	16	1	US-08-077-797A-15	Sequence 15, Appl	684	16	53.3	18	1	US-08-485-302-12	Sequence 12, Appl
612	16	53.3	16	1	US-08-077-797A-49	Sequence 49, Appl	685	16	53.3	18	1	US-08-485-302-34	Sequence 34, Appl
613	16	53.3	16	1	US-08-222-851-6	Sequence 6, Appl	686	16	53.3	18	1	US-08-485-302-35	Sequence 35, Appl

687	16	53.3	18	1	US-08-485-302-40	Sequence 40, Appl	760	16	53.3	20	1	US-08-440-861-56	Sequence 56, Appl
688	16	53.3	18	1	US-08-485-302-48	Sequence 48, Appl	761	16	53.3	20	1	US-08-786-748A-97	Sequence 97, Appl
689	16	53.3	18	1	US-08-426-550-11	Sequence 11, Appl	762	16	53.3	20	1	US-08-786-748A-105	Sequence 105, App
690	16	53.3	18	1	US-08-426-550-12	Sequence 12, Appl	763	16	53.3	20	1	US-08-439-817-57	Sequence 57, Appl
691	16	53.3	18	1	US-08-426-550-13	Sequence 13, Appl	764	16	53.3	20	1	US-08-439-817-56	Sequence 66, Appl
692	16	53.3	18	1	US-07-965-667A-15	Sequence 15, Appl	765	16	53.3	20	1	US-08-399-696-107	Sequence 107, App
693	16	53.3	18	1	US-08-487-568-40	Sequence 40, Appl	766	16	53.3	20	1	US-08-399-696-112	Sequence 112, App
694	16	53.3	18	1	US-08-787-547-7	Sequence 7, Appl1	767	16	53.3	20	1	US-08-484-635-130	Sequence 130, App
695	16	53.3	18	2	US-08-480-190-61	Sequence 1, Appl1	768	16	53.3	20	1	US-08-485-508-77	Sequence 77, Appl
696	16	53.3	18	2	US-08-480-190-61	Sequence 61, Appl	769	16	53.3	20	1	US-08-485-508-86	Sequence 86, Appl
697	16	53.3	18	2	US-08-764-640-154	Sequence 154, App	770	16	53.3	20	1	US-08-381-984-22	Sequence 22, Appl
698	16	53.3	18	2	US-08-637-759B-34	Sequence 54, Appl	771	16	53.3	20	1	US-08-381-984-23	Sequence 23, Appl
699	16	53.3	18	2	US-08-488-379-1	Sequence 1, Appl1	772	16	53.3	20	1	US-08-483-926A-6	Sequence 6, Appl1
700	16	53.3	18	2	US-08-488-379-61	Sequence 61, Appl	773	16	53.3	20	2	US-08-480-190-207	Sequence 207, App
701	16	53.3	18	2	US-08-685-589A-211	Sequence 211, App	774	16	53.3	20	2	US-08-854-768-6	Sequence 6, Appl1
702	16	53.3	18	2	US-08-685-589A-214	Sequence 214, App	775	16	53.3	20	2	US-08-484-631-130	Sequence 130, App
703	16	53.3	18	2	US-08-685-589A-215	Sequence 215, App	776	16	53.3	20	2	US-08-621-803-120	Sequence 120, App
704	16	53.3	18	2	US-08-685-589A-230	Sequence 230, App	777	16	53.3	20	2	US-08-485-445A-159	Sequence 159, App
705	16	53.3	18	2	US-08-709-004B-3	Sequence 3, Appl1	778	16	53.3	20	2	US-08-485-445A-160	Sequence 160, App
706	16	53.3	18	2	US-08-709-004B-4	Sequence 4, Appl1	779	16	53.3	20	2	US-08-749-852-53	Sequence 53, Appl
707	16	53.3	18	2	US-09-017-205-21	Sequence 21, Appl	780	16	53.3	20	2	US-08-749-852-55	Sequence 55, Appl
708	16	53.3	18	2	US-09-017-205-65	Sequence 65, Appl	781	16	53.3	20	2	US-08-637-759B-112	Sequence 112, App
709	16	53.3	18	2	US-09-017-205-66	Sequence 66, Appl	782	16	53.3	20	2	US-08-488-379-207	Sequence 207, App
710	16	53.3	18	2	US-08-031-538-37	Sequence 37, Appl	783	16	53.3	20	2	US-08-617-929-3	Sequence 3, Appl1
711	16	53.3	18	2	US-08-752-852A-85	Sequence 85, Appl	784	16	53.3	20	2	US-08-466-975A-17	Sequence 17, Appl
712	16	53.3	18	2	US-08-752-852A-86	Sequence 86, Appl	785	16	53.3	20	2	US-08-238-821B-48	Sequence 48, Appl
713	16	53.3	18	2	US-08-752-852A-135	Sequence 135, App	786	16	53.3	20	2	US-08-954-724-8	Sequence 8, Appl1
714	16	53.3	18	2	US-08-752-852A-136	Sequence 136, App	787	16	53.3	20	2	US-08-954-724-9	Sequence 9, Appl1
715	16	53.3	18	2	US-08-752-852A-137	Sequence 137, App	788	16	53.3	20	2	US-08-954-724-12	Sequence 12, Appl
716	16	53.3	18	2	US-08-752-852A-139	Sequence 139, App	789	16	53.3	20	2	US-08-954-724-13	Sequence 13, Appl
717	16	53.3	18	2	US-08-752-852A-140	Sequence 140, App	790	16	53.3	20	2	US-08-391-671A-17	Sequence 17, Appl
718	16	53.3	18	2	US-08-752-852A-143	Sequence 143, App	791	16	53.3	20	2	US-08-845-926-17	Sequence 17, Appl
719	16	53.3	18	2	US-08-752-852A-144	Sequence 144, App	792	16	53.3	20	2	US-08-845-926-18	Sequence 18, Appl
720	16	53.3	18	2	US-08-752-852A-235	Sequence 235, App	793	16	53.3	20	2	US-08-845-926-19	Sequence 19, Appl
721	16	53.3	18	2	US-08-889-291-7	Sequence 7, Appl1	794	16	53.3	20	2	US-08-845-926-22	Sequence 22, Appl
722	16	53.3	18	4	PCT-US93-07545-1	Sequence 1, Appl1	795	16	53.3	20	2	US-08-932-682-97	Sequence 97, Appl
723	16	53.3	18	4	PCT-US93-07545-61	Sequence 61, Appl	796	16	53.3	20	2	US-08-932-682-105	Sequence 105, App
724	16	53.3	18	4	PCT-US93-10197-15	Sequence 15, Appl	797	16	53.3	20	2	US-08-965-947-8	Sequence 8, Appl1
725	16	53.3	18	5	5258287-46	Patent No. 5258287	798	16	53.3	20	2	US-08-965-947-9	Sequence 9, Appl1
726	16	53.3	18	5	5258287-52	Patent No. 5258287	799	16	53.3	20	2	US-08-965-947-12	Sequence 12, Appl
727	16	53.3	19	1	US-07-654-839-2	Sequence 2, Appl1	800	16	53.3	20	2	US-08-965-947-13	Sequence 13, Appl
728	16	53.3	19	1	US-08-290-448A-16	Sequence 16, Appl	801	16	53.3	20	2	US-08-965-947-13	Sequence 13, Appl
729	16	53.3	19	1	US-08-290-448A-16	Sequence 16, Appl	802	16	53.3	20	2	US-08-031-538-40	Sequence 40, Appl
730	16	53.3	19	1	US-08-222-851-5	Sequence 5, Appl1	803	16	53.3	20	2	US-08-737-045-6	Sequence 6, Appl1
731	16	53.3	19	1	US-08-175-069A-16	Sequence 16, Appl	804	16	53.3	20	3	US-08-827-570-130	Sequence 130, App
732	16	53.3	19	2	US-08-764-640-158	Sequence 158, App	805	16	53.3	20	4	PCT-US93-07545-207	Sequence 207, App
733	16	53.3	19	2	US-08-764-640-164	Sequence 164, App	806	16	53.3	20	4	PCT-US95-00498-159	Sequence 159, App
734	16	53.3	19	2	US-08-729-152-15	Sequence 15, Appl	807	16	53.3	20	4	PCT-US95-00556-159	Sequence 159, App
735	16	53.3	19	2	US-08-729-152-26	Sequence 26, Appl	808	16	53.3	20	4	PCT-US95-05744-48	Sequence 48, Appl
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737	16	53.3	19	5	5258287-47	Patent No. 5258287	810	16	53.3	20	4	PCT-US95-09307-12	Sequence 12, Appl
738	16	53.3	20	1	US-07-755-161A-1	Sequence 1, Appl1	811	16	50.0	5	1	US-07-657-769B-19	Sequence 19, Appl
739	16	53.3	20	1	US-07-755-161A-2	Sequence 2, Appl1	812	15	50.0	5	1	US-07-657-769B-22	Sequence 22, Appl
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741	16	53.3	20	1	US-07-891-174-2	Sequence 2, Appl1	814	15	50.0	6	1	US-08-338-890B-5	Sequence 5, Appl1
742	16	53.3	20	1	US-08-311-611A-159	Sequence 159, App	815	15	50.0	6	2	US-08-340-208B-4	Sequence 4, Appl1
743	16	53.3	20	1	US-08-204-487-2	Sequence 2, Appl1	816	15	50.0	6	2	US-08-340-208B-5	Sequence 5, Appl1
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752	16	53.3	20	1	US-08-306-473A-159	Sequence 159, App	825	15	50.0	13	4	PCT-US93-09626-35	Sequence 35, Appl
753	16	53.3	20	1	US-08-256-771-22	Sequence 22, Appl	826	15	50.0	14	1	US-08-173-510B-71	Sequence 71, Appl
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837	15	50.0	15	4	US-08-292-345B-10	Sequence 28, Appl	910	14	46.7	9	1	US-08-082-847-32	Sequence 32, Appl
838	15	50.0	15	4	US-08-292-345B-10	Sequence 29, Appl	911	14	46.7	9	1	US-08-082-847-33	Sequence 33, Appl
839	15	50.0	15	4	US-08-292-345B-10	Sequence 22, Appl	912	14	46.7	9	1	US-08-082-847-34	Sequence 34, Appl
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842	15	50.0	15	4	US-08-292-345B-10	Sequence 22, Appl	915	14	46.7	9	1	US-08-082-847-37	Sequence 37, Appl
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844	15	50.0	15	4	US-08-292-345B-10	Sequence 22, Appl	917	14	46.7	9	1	US-08-687-226-66	Sequence 66, Appl
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866	15	50.0	15	5	US-08-484-530-11	Sequence 11, Appl	939	14	46.7	12	2	US-08-406-330-45	Sequence 45, Appl
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873	15	50.0	15	5	US-08-827-618A-48	Sequence 48, Appl	946	14	46.7	13	2	US-09-207-621-66	Sequence 66, Appl
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899	14	46.7	14	6	US-08-082-847-29	Sequence 29, Appl	972	14	46.7	15	1	US-08-473-344-47	Sequence 47, Appl
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987 14 46.7 17 1 US-08-190-788A-169 Sequence 169, App
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989 14 46.7 17 1 US-08-465-391A-169 Sequence 169, App
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992 14 46.7 17 2 US-08-463-076E-222 Sequence 222, App
993 14 46.7 18 1 US-07-830-330-11 Sequence 11, Appl
994 14 46.7 18 1 US-07-789-184-212 Sequence 212, App
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ALIGNMENTS

RESULT 1
US-08-406-330-4
; Sequence 4, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-5

Query Match 90.0%; Score 27; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 4 WRYSEY 9
RESULT 3
US-08-556-597-4
; Sequence 4, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York

COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-4

Query Match 90.0%; Score 27; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 4
US-08-556-597-5
Sequence 5, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
HUMAN PLATELET GLYCOPROTEIN Ib/IX
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101

TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-5

Query Match 90.0%; Score 27; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 5
US-08-406-330-38
Sequence 38, Application US/08406330
Patent No. 5817748
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
HUMAN PLATELET GLYCOPROTEIN Ib/IX
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-38

Query Match 86.7%; Score 26; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 9.9e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
|| ||
Db 3 WRYSEY 8

RESULT 6
US-08-556-597-38
; Sequence 38, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556.597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-556-597-38

Query Match 86.7%; Score 26; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 9.9e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WRXXEY 6
|| ||
Db 3 WRYREY 8

RESULT 7
US-08-406-330-1
; Sequence 1, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406.330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-406-330-1

Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 WRXXEY 6
|| ||
Db 4 WRYREY 9

RESULT 8
US-08-406-330-3
; Sequence 3, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406.330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-3

Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
|| ||
Db 4 WRVEY 9

RESULT 9
US-08-406-330-6
; Sequence 6, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-6

Query Match 85.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
|| ||
Db 1 WRQREY 6

RESULT 10
US-08-556-597-1
; Sequence 1, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.

; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-1

Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
|| ||
Db 4 WRVEY 9

RESULT 11
US-08-556-597-3
; Sequence 3, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:

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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-556-597-3

Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
Db 4 WRVFEY 9

RESULT 12
US-08-556-597-6
; Sequence 6, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

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US-08-556-597-6

Query Match 86.7%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
Db 1 WRQREY 6

RESULT 13
US-08-406-330-8
; Sequence 8, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-406-330-8

Query Match 83.3%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
Db 5 WRNWEY 10

RESULT 14
US-08-556-597-8
; Sequence 8, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX

```

NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-8

Query Match 83.3%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 5 WRNWEY 10

RESULT 15
US-08-077-797A-42
Sequence 42, Application US/08077797A
Patent No. 5679548
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
APPLICANT: Rosenblum, Jonathan
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE METAL
TITLE OF INVENTION: BINDING SITES AND COMPOSITIONS THEREOF
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5679548th Torrey Pines Road, TPC8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,797A
FILING DATE: 14-JUN-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012,566
FILING DATE: 02-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1276P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
US-08-077-797A-42

Query Match 80.0%; Score 24; DB 1; Length 16;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WRXXEY 6
|| ||
DB 11 WRTMDY 16

Search completed: May 2, 2000, 00:18:30
Job time: 128 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 2, 2000, 00:17:12 ; Search time 13.65 Seconds
(without alignments)

20.734 Million cell updates/sec

Title: US-09-258-947-174

Perfect score: 30

Sequence: 1 WRXVEY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 3999

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

PIR_G2:*
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	63.3	13	2 S04360	lacB protein - Sta
2	18	60.0	15	2 G49655	T-cell-receptor be
3	16	53.3	7	2 S33245	neuromodulatory pe
4	16	53.3	9	2 B57444	neuropeptide Grb-A
5	16	53.3	9	2 C57444	neuropeptide Grb-A
6	16	53.3	11	2 A34662	Achatina cardio-ex
7	16	53.3	11	2 B41946	T-cell receptor ga
8	16	53.3	12	1 A53709	alpha-conotoxin Im
9	16	53.3	12	2 S18362	aspartate transami
10	16	53.3	13	2 S54344	glyceraldehyde-3-p
11	16	53.3	13	2 PC4391	cysteine proteinas
12	16	53.3	14	1 LFEWC	trp operon leader
13	16	53.3	14	1 LFEWC	trp operon leader
14	16	53.3	14	1 LFEWC	trp operon leader
15	16	53.3	14	2 PT0026	calotropin DI - mu
16	16	53.3	14	2 PT0026	karatatin - karata
17	16	53.3	15	2 P00232	cystatin CI-4a - m
18	16	53.3	15	2 PH1762	T-cell receptor al
19	16	53.3	16	2 E37290	homeotic protein G
20	16	53.3	17	2 I49048	trp leader peptide
21	16	53.3	17	2 A29834	integrase homolog
22	16	53.3	17	2 E40442	trp leader peptide
23	16	53.3	18	2 S46418	NT11 protein - cur
24	16	53.3	18	2 I68647	retinoblastoma sus
25	16	53.3	19	2 PC1251	testin II - rat (f
26	16	53.3	19	2 S60110	hypothetical prote
27	16	53.3	19	2 I49037	TCR delta chain V-
28	16	53.3	20	2 S46205	cosmain (EC 3.4.2
29	16	53.3	20	2 S46204	ananain (EC 3.4.22
30	16	53.3	20	2 S39049	Cytotoxin-binding

31	16	53.3	20	2 A40451	dormancy-related p
32	16	53.3	20	2 A44773	pollen allergen I
33	16	53.3	20	2 S78760	ribosomal protein
34	15	50.0	12	2 PH1611	Ig H chain V-D-J r
35	15	50.0	14	2 F49037	TCR delta chain V-
36	15	50.0	19	2 A44854	L-2,4-diaminobuty
37	15	50.0	20	2 C49164	chromogranin-B - r
38	15	50.0	20	2 C56894	intracrystalline c
39	15	50.0	20	2 A56894	intracrystalline c
40	15	50.0	20	2 B56894	intracrystalline c
41	14	46.7	10	2 E49033	T-cell receptor ga
42	14	46.7	17	2 H49048	T-cell receptor be
43	14	46.7	19	2 A60505	hemoglobin beta ch
44	14	46.7	20	2 B60505	hemoglobin beta ch
45	13	43.3	7	2 S33244	neuromodulatory pe
46	13	43.3	7	2 S33246	neuromodulatory pe
47	13	43.3	7	4 I55382	hypothetical pepti
48	13	43.3	10	1 RHLMGS	gonadoliberin - se
49	13	43.3	10	2 S59625	beta-galactosidase
50	13	43.3	10	2 A49187	gonadotropin-relea
51	13	43.3	12	1 OOGM2	urotensin II - lon
52	13	43.3	12	2 S42765	urotensin II - tel
53	13	43.3	12	2 JS0423	urotensin II-A pep
54	13	43.3	12	2 S26541	T-cell receptor be
55	13	43.3	12	2 S69123	proton-translocati
56	13	43.3	12	2 A40763	sucrose-6-phosphat
57	13	43.3	12	2 JS0424	urotensin II-B pep
58	13	43.3	12	2 H41946	T-cell receptor ga
59	13	43.3	13	2 PQ0445	urotensin II - lau
60	13	43.3	13	2 A61514	glutathione transf
61	13	43.3	13	2 PH0138	T-cell receptor be
62	13	43.3	13	2 B56884	dipeptidyl-peptida
63	13	43.3	14	1 QMVHXX	mastoparan X - hor
64	13	43.3	14	1 QMWAPP	polistes mastopara
65	13	43.3	14	2 C60414	somatostatin - sli
66	13	43.3	14	2 B60842	somatostatin I - c
67	13	43.3	14	2 A60622	somatostatin - spo
68	13	43.3	14	2 A60840	somatostatin I - E
69	13	43.3	14	2 S00172	somatostatin I - s
70	13	43.3	14	2 PH0135	T-cell receptor be
71	13	43.3	14	2 JH0328	probursin tetrade
72	13	43.3	15	2 S21241	oligo-1,6-glucosid
73	13	43.3	15	2 S21240	alpha-glucosidase
74	13	43.3	15	2 S21202	glucan 1,4-alpha-g
75	13	43.3	16	2 A29541	little gastrin - C
76	13	43.3	16	2 S22040	cob protein - comm
77	13	43.3	17	2 A60071	gastrin - rhesus m
78	13	43.3	17	2 B44923	carboxypeptidase 3
79	13	43.3	18	2 A31817	fasciclin I - Amer
80	13	43.3	18	2 S27141	hypothetical prote
81	13	43.3	18	2 A40256	interleukin-7 rece
82	13	43.3	19	2 G49048	T-cell receptor be
83	13	43.3	19	2 B61409	genome polypeptin
84	13	43.3	20	2 PC2347	base nonspecific a
85	13	43.3	20	2 C54052	phosphoribosyl-NMP
86	13	43.3	20	2 S16202	pyrroline-5-carbox
87	13	43.3	20	2 D37396	pollen allergen Fe
88	13	43.3	20	2 D25507	proteinase inhibit
89	13	43.3	20	2 S74101	alkaline phosphata
90	13	43.3	20	2 PC2248	lambda 112 protein
91	13	43.3	20	2 A61506	alpha-1-antitrypsi
92	12	40.0	5	2 B37325	pap fibribial regul
93	12	40.0	7	2 A38081	amine oxidase (cop
94	12	40.0	7	2 I48293	transforming prote
95	12	40.0	8	2 S16324	hypothetical prote
96	12	40.0	9	1 AKLOIM	lacustamycininhibi
97	12	40.0	9	2 S70332	endosperm protein,
98	12	40.0	9	2 S70345	amine oxidase (cop
99	12	40.0	9	2 A57444	neuropeptide Grb-A
100	12	40.0	9	2 S07241	litorin - Rohde's
101	12	40.0	9	2 A61357	phyllacaerulein -
102	12	40.0	9	2 PH0108	late gl-69 protein
103	12	40.0	10	1 RHAQ2	gonadoliberin II -

104 12 40.0 10 1 A61126 gonadoliberin - sp
105 12 40.0 10 2 S30348 clotting protein -
106 12 40.0 10 2 B46030 gonadoliberin II -
107 12 40.0 10 2 A43405 6-phosphofructo-2-
108 12 40.0 10 2 P40916 T-cell receptor be
109 12 40.0 11 2 A58838 hemolysin - Porphy
110 12 40.0 11 2 S41747 chaperonin 10 homo
111 12 40.0 11 2 A38590 transforming prote
112 12 40.0 11 2 P41375 T antigen variant
113 12 40.0 11 3 P00731 Unidentified 5.7/3
114 12 40.0 12 2 A29169 phospholipase A2 (
115 12 40.0 12 2 C49215 urease (EC 3.5.1.5
116 12 40.0 12 2 S6557 T-cell receptor be
117 12 40.0 12 2 S26553 T-cell receptor be
118 12 40.0 12 2 S70344 amine oxidase (cop
119 12 40.0 12 2 I54259 L-lactate dehydrog
120 12 40.0 12 2 P40663 dystrophin-ascia
121 12 40.0 12 2 P40746 T-cell receptor be
122 12 40.0 12 2 P41470 T-cell receptor be
123 12 40.0 12 2 S33168 z protein - guinea
124 12 40.0 13 2 S39413 tubulin beta chain
125 12 40.0 13 2 S4316 photosystem I 9K c
126 12 40.0 13 2 S60046 early nodulin 40 -
127 12 40.0 13 2 A33660 osteoclast functio
128 12 40.0 13 2 P70293 Ig heavy chain CRD
129 12 40.0 13 2 S75567 T cell receptor V-
130 12 40.0 13 2 S47373 T-cell antigen rec
131 12 40.0 13 2 P41595 Ig H chain V-D-J r
132 12 40.0 13 2 P40928 T-cell receptor be
133 12 40.0 14 2 P40142 carbon-monoxide de
134 12 40.0 14 2 A61306 ribonuclease M (EC
135 12 40.0 14 2 S23369 T-cell receptor al
136 12 40.0 14 2 S29878 Na+/K+-exchanging
137 12 40.0 14 2 S68095 calcium-binding pr
138 12 40.0 15 2 B6997 unspecific monooxy
139 12 40.0 15 2 P40175 styral glycoprotei
140 12 40.0 15 2 P00174 styral glycoprotei
141 12 40.0 15 2 P00195 Sfll-glycoprotein
142 12 40.0 15 2 I52734 gene c-Ki-ras prot
143 12 40.0 15 2 A61266 glucuronosyltransf
144 12 40.0 15 2 A35389 urease (EC 3.5.1.5
145 12 40.0 15 2 A60763 endo-1,3-beta-gluc
146 12 40.0 15 2 S36893 ribosomal protein
147 12 40.0 15 2 P40018 photosystem I 9K p
148 12 40.0 15 2 P00192 styral glycoprotei
149 12 40.0 15 2 P40185 27K protein A 3.4/
150 12 40.0 15 2 PC4269 unidentified QR310
151 12 40.0 15 2 S28981 tubulin alpha-4 ch
152 12 40.0 15 2 A54397 ubiquitin-carrier
153 12 40.0 15 2 I65478 c-Ki-ras - hamster
154 12 40.0 15 2 E49037 TCR delta chain V-
155 12 40.0 16 2 E41425 cytochrome P450 1F
156 12 40.0 16 2 P40048 protein QA100047 -
157 12 40.0 16 2 P70237 Ig heavy chain CDR
158 12 40.0 16 2 P70296 Ig heavy chain CDR
159 12 40.0 16 2 P41302 Ig heavy chain DJ
160 12 40.0 16 2 A45133 casein kinase II (
161 12 40.0 16 2 P41604 Ig H chain V-D-J r
162 12 40.0 16 2 A48839 T-cell receptor al
163 12 40.0 16 2 D49037 TCR delta chain V-
164 12 40.0 17 2 B28027 protein P4 - curle
165 12 40.0 17 2 P70234 Ig heavy chain CRD
166 12 40.0 17 2 P40794 T-cell receptor al
167 12 40.0 17 2 A61019 17K basolateral pl
168 12 40.0 17 2 A45592 lactase-phlorizin
169 12 40.0 17 2 B48943 phage antigenic de
170 12 40.0 17 2 P40005 very-high-density
171 12 40.0 18 2 B49215 urease (EC 3.5.1.5
172 12 40.0 18 2 P41368 Ig heavy chain DJ
173 12 40.0 18 2 PS0211 L-ascorbate peroxi
174 12 40.0 18 2 S54272 CTC 75 protein - h
175 12 40.0 18 2 S23379 sorbitol dehydroge
176 12 40.0 18 2 P41621 Ig H chain V-D-J r

177 12 40.0 18 2 S48862 murine cyclin H -
178 12 40.0 18 3 P00736 Acetolactate synth
179 12 40.0 19 2 S56049 kidney stone prote
180 12 40.0 19 2 C71871 glutathione transf
181 12 40.0 19 2 C32735 thyroglobulin - pi
182 12 40.0 19 2 B32735 thyroglobulin - sh
183 12 40.0 19 2 C48363 2-hydroxyglutaryl-
184 12 40.0 19 2 P40062 beta-galactoside-b
185 12 40.0 19 2 S57558 T cell receptor V-
186 12 40.0 19 2 A53875 creatine kinase (E
187 12 40.0 20 2 P40110 style glycoprotein
188 12 40.0 20 2 S33787 pancreatic elastas
189 12 40.0 20 2 B61333 chymotrypsin (EC 3
190 12 40.0 20 2 S32502 calpain (EC 3.4.22
191 12 40.0 20 2 P40133 pepsin (EC 3.4.23.
192 12 40.0 20 2 D49215 urease (EC 3.5.1.5
193 12 40.0 20 2 D49164 chromogranin-B r
194 12 40.0 20 2 I79432 MHC class II histo
195 12 40.0 20 2 B33761 actin - Acanthamo
196 12 40.0 20 2 A31049 calsequestrin, fas
197 12 40.0 20 2 A42934 heat shock protein
198 12 40.0 20 2 S03335 photosystem II pho
199 12 40.0 20 2 P40046 citrate (sl)-synth
200 12 40.0 20 2 S65605 dimeric protein (B
201 12 40.0 20 2 S43627 cytochrome-c oxida
202 12 40.0 20 2 P40459 basic eosinophil p
203 12 40.0 20 2 S56756 link protein - rat
204 12 40.0 3 2 F37196 bradykinin-potenti
205 11 36.7 4 2 A34626 RPKH-related neuro
206 11 36.7 4 2 S68059 low molecularweig
207 11 36.7 4 2 B53284 T-cell receptor be
208 11 36.7 4 2 P40661 T-cell receptor be
209 11 36.7 5 2 A60803 neuropeptide - sea
210 11 36.7 5 2 JH0253 gut pentapeptide -
211 11 36.7 5 2 G37196 bradykinin-potenti
212 11 36.7 5 2 P40281 Ig heavy chain CRD
213 11 36.7 5 2 P40308 Ig heavy chain CRD
214 11 36.7 5 2 A32516 cholecystokinin-5
215 11 36.7 5 2 P40729 T-cell receptor be
216 11 36.7 5 2 P40580 T-cell receptor be
217 11 36.7 6 2 S66195 alcohol dehydrogen
218 11 36.7 6 2 B48395 dnaA protein - Pse
219 11 36.7 6 2 A31263 dihydrofolate redu
220 11 36.7 6 2 B31263 dihydrofolate redu
221 11 36.7 6 2 P40028 pev-kinin 2 - pena
222 11 36.7 6 2 A61068 locusfakinin - mig
223 11 36.7 6 2 I79584 gene TCRD protein
224 11 36.7 6 2 B35640 cerebellar degener
225 11 36.7 6 2 P40629 T-cell receptor be
226 11 36.7 6 2 P40532 T-cell receptor be
227 11 36.7 6 2 P40519 T-cell receptor be
228 11 36.7 6 2 P40637 T-cell receptor be
229 11 36.7 6 2 P40641 T-cell receptor be
230 11 36.7 6 2 P40726 T-cell receptor be
231 11 36.7 6 2 F41946 T-cell receptor ga
232 11 36.7 7 2 A58512 venom heptapeptide
233 11 36.7 7 2 S57274 triacylglycerol li
234 11 36.7 7 2 S09652 hypothetical prote
235 11 36.7 7 2 P40649 alpha-dextrin endo
236 11 36.7 7 2 P40029 pev-kinin 1 - pena
237 11 36.7 7 2 S33567 tubulin beta-3 cha
238 11 36.7 7 2 S21230 dermorphin (trip(4)
239 11 36.7 7 2 A61081 typtophyllin, basi
240 11 36.7 7 2 E48394 glycoprotein compo
241 11 36.7 7 2 P41602 Ig H chain V-D-J r
242 11 36.7 7 2 P40526 T-cell receptor be
243 11 36.7 7 2 P40628 T-cell receptor be
244 11 36.7 7 2 P40642 T-cell receptor be
245 11 36.7 7 2 P40722 T-cell receptor be
246 11 36.7 7 2 P40688 T-cell receptor be
247 11 36.7 7 2 P40586 T-cell receptor be
248 11 36.7 7 2 P40728 T-cell receptor be
249 11 36.7 7 2 P40008 glucuronosyltransf

250	11	36.7	7	2	B48394	major fat-globule	323	11	36.7	10	2	S09138	hypertrehalosemic
251	11	36.7	7	3	PQ0727	H2 class I protein	324	11	36.7	10	2	A31571	hypertrehalosemic/
252	11	36.7	7	4	A58725	virotoxin - gastro	325	11	36.7	10	2	B33995	hypotrehalosemic h
253	11	36.7	8	2	A61348	red pigment-concen	326	11	36.7	10	2	A60647	neuromedin C - bov
254	11	36.7	8	2	A28004	adipokinetiC hormo	327	11	36.7	10	2	A61337	caerulein - frog (
255	11	36.7	8	2	S08995	hypertrehalosemic	328	11	36.7	10	2	C39191	hypothetical prote
256	11	36.7	8	2	S08996	hypertrehalosemic	329	11	36.7	10	2	A40753	aldehyde ferredoxi
257	11	36.7	8	2	S10596	hypertrehalosemic	330	11	36.7	10	2	A40753	processing enzyme,
258	11	36.7	8	2	A48823	adipokinetiC hormo	331	11	36.7	10	2	A27617	triose-phosphate i
259	11	36.7	8	2	B49823	adipokinetiC hormo	332	11	36.7	10	2	PQ0753	beta-fructofuranos
260	11	36.7	8	2	A44960	neuropeptide Led-C	333	11	36.7	10	2	S63696	DNA polymerase - y
261	11	36.7	8	2	B44960	neuropeptide Led-C	334	11	36.7	10	2	A46030	gonadoliberin I -
262	11	36.7	8	2	S15422	adipokinetiC hormo	335	11	36.7	10	2	A21114	gonadoliberin - ch
263	11	36.7	8	2	A43976	hypertrehalosemic	336	11	36.7	10	2	S39030	lysyl-bradykinin -
264	11	36.7	8	2	B43976	hypertrehalosemic	337	11	36.7	10	2	PQ0177	neuromedin C - lau
265	11	36.7	8	2	A33995	adipokinetiC hormo	338	11	36.7	10	2	A13687	caerulein-like pep
266	11	36.7	8	2	S11545	adipokinetiC hormo	339	11	36.7	10	2	B37196	bradykinin-potentl
267	11	36.7	8	2	S55310	adipokinetiC hormo	340	11	36.7	10	2	H37196	bradykinin-potentl
268	11	36.7	8	2	A58641	adipokinetiC hormo	341	11	36.7	10	2	A35555	hypothetical prote
269	11	36.7	8	2	A58620	adipokinetiC hormo	342	11	36.7	10	2	PT0245	Ig heavy chain CRD
270	11	36.7	8	2	PQ0012	cholecystokinin -	343	11	36.7	10	2	PT0289	Ig heavy chain CRD
271	11	36.7	8	2	A43001	cholecystokinin -	344	11	36.7	10	2	PT0310	Ig heavy chain CRD
272	11	36.7	8	2	S19288	acylase - Klyuvera	345	11	36.7	10	2	PT0322	Ig heavy chain CRD
273	11	36.7	8	2	A39308	glycine reductase	346	11	36.7	10	2	PH1344	Ig heavy chain DJ
274	11	36.7	8	2	C61512	variant surface gl	347	11	36.7	10	2	S23370	T-cell receptor al
275	11	36.7	8	2	D61512	variant surface gl	348	11	36.7	10	2	F49033	T-cell receptor ga
276	11	36.7	8	2	A05169	neuropeptide M-I -	349	11	36.7	10	2	F33932	Ig mu chain J regi
277	11	36.7	8	2	JS0315	leucokinin V - Ma	350	11	36.7	10	2	E41946	T-cell receptor ga
278	11	36.7	8	2	JS0316	leucokinin VI - Ma	351	11	36.7	10	2	A1946	T-cell receptor ga
279	11	36.7	8	2	JS0317	leucokinin VII - M	352	11	36.7	10	2	B38887	T-cell receptor ga
280	11	36.7	8	2	JS0318	leucokinin VIII -	353	11	36.7	10	2	PH0923	T-cell receptor be
281	11	36.7	8	2	S21663	neuropeptide - flo	354	11	36.7	10	2	T13976	cytochrome c oxida
282	11	36.7	8	2	A35065	clonin - sea squir	355	11	36.7	10	2	T12303	cytochrome c oxida
283	11	36.7	8	2	A31570	angiotensin-conver	356	11	36.7	10	2	T14019	cytochrome c oxida
284	11	36.7	8	2	A41117	acetylcholinestera	357	11	36.7	10	2	T14019	cytochrome c oxida
285	11	36.7	8	2	PT0724	T-cell receptor be	358	11	36.7	10	2	T14043	cytochrome c oxida
286	11	36.7	8	2	A38887	T-cell receptor ga	359	11	36.7	10	2	T14054	cytochrome c oxida
287	11	36.7	8	2	T13818	cytochrome oxidase	360	11	36.7	10	2	T12308	cytochrome c oxida
288	11	36.7	9	1	QDRB	delta sleep-induci	361	11	36.7	10	2	T12312	cytochrome c oxida
289	11	36.7	9	2	A24244	adipokinetiC hormo	362	11	36.7	10	2	T12329	cytochrome c oxida
290	11	36.7	9	2	I55386	lysosome-associate	363	11	36.7	10	2	T12316	cytochrome c oxida
291	11	36.7	9	2	A43848	cell surface adhes	364	11	36.7	10	2	T14212	cytochrome c oxida
292	11	36.7	9	2	D57444	neuropeptide Grb-A	365	11	36.7	10	2	T12321	cytochrome c oxida
293	11	36.7	9	2	A60522	sperm-activating p	366	11	36.7	10	2	T14215	cytochrome c oxida
294	11	36.7	9	2	S07205	litorin 2-Glu - Au	367	11	36.7	10	2	T14223	cytochrome c oxida
295	11	36.7	9	2	S07204	litorin I - Austr	368	11	36.7	10	2	T14219	cytochrome c oxida
296	11	36.7	9	2	JS0302	xenopsin-related p	369	11	36.7	10	2	S53789	neuropeptide Pec-H
297	11	36.7	9	2	PT0231	Ig heavy chain CDR	370	11	36.7	11	1	LFTWE	probable trpEG lea
298	11	36.7	9	2	PT0270	Ig heavy chain CRD	371	11	36.7	11	2	S66196	alcohol dehydrogen
299	11	36.7	9	2	PT0272	Ig heavy chain CRD	372	11	36.7	11	2	B49164	chromogranin-B - r
300	11	36.7	9	2	PT0288	Ig heavy chain CRD	373	11	36.7	11	2	S32575	ribosomal protein
301	11	36.7	9	2	PT0299	Ig heavy chain CRD	374	11	36.7	11	2	C53652	rhlR protein - Pse
302	11	36.7	9	2	PT0324	Ig heavy chain CRD	375	11	36.7	11	2	H54346	pyruvate synthase
303	11	36.7	9	2	A37027	macrophage chemota	376	11	36.7	11	2	S70338	napin small chain
304	11	36.7	9	2	I46023	growth hormone rec	377	11	36.7	11	2	JQ2307	hypothetical 1.5K
305	11	36.7	9	2	PT0634	T-cell receptor be	378	11	36.7	11	2	JQ2317	hypothetical 1.5K
306	11	36.7	9	2	PT0562	T-cell receptor be	379	11	36.7	11	2	S45698	gamma-MSH-like pro
307	11	36.7	9	2	I58350	gene c-mpl protein	380	11	36.7	11	2	S05002	corazonin - Americ
308	11	36.7	9	2	A60320	xenopsin-related p	381	11	36.7	11	2	PT0249	Ig heavy chain CRD
309	11	36.7	9	2	S78426	52.5K protein - Pa	382	11	36.7	11	2	PT0273	Ig heavy chain CRD
310	11	36.7	9	2	S56004	glucan 1,3-beta-gl	383	11	36.7	11	2	PT0302	Ig heavy chain CRD
311	11	36.7	10	1	XAVI68	angiotensin-conver	384	11	36.7	11	2	PH1343	Ig heavy chain DJ
312	11	36.7	10	1	XASNPC	angiotensin-conver	385	11	36.7	11	2	S68649	spermathecin AQN-3
313	11	36.7	10	1	RHPGG	gonadoliberin - pi	386	11	36.7	11	2	A33571	folliculin - bovi
314	11	36.7	10	1	RHSHG	gonadoliberin - sh	387	11	36.7	11	2	A41946	T-cell receptor ga
315	11	36.7	10	1	RHAQ1	gonadoliberin I'-	388	11	36.7	11	2	C38887	T-cell receptor ga
316	11	36.7	10	2	S71868	glutathione transf	389	11	36.7	11	2	I41946	T-cell receptor ga
317	11	36.7	10	2	JC1367	thyroliberin poten	390	11	36.7	11	2	A49037	T-cell receptor ga
318	11	36.7	10	2	A60421	hypertrehalosemic	391	11	36.7	11	2	B49037	TcR gamma V-J regl
319	11	36.7	10	2	S08997	hypertrehalosemic	392	11	36.7	11	2	C49037	TcR gamma V-J regl
320	11	36.7	10	2	S08998	hypertrehalosemic	393	11	36.7	11	2	S21704	asparagine-tRNA 1
321	11	36.7	10	2	A26381	hypertrehalosemic	394	11	36.7	11	2	T12264	cytochrome-c oxida
322	11	36.7	10	2	JC1416	hypertrehalosemic	395	11	36.7	11	2	T12253	cytochrome-c oxida

396	11	36.7	11	2	T12244	cytochrome-c oxida	469	11	36.7	14	2	PH1759	T cell receptor al
397	11	36.7	11	2	T12248	cytochrome-c oxida	470	11	36.7	14	2	PH1766	T cell receptor al
398	11	36.7	11	3	PQ0702	Unidentified 6.7/2	471	11	36.7	14	2	PH1767	T cell receptor al
399	11	36.7	12	2	I64829	gene HEXA protein	472	11	36.7	14	2	PH1768	T cell receptor al
400	11	36.7	12	2	S26548	T-cell receptor be	473	11	36.7	14	2	PH1769	T cell receptor V-
401	11	36.7	12	2	PH1675	Ig heavy chain V r	474	11	36.7	14	2	S57572	spermdhesin AWN h
402	11	36.7	12	2	I41235	glutamine--tRNA l1	475	11	36.7	14	2	S58426	leukotriene B-4 l2
403	11	36.7	12	2	A26093	microbial collagen	476	11	36.7	14	2	A47421	Ig H chain V-D-J r
404	11	36.7	12	2	G64003	hypothetical prote	477	11	36.7	14	2	PH1625	Ig H chain V-D-J r
405	11	36.7	12	2	PQ0776	NADH dehydrogenase	478	11	36.7	14	2	PH1626	Ig H chain V-D-J r
406	11	36.7	12	2	A49637	MHC class II histo	479	11	36.7	14	2	PH1627	Ig H chain V-D-J r
407	11	36.7	12	2	I77529	estrogen receptor	480	11	36.7	14	2	PH1594	Ig H chain V-D-J r
408	11	36.7	12	2	PT0274	Ig heavy chain CRD	481	11	36.7	14	2	PH0801	T-cell receptor al
409	11	36.7	12	2	PH1324	Ig heavy chain DJ	482	11	36.7	14	2	PH0747	T-cell receptor be
410	11	36.7	12	2	PH1308	Ig heavy chain DJ	483	11	36.7	14	2	S39931	S-allole-associate
411	11	36.7	12	2	S43957	Ig mu chain V regi	484	11	36.7	14	3	PC2373	IMP dehydrogenase
412	11	36.7	12	2	S49110	interleukin-10 - h	485	11	36.7	15	2	A26997	unspecific monooxy
413	11	36.7	12	2	S43170	kinesin light chai	486	11	36.7	15	2	S24159	leukocyte elastase
414	11	36.7	12	2	A49033	T-cell receptor de	487	11	36.7	15	2	E49021	Ig heavy chain J8
415	11	36.7	12	2	A19033	T-cell receptor de	488	11	36.7	15	2	PH1319	Ig heavy chain DJ
416	11	36.7	12	2	PN0046	ATP synthase D cha	489	11	36.7	15	2	S30382	Ig heavy chain J r
417	11	36.7	12	2	S25039	Ig heavy chain V r	490	11	36.7	15	2	S26791	Ig heavy chain V r
418	11	36.7	12	2	A42324	cytochrome P450c27	491	11	36.7	15	2	S02381	probable membrane
419	11	36.7	12	2	I58273	thyroglobulin - ra	492	11	36.7	15	2	S39012	proteinase - Therm
420	11	36.7	12	2	I57678	gene rFUP-A protei	493	11	36.7	15	2	PH0216	agarase (EC 3.2.1.1
421	11	36.7	13	1	XAV198	angiotensin-conver	494	11	36.7	15	2	S21411	modulation protein
422	11	36.7	13	1	MTCMAD	melanotropin alpha	495	11	36.7	15	2	S33781	acetylactate synth
423	11	36.7	13	1	MTCMAD	melanotropin alpha	496	11	36.7	15	2	C43334	orf3 3' to andR -
424	11	36.7	13	2	A37196	bradykinin-potenti	497	11	36.7	15	2	B60763	endo-1,3-beta-gluc
425	11	36.7	13	2	PH1676	Ig heavy chain V r	498	11	36.7	15	2	A48372	benzoyl-CoA ligase
426	11	36.7	13	2	A59044	epsilon-conotoxin	499	11	36.7	15	2	T09463	ribosomal protein
427	11	36.7	13	2	I54984	aeg-46.5 protein -	500	11	36.7	15	2	S32450	pol polyprotein -
428	11	36.7	13	2	A60409	bombesin-like pept	501	11	36.7	15	2	PA0036	glycine cleavage s
429	11	36.7	13	2	A60174	tryptophyllin-13 -	502	11	36.7	15	2	S08209	hypothetical prote
430	11	36.7	13	2	A60379	factor X activator	503	11	36.7	15	2	P00750	self-incompatibili
431	11	36.7	13	2	B28810	glutathione transf	504	11	36.7	15	2	B56891	gamma 2 gliadin -
432	11	36.7	13	2	PT0304	Ig heavy chain CRD	505	11	36.7	15	2	PA0099	phenotypic variati
433	11	36.7	13	2	S23372	T-cell receptor al	506	11	36.7	15	2	S10388	Ig heavy chain J r
434	11	36.7	13	2	S61798	T-cell-specific tr	507	11	36.7	15	2	S10386	Ig heavy chain J r
435	11	36.7	13	2	B25448	Ig kappa-1 chain,	508	11	36.7	15	2	A47628	FC gamma receptor
436	11	36.7	13	2	S32551	glutathione transf	509	11	36.7	15	2	PH1365	Ig heavy chain DJ
437	11	36.7	13	2	PH1636	Ig H chain V-D-J r	510	11	36.7	15	2	PH1366	Ig heavy chain DJ
438	11	36.7	13	2	PH1620	Ig H chain V-D-J r	511	11	36.7	15	2	PH1342	Ig heavy chain DJ
439	11	36.7	13	2	G37266	Ig heavy chain C r	512	11	36.7	15	2	PH1318	Ig heavy chain DJ
440	11	36.7	13	2	D37267	Ig heavy chain C r	513	11	36.7	15	2	PH1320	Ig heavy chain DJ
441	11	36.7	13	2	B26406	Ig kappa chain J r	514	11	36.7	15	2	S43956	Ig mu chain V regi
442	11	36.7	13	2	A47630	Ig kappa chain J r	515	11	36.7	15	2	PH1788	T cell receptor al
443	11	36.7	13	2	I51905	collecting duct wa	516	11	36.7	15	2	S38976	chromogranin A - b
444	11	36.7	13	2	S65558	serine proteinase	517	11	36.7	15	2	PQ0073	T-cell receptor be
445	11	36.7	13	3	PC3369	Unidentified 85K p	518	11	36.7	15	2	PA0099	7 alpha-hydroxy-4-
446	11	36.7	14	1	BSTDY	bombesin - fire-be	519	11	36.7	15	2	A45103	Ig H chain V-D-J r
447	11	36.7	14	1	BSTDY	bombesin - yellow-	520	11	36.7	15	2	PH1613	Ig H chain V-D-J r
448	11	36.7	14	2	PH1677	Ig heavy chain V r	521	11	36.7	15	2	PH1590	Ig H chain V-D-J r
449	11	36.7	14	2	PH1705	Ig heavy chain V r	522	11	36.7	15	2	PH1612	Ig H chain V-D-J r
450	11	36.7	14	2	PT0077	proteochondotin c	523	11	36.7	15	2	S26745	Ig heavy chain J r
451	11	36.7	14	2	S05709	homeotic protein c	524	11	36.7	15	2	PH0782	T-cell receptor al
452	11	36.7	14	2	A44515	trp EG leader pept	525	11	36.7	15	2	PA0031	mixed lymphocyte r
453	11	36.7	14	2	B44854	L-2,4-diaminobuty	526	11	36.7	15	2	PL0109	complement factor
454	11	36.7	14	2	S33801	chaperone, TCP1-re	527	11	36.7	15	4	I38032	hypothetical MNL/T
455	11	36.7	14	2	S33802	chaperone, TCP1-re	528	11	36.7	16	1	A49761	locustapapyrokinin -
456	11	36.7	14	2	A35105	hypothetical prote	529	11	36.7	16	1	MDPFS	melanotropin beta
457	11	36.7	14	2	PC1215	homeotic protein E	530	11	36.7	16	2	S03405	hydrogenase (EC 1.
458	11	36.7	14	2	S13336	mastoparan B - hor	531	11	36.7	16	2	I57530	gene c-fms protein
459	11	36.7	14	2	S03530	Ig heavy chain J r	532	11	36.7	16	2	A60551	leukocyte elastase
460	11	36.7	14	2	I54284	C1-inhibitor - hum	533	11	36.7	16	2	A36300	T-cell receptor ga
461	11	36.7	14	2	PT0223	Ig heavy chain CDR	534	11	36.7	16	2	S03532	Ig heavy chain J r
462	11	36.7	14	2	PH1348	Ig heavy chain DJ	535	11	36.7	16	2	D49021	Ig heavy chain J7
463	11	36.7	14	2	PH1327	Ig heavy chain DJ	536	11	36.7	16	2	S03083	Ig heavy chain J r
464	11	36.7	14	2	PH1356	Ig heavy chain DJ	537	11	36.7	16	2	S26746	Ig heavy chain J r
465	11	36.7	14	2	PH1332	Ig heavy chain DJ	538	11	36.7	16	2	C37290	homeotic protein G
466	11	36.7	14	2	PH1322	Ig heavy chain DJ	539	11	36.7	16	2	S05703	homeotic protein c
467	11	36.7	14	2	PH1757	T cell receptor al	540	11	36.7	16	2	S66613	protein p12E - Fx1
468	11	36.7	14	2	PH1758	T cell receptor al	541	11	36.7	16	2	B44820	7K protein - Esche

542	11	36.7	16	2	PC1299	subtilisin (EC 3.4	615	11	36.7	18	2	I40062	shikimate 5-dehydr
543	11	36.7	16	2	A24099	crystal protein, 2	616	11	36.7	18	2	S21569	1H-4-oxoquinoline
544	11	36.7	16	2	A47393	neuroepitide calla	617	11	36.7	18	2	A43334	orfl 5' of aadr -
545	11	36.7	16	2	A20190	hypodermin B - ear	618	11	36.7	18	2	A61577	24k serine protein
546	11	36.7	16	2	S28213	glutathione transf	619	11	36.7	18	2	T03799	leader peptide trp
547	11	36.7	16	2	A48630	bothrojaracin - ja	620	11	36.7	18	2	S20322	gluten - wheat
548	11	36.7	16	2	PT0282	Ig heavy chain CDR	621	11	36.7	18	2	JU0124	polyphemus I - A
549	11	36.7	16	2	PH1346	Ig heavy chain DJ	622	11	36.7	18	2	JU0125	polyphemus II -
550	11	36.7	16	2	I37452	protein kinase - h	623	11	36.7	18	2	S19914	choline O-acetyltr
551	11	36.7	16	2	F24687	T-cell receptor be	624	11	36.7	18	2	I52623	FSHR - human (frag
552	11	36.7	16	2	I79565	TCL3 oncogene (put	625	11	36.7	18	2	PT0239	Ig heavy chain CDR
553	11	36.7	16	2	S23184	redoxendonuclease	626	11	36.7	18	2	PT0286	Ig heavy chain CDR
554	11	36.7	16	2	S13898	alkaline phosphata	627	11	36.7	18	2	PH1349	Ig heavy chain DJ
555	11	36.7	16	2	PH1637	Ig H chain V-D-J r	628	11	36.7	18	2	PH1350	Ig heavy chain DJ
556	11	36.7	16	2	PH1638	Ig H chain V-D-J r	629	11	36.7	18	2	S43958	Ig mu chain V regi
557	11	36.7	16	2	C33932	Ig mu chain J regi	630	11	36.7	18	2	A24749	neuropeptide A - b
558	11	36.7	16	2	PH0748	T-cell receptor be	631	11	36.7	18	2	C56211	progesterone recep
559	11	36.7	16	2	A46236	transforming prote	632	11	36.7	18	2	S39009	oviductin - golden
560	11	36.7	16	2	S33589	beta-crystallin A4	633	11	36.7	18	2	A35678	hypothetical prote
561	11	36.7	16	2	S55307	glutathione transf	634	11	36.7	18	2	I35141	T-cell receptor de
562	11	36.7	16	2	B23692	transcription fact	635	11	36.7	18	2	C49254	TcR C gamma 1 chai
563	11	36.7	17	1	GMSH	gastrin - sheep	636	11	36.7	18	2	G49037	TcR delta chain V-
564	11	36.7	17	2	S66198	alcohol dehydrogen	637	11	36.7	19	1	EWSMAN	ancovenin - Strept
565	11	36.7	17	2	S03531	Ig heavy chain J5	638	11	36.7	19	2	A28702	cytochrome P450-C-
566	11	36.7	17	2	S24570	Ig heavy chain J r	639	11	36.7	19	2	I49422	L-lactate dehydrog
567	11	36.7	17	2	S26744	Ig heavy chain J r	640	11	36.7	19	2	I45957	protein kinase (EC
568	11	36.7	17	2	S26747	Ig heavy chain J r	641	11	36.7	19	2	S60633	H+-transporting AT
569	11	36.7	17	2	B44873	caldesmon (fragmen	642	11	36.7	19	2	I45950	opiate peptide e-1
570	11	36.7	17	2	I57941	beta 3-adrenergic	643	11	36.7	19	2	S43960	Ig mu chain V regi
571	11	36.7	17	2	I51910	Sp-A2 - human (fra	644	11	36.7	19	2	PH1304	Ig heavy chain DJ
572	11	36.7	17	2	A41053	glutamate receptor	645	11	36.7	19	2	PH1307	Ig heavy chain DJ
573	11	36.7	17	2	A44560	terephthalate 1,2-	646	11	36.7	19	2	PT0244	Ig heavy chain CDR
574	11	36.7	17	2	A27636	cytotoxin B - Clos	647	11	36.7	19	2	A28814	Ig kappa chain V r
575	11	36.7	17	2	S18534	hypothetical prote	648	11	36.7	19	2	I53673	amyloid protein -
576	11	36.7	17	2	S19614	globin - polychaet	649	11	36.7	19	2	A58700	actagardine - "Act
577	11	36.7	17	2	A38824	tachyplesin I - ho	650	11	36.7	19	2	B56613	virion morphogenes
578	11	36.7	17	2	JX0125	tachyplesin III -	651	11	36.7	19	2	A48354	nonstructural prot
579	11	36.7	17	2	PC1318	large granule L6 c	652	11	36.7	19	2	I40063	shikimate 5-dehydr
580	11	36.7	17	2	A30068	tachyplesin - hors	653	11	36.7	19	2	S63489	dissimilatory sulf
581	11	36.7	17	2	JU0123	tachyplesin II - h	654	11	36.7	19	2	S32675	nitrogen fixation
582	11	36.7	17	2	A40442	integrase homolog	655	11	36.7	19	2	S29212	protein C - oat (f
583	11	36.7	17	2	F40442	integrase homolog	656	11	36.7	19	2	S19532	globin - polychaet
584	11	36.7	17	2	S03533	Ig heavy chain J r	657	11	36.7	19	2	I19613	tachyplesin I prec
585	11	36.7	17	2	PT0235	Ig heavy chain CDR	658	11	36.7	19	2	JX0124	small granule S2 c
586	11	36.7	17	2	PH1367	Ig heavy chain DJ	659	11	36.7	19	2	PC1309	gene hMLH1 protein
587	11	36.7	17	2	PH1331	Ig heavy chain DJ	660	11	36.7	19	2	I52721	Ig heavy chain DJ
588	11	36.7	17	2	PH1357	Ig heavy chain DJ	661	11	36.7	19	2	PH1352	Ig heavy chain DJ
589	11	36.7	17	2	A34704	protein-tyrosine k	662	11	36.7	19	2	PH1353	Ig heavy chain DJ
590	11	36.7	17	2	I54262	pyruvate dehydroge	663	11	36.7	19	2	PH1339	Ig heavy chain DJ
591	11	36.7	17	2	I58129	type I keratin K16	664	11	36.7	19	2	PH1315	Ig heavy chain DJ
592	11	36.7	17	2	I78538	type I keratin K17	665	11	36.7	19	2	PH1330	Ig heavy chain DJ
593	11	36.7	17	2	S10786	enamelin, 26K - bo	666	11	36.7	19	2	S57515	T cell receptor be
594	11	36.7	17	2	PH1630	Ig H chain V-D-J r	667	11	36.7	19	2	S57516	T cell receptor be
595	11	36.7	17	2	I53392	CD33 antigen homol	668	11	36.7	19	2	D32071	T-cell receptor de
596	11	36.7	17	2	I67524	CD33 antigen homol	669	11	36.7	19	2	S03519	T-cell receptor ga
597	11	36.7	17	2	I67526	CD33 antigen homol	670	11	36.7	19	2	S03076	T-cell receptor ga
598	11	36.7	17	2	PS0384	Ig heavy chain J r	671	11	36.7	19	2	I46654	T-cell receptor de
599	11	36.7	17	2	A61211	anantin - Streptom	672	11	36.7	19	2	PH1624	Ig H chain V-D-J r
600	11	36.7	18	1	MTHOB	melanotropin beta	673	11	36.7	19	2	S12268	Qa-2 antigen - mou
601	11	36.7	18	1	MTDFBC	melanotropin beta	674	11	36.7	19	2	PH0793	T-cell receptor al
602	11	36.7	18	2	S24780	protein-tyrosine k	675	11	36.7	19	2	B46592	lactase-phlorizin
603	11	36.7	18	2	S74195	epoxide hydrolase	676	11	36.7	19	2	S02269	UDPglucose-glycog
604	11	36.7	18	2	G02018	proteasome chain L	677	11	36.7	19	2	I54264	rhodopsin single b
605	11	36.7	18	2	S04229	N4-(beta-N-acetyl	678	11	36.7	20	1	DIRT	dental fluid tra
606	11	36.7	18	2	D49570	plasma membrane ca	679	11	36.7	20	2	A23739	cytochrome P450 MU
607	11	36.7	18	2	S43834	DNA topoisomerase	680	11	36.7	20	2	S21176	testosterone 6beta
608	11	36.7	18	2	A25941	Ig heavy chain J-H	681	11	36.7	20	2	A60728	cytochrome P450 3A
609	11	36.7	18	2	S03528	Ig heavy chain J1	682	11	36.7	20	2	B61080	5-carboxymethyl-2-
610	11	36.7	18	2	PH1323	Ig heavy chain DJ	683	11	36.7	20	2	S77981	cytochrome-c oxida
611	11	36.7	18	2	A32220	T-cell receptor de	684	11	36.7	20	2	B37520	glutathione transf
612	11	36.7	18	2	S29264	ovohemerythrin - d	685	11	36.7	20	2	S29100	glutathione transf
613	11	36.7	18	2	S55501	thrombospondin pre	686	11	36.7	20	2	S29099	glutathione transf
614	11	36.7	18	2	S52125	gamma2-gliadin P25	687	11	36.7	20	2	S30381	glutathione transf

688	11	36.7	20	2	S71869	glutathione transf	761	9	30.0	8	2	PT0311	Ig heavy chain CRD
689	11	36.7	20	2	PQ0751	self-incompatibili	762	9	30.0	8	2	B45800	serum albumin - do
690	11	36.7	20	2	PH0111	style glycoprotein	763	9	30.0	8	2	S29272	tocopherol-binding
691	11	36.7	20	2	A56900	chymotrypsin I (EC	764	9	30.0	8	2	S68325	blood cell protein
692	11	36.7	20	2	I49423	cytotoxic T-lympho	765	9	30.0	9	1	ABHUSK	kinetensin - human
693	11	36.7	20	2	A37111	ribulose-bisphosph	766	9	30.0	9	2	S38850	Ig heavy chain V r
694	11	36.7	20	2	PN0171	peptidylprolyl iso	767	9	30.0	9	3	PW0002	light-harvesting c
695	11	36.7	20	2	PL0192	Ig lambda 2 chain	768	9	30.0	10	1	GMROL2	leucosulfakinin-II
696	11	36.7	20	2	PT0248	Ig heavy chain CDR	769	9	30.0	10	2	A44646	neurotoxin-associa
697	11	36.7	20	2	A49048	T-cell receptor be	770	9	30.0	10	2	I44644	neurotoxin-associa
698	11	36.7	20	2	F49048	T-cell receptor be	771	9	30.0	10	2	F41839	ribosomal protein
699	11	36.7	20	2	PC1240	calcium-binding pr	772	9	30.0	10	2	S62208	polyferredoxin - M
700	11	36.7	20	2	A05313	apolipoprotein A-I	773	9	30.0	10	2	A44871	monodehydroascorba
701	11	36.7	20	2	A36045	thrombospondin hom	774	9	30.0	10	2	PS0451	24K protein 4302 -
702	11	36.7	20	2	S04988	gag core shell pro	775	9	30.0	10	2	S62880	polygalacturonase
703	11	36.7	20	2	A44927	major outer membra	776	9	30.0	10	2	B60656	leucosulfakinin II
704	11	36.7	20	2	S45637	oxidoreductase - p	777	9	30.0	10	2	S33844	alpha-2-macroglobu
705	11	36.7	20	2	I64036	hypothetical prote	778	9	30.0	10	2	PH1592	Ig H chain V-D-J r
706	11	36.7	20	2	S63490	dissimilatory sulfi	779	9	30.0	10	2	PT0215	T-cell receptor be
707	11	36.7	20	2	PH1380	alpha-amylase (EC	780	9	30.0	10	2	A56758	urechistachykinin
708	11	36.7	20	2	S29636	jacalin beta-I cha	781	9	30.0	11	1	GMROL	leucosulfakinin -
709	11	36.7	20	2	S29635	jacalin beta chain	782	9	30.0	11	2	S19775	wound-induced prot
710	11	36.7	20	2	S03987	agglutinin beta-2	783	9	30.0	11	2	A60656	perisulfakinin - A
711	11	36.7	20	2	A60372	pollen allergen Po	784	9	30.0	11	2	PH1632	Ig H chain V-D-J r
712	11	36.7	20	2	S35460	alliin lyase (EC 4	785	9	30.0	11	2	PH1600	Ig H chain V-D-J r
713	11	36.7	20	2	S09090	acyl coenzyme A--6	786	9	30.0	11	2	PH1583	Ig H chain V-D-J r
714	11	36.7	20	2	PC2084	serine proteinase	787	9	30.0	11	2	PH1584	Ig H chain V-D-J r
715	11	36.7	20	2	S38763	S-adenosyl-L-methi	788	9	30.0	11	2	PT0214	T-cell receptor be
716	11	36.7	20	2	S48654	plasmepsin II - pl	789	9	30.0	11	2	S18385	NAD5-cytochrome P4
717	11	36.7	20	2	PC1152	equinotoxin ID - s	790	9	30.0	12	2	S28546	T-cell receptor be
718	11	36.7	20	2	A34817	collagenolytic pro	791	9	30.0	12	2	S28547	T-cell receptor be
719	11	36.7	20	2	A56899	serum heterodimer,	792	9	30.0	12	2	S26544	T-cell receptor be
720	11	36.7	20	2	A47105	dystroglycan - chi	793	9	30.0	12	2	S15815	translation elonga
721	11	36.7	20	2	S08605	hypothetical prote	794	9	30.0	12	2	B44818	extracellular lipa
722	11	36.7	20	2	S10876	hypothetical prote	795	9	30.0	12	2	JU0356	cycloleonorinin -
723	11	36.7	20	2	S27142	hypothetical prote	796	9	30.0	12	2	S10624	lipovitellin - Afr
724	11	36.7	20	2	S58382	hypothetical prote	797	9	30.0	12	2	S51737	T-cell receptor be
725	11	36.7	20	2	PH1358	Ig heavy chain DJ	798	9	30.0	12	2	PH1587	Ig H chain V-D-J r
726	11	36.7	20	2	PH1341	Ig heavy chain DJ	799	9	30.0	12	2	PH1605	Ig H chain V-D-J r
727	11	36.7	20	2	PH1326	Ig heavy chain DJ	800	9	30.0	12	2	PH1606	Ig H chain V-D-J r
728	11	36.7	20	2	S60350	kallikrein, pankre	801	9	30.0	12	2	PH1581	Ig H chain V-D-J r
729	11	36.7	20	2	S15861	estrogen receptor	802	9	30.0	12	2	PH1458	T-cell receptor be
730	11	36.7	20	2	A38689	1-phosphatidylinos	803	9	30.0	12	2	PH1462	T-cell receptor be
731	11	36.7	20	2	PQ0071	T-cell receptor be	804	9	30.0	12	2	PH1461	T-cell receptor be
732	11	36.7	20	2	S68341	procathepsin L - g	805	9	30.0	12	2	PH1457	T-cell receptor be
733	11	36.7	20	2	S66222	defensin AMP2 - Da	806	9	30.0	12	2	PH1459	T-cell receptor be
734	11	36.7	20	3	PW0003	light-harvesting c	807	9	30.0	12	2	PH0771	T-cell receptor be
735	10	33.3	9	2	S30494	cat gene leader pe	808	9	30.0	12	2	PH0931	T-cell receptor be
736	10	33.3	9	2	B24362	chloramphenicol O-	809	9	30.0	13	2	S29488	GTP-binding protei
737	10	33.3	9	2	PH1591	Ig H chain V-D-J r	810	9	30.0	13	2	S23356	hypothetical prote
738	10	33.3	12	2	S47363	T-cell antigen rec	811	9	30.0	13	2	S47356	T-cell antigen rec
739	10	33.3	13	2	PH0805	T-cell receptor al	812	9	30.0	13	2	S47357	T-cell antigen rec
740	10	33.3	14	2	PH1623	Ig H chain V-D-J r	813	9	30.0	13	2	S47359	T-cell antigen rec
741	10	33.3	14	2	PH1586	Ig H chain V-D-J r	814	9	30.0	13	2	S47361	T-cell antigen rec
742	10	33.3	15	2	A56786	plmeloyl-CoA synth	815	9	30.0	13	2	S47365	T-cell antigen rec
743	10	33.3	15	2	B45133	casein kinase II (816	9	30.0	13	2	S47368	T-cell antigen rec
744	10	33.3	15	2	A35417	28K serine protein	817	9	30.0	13	2	S47372	T-cell antigen rec
745	10	33.3	15	2	I67525	CD33 antigen homol	818	9	30.0	13	2	S47376	T-cell antigen rec
746	10	33.3	16	2	PT0234	Ig heavy chain CDR	819	9	30.0	13	2	S47377	T-cell antigen rec
747	10	33.3	18	2	S14661	photosystem I prot	820	9	30.0	13	2	S47378	T-cell antigen rec
748	10	33.3	18	2	H64711	hypothetical prote	821	9	30.0	13	2	S47382	T-cell antigen rec
749	10	33.3	19	2	S43641	carboxylesterase (822	9	30.0	13	2	S47383	T-cell antigen rec
750	10	33.3	19	2	PC1324	hypothetical prote	823	9	30.0	13	2	S47384	T-cell antigen rec
751	10	33.3	19	2	PC1322	hypothetical prote	824	9	30.0	13	2	S47385	T-cell antigen rec
752	10	33.3	19	2	A38382	15K protein A - ra	825	9	30.0	13	2	S47388	T-cell antigen rec
753	10	33.3	20	2	A54519	tubulin alpha chai	826	9	30.0	13	2	S47389	T-cell antigen rec
754	10	33.3	20	2	S19616	globin - polychaet	827	9	30.0	13	2	S47392	T-cell antigen rec
755	10	33.3	20	2	B38382	15K protein B - ra	828	9	30.0	13	2	S47394	T-cell antigen rec
756	9	30.0	3	2	A43391	TRH-like tripeptid	829	9	30.0	13	2	S65612	tubulin alpha-chai
757	9	30.0	5	2	D60274	major protein anti	830	9	30.0	13	2	PH1593	Ig H chain V-D-J r
758	9	30.0	5	2	S68326	blood cell protein	831	9	30.0	13	2	PH1596	Ig H chain V-D-J r
759	9	30.0	6	2	B44510	hypothetical prote	832	9	30.0	13	2	PH1585	Ig H chain V-D-J r
760	9	30.0	6	2	PT0662	T-cell receptor be	833	9	30.0	13	2	PH1479	T-cell receptor be

834	9	30.0	13	3	PC3371	atp protein - Baci	907	9	30.0	16	2	C28587	T-cell receptor be
835	9	30.0	14	2	C40944	hypothetical prote	908	9	30.0	16	2	S10808	protein kinase C 1
836	9	30.0	14	2	S39932	S-allele-associate	909	9	30.0	16	2	FS3284	T-cell receptor be
837	9	30.0	14	2	S29209	avenin alpha-2 - o	910	9	30.0	16	2	FS3284	T-cell receptor be
838	9	30.0	14	2	S07768	soluble hydrognas	911	9	30.0	16	2	PH1634	Ig H chain V-D-J r
839	9	30.0	14	2	C39170	acyl-[acyl-carrier	912	9	30.0	16	2	PH1622	Ig H chain V-D-J r
840	9	30.0	14	2	PA0015	seed storage prote	913	9	30.0	16	2	PH1589	Ig H chain V-D-J r
841	9	30.0	14	2	PS0252	16K protein 5404 -	914	9	30.0	16	2	PH1588	Ig H chain V-D-J r
842	9	30.0	14	2	E33098	214K exoantigen (v	915	9	30.0	16	2	PH1580	Ig H chain V-D-J r
843	9	30.0	14	2	C33098	223K exoantigen -	916	9	30.0	16	2	PH0763	T-cell receptor be
844	9	30.0	14	2	S45655	cathepsin L (EC 3.	917	9	30.0	16	2	PH0766	T-cell receptor be
845	9	30.0	14	2	S00150	ovostatin - duck (918	9	30.0	16	2	IS2226	aldehyde dehydroge
846	9	30.0	14	2	B20872	alpha-2-macroglobu	919	9	30.0	16	2	PH1607	Ig H chain V-D-J r
847	9	30.0	14	2	PT0232	Ig heavy chain CRD	920	9	30.0	17	2	B43404	T-cell receptor be
848	9	30.0	14	2	PT0252	Ig heavy chain CRD	921	9	30.0	17	2	C24166	photosystem II ext
849	9	30.0	14	2	PT0294	Ig heavy chain CRD	922	9	30.0	17	2	A44896	heat shock protei
850	9	30.0	14	2	I49514	B144 protein A - m	923	9	30.0	17	2	B42965	talain (glycosylate
851	9	30.0	14	2	PH1614	Ig H chain V-D-J r	924	9	30.0	17	2	S57514	T cell receptor be
852	9	30.0	14	2	PH1615	Ig H chain V-D-J r	925	9	30.0	17	2	S57519	T cell receptor be
853	9	30.0	14	2	PH1617	Ig H chain V-D-J r	926	9	30.0	17	2	S57556	T cell receptor be
854	9	30.0	14	2	PH1597	Ig H chain V-D-J r	927	9	30.0	17	2	S57555	T cell receptor be
855	9	30.0	14	2	PH1598	Ig H chain V-D-J r	928	9	30.0	17	2	B49255	T-cell receptor be
856	9	30.0	14	2	PH1601	Ig H chain V-D-J r	929	9	30.0	17	2	C49255	T-cell receptor be
857	9	30.0	14	2	PH1608	Ig H chain V-D-J r	930	9	30.0	17	2	S51736	T-cell receptor be
858	9	30.0	14	2	PH1471	T-cell receptor be	931	9	30.0	18	2	B40741	T-cell receptor be
859	9	30.0	14	2	PH0765	T-cell receptor be	932	9	30.0	18	2	S08559	ribosomal protein
860	9	30.0	14	2	PH0755	T-cell receptor be	933	9	30.0	18	2	JP0102	fibrinogen beta ch
861	9	30.0	14	2	PH0915	T-cell receptor be	934	9	30.0	18	2	A56871	retinol-binding pr
862	9	30.0	14	2	C48394	major fat-globule	935	9	30.0	18	2	D56049	kidney stone prote
863	9	30.0	14	2	A56632	neofutakinin-II -	936	9	30.0	18	2	A45138	arsenite oxidase I
864	9	30.0	14	2	S39930	S-allele-associate	937	9	30.0	18	2	E47088	methanol:N'-dime
865	9	30.0	15	2	S29207	avenin gamma-4 - o	938	9	30.0	18	2	A56791	keratin B2 homolog
866	9	30.0	15	2	PL0143	carbon-monoxide de	939	9	30.0	18	2	F49255	T-cell receptor be
867	9	30.0	15	2	PL0141	carbon-monoxide de	940	9	30.0	18	2	A54904	T-cell receptor be
868	9	30.0	15	2	S36889	ribosomal protein	941	9	30.0	18	2	C56046	urinary tract ston
869	9	30.0	15	2	S74129	superoxide dismuta	942	9	30.0	18	2	B44239	amine oxidase (cop
870	9	30.0	15	2	PQ0193	stylar glycoprotei	943	9	30.0	18	2	PQ0072	T-cell receptor be
871	9	30.0	15	2	PQ0194	Sz-glycoprotein -	944	9	30.0	18	2	PH1629	Ig H chain V-D-J r
872	9	30.0	15	2	PS0455	superoxide dismuta	945	9	30.0	18	2	B48839	T-cell receptor be
873	9	30.0	15	2	S27248	pseudogermin - whe	946	9	30.0	19	2	PS0186	superoxide dismuta
874	9	30.0	15	2	PA0076	fructose-bisphosph	947	9	30.0	19	2	PA0012	superoxide dismuta
875	9	30.0	15	2	PA0088	protein QF200051 -	948	9	30.0	19	2	B60894	gamma crystallin I
876	9	30.0	15	2	PA0071	superoxide dismuta	949	9	30.0	19	2	A60894	gamma crystallin I
877	9	30.0	15	2	A31435	adherence lectin h	950	9	30.0	19	2	A44239	amine oxidase (cop
878	9	30.0	15	2	S29485	Grp-binding protei	951	9	30.0	19	2	C40634	orf21 5' of eryK -
879	9	30.0	15	2	S77987	cytochrome-c oxida	952	9	30.0	19	2	PA0010	seed storage prote
880	9	30.0	15	2	A41436	alpha-macroglobuli	953	9	30.0	19	2	JC2059	homobox 4 protein
881	9	30.0	15	2	B41436	ovostatin - green	954	9	30.0	19	2	E60977	14-3-3 protein hom
882	9	30.0	15	2	PH0136	T-cell receptor be	955	9	30.0	19	2	I49039	T-cell receptor be
883	9	30.0	15	2	D28587	T-cell receptor be	956	9	30.0	19	2	S22232	vitronectin - goat
884	9	30.0	15	2	F28587	T-cell receptor be	957	9	30.0	19	2	S22233	vitronectin - shee
885	9	30.0	15	2	B33527	fructose-2,6-bisph	958	9	30.0	19	2	PH1609	Ig H chain V-D-J r
886	9	30.0	15	2	I53284	T-cell receptor be	959	9	30.0	19	2	A49254	TCR delta chain V-
887	9	30.0	15	2	PH1631	Ig H chain V-D-J r	960	9	30.0	20	2	S29495	enhancing factor -
888	9	30.0	15	2	PH1610	Ig H chain V-D-J r	961	9	30.0	20	2	A20899	fructose-bisphosph
889	9	30.0	15	2	PH1582	Ig H chain V-D-J r	962	9	30.0	20	2	D60894	gamma crystallin V
890	9	30.0	15	2	PH1378	T antigen variant	963	9	30.0	20	2	PN0154	microbial serine p
891	9	30.0	15	2	PH1377	T antigen variant	964	9	30.0	20	2	PS0087	metalloendopeptid
892	9	30.0	15	2	PH0760	T-cell receptor be	965	9	30.0	20	2	PQ0215	R-phycocerythrin ga
893	9	30.0	15	2	PH0770	T-cell receptor be	966	9	30.0	20	2	H22565	hypothetical prote
894	9	30.0	15	2	PH0764	T-cell receptor be	967	9	30.0	20	2	B30208	cathepsin L (EC 3.
895	9	30.0	15	2	B28501	lipoprotein lipase	968	9	30.0	20	2	S68785	octopamine recepto
896	9	30.0	15	2	S63429	pyrogallol hydroxy	969	9	30.0	20	2	S28779	larval serum prote
897	9	30.0	16	2	S10807	protein kinase C i	970	9	30.0	20	2	A60293	galactose-1-phosph
898	9	30.0	16	2	S10809	protein kinase C i	971	9	30.0	20	2	I54189	T-cell receptor be
899	9	30.0	16	2	C45143	protein-tyrosine-p	972	9	30.0	20	2	D49255	Prinase (EC 2.7.7.
900	9	30.0	16	2	A59042	alpha-conotoxin Ep	973	9	30.0	20	2	C49404	T-cell receptor be
901	9	30.0	16	2	A59045	alpha-conotoxin Au	974	9	30.0	20	3	PQ0710	photosystem I 10.4
902	9	30.0	16	2	A54877	alpha-conotoxin Pn	975	8	26.7	5	2	PQ0689	fulicin - giant Af
903	9	30.0	16	2	B54877	alpha-conotoxin Pn	976	8	26.7	5	2	A44692	hydrogensulfite re
904	9	30.0	16	2	PH1778	T cell receptor al	977	8	26.7	6	2	S11556	glucose isomerase
905	9	30.0	16	2	G49039	T-cell receptor be	978	8	26.7	7	2	S17976	probable Na+-trans
906	9	30.0	16	2	B28587	T-cell receptor be	979	8	26.7	8	2	S45651	

980 translation elonga 8 26.7 9 2 D58503
 981 huto protein - kie 8 26.7 9 2 C36730
 982 glycine cleavage s 8 26.7 9 2 PS0253
 983 venom protein HR-3 8 26.7 9 2 S10920
 984 cytochrome-c oxida 8 26.7 9 2 S77984
 985 gene hGRP protein 8 26.7 9 2 I52705
 986 19 heavy chain CRD 8 26.7 9 2 P70315
 987 ornithine aminotra 8 26.7 9 2 I77348
 988 alpha-2-macroglobu 8 26.7 9 2 S66635
 989 beta-neoendorphin 8 26.7 10 2 A60410
 990 bacterioferritin - 8 26.7 10 2 S48182
 991 formaldehyde dehyd 8 26.7 10 2 D46285
 992 ermG leader peptid 8 26.7 11 2 A26330
 993 Pyrroloquinoline q 8 26.7 11 2 S58444
 994 dnan protein - Str 8 26.7 11 2 T10965
 995 kassinin-like pept 8 26.7 11 2 B60409
 996 kassinin-like pept 8 26.7 11 2 C60409
 997 kassinin-like pept 8 26.7 11 2 D60409
 998 substance P-like p 8 26.7 11 2 E60409
 999 substance P-like p 8 26.7 11 2 F60409
 1000 glucocerebrosidase 8 26.7 11 2 I52980

ALIGNMENTS

RESULT 1
 S04360
 lacB protein - Staphylococcus aureus (fragment)
 C:Species: Staphylococcus aureus
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Mar-1993
 C:Accession: S04360
 R:Rosey, E.L.; Stewart, G.C.
 Nucleic Acids Res. 17, 3980, 1989
 A:Title: The nucleotide sequence of the lacC and lacD genes of Staphylococcus aureus.
 A:Reference number: S04358; MUID:89282406
 A:Accession: S04360
 A:Molecule type: DNA
 A:Residues: 1-13 <ROS>
 A:Cross-references: EMBL:X14827
 C:Genetics:
 A:Gene: lacB

Query Match 63.3%; Score 19; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.2e+02;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 | | |
 Db 6 WDRGEY 11

RESULT 2
 G49655
 T-cell-receptor beta chain variable region (clone 1) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
 C:Accession: G49655; F49655; A49655
 R:Grom, A.A.; Thompson, S.D.; Luvyink, L.; Passo, M.; Choi, E.; Glass, D.N.
 Proc. Natl. Acad. Sci. U.S.A. 90 11104-11108, 1993
 A:Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juveni
 A:Reference number: A49655; MUID:94068553
 A:Accession: G49655
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-15 <GR1>
 A:Experimental source: hip joint, synovial tissues
 A:Note: this was designated clone 1
 A:Accession: F49655
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid

A:Residues: 1-15 <GR2>
 A:Experimental source: hip joint, synovial tissues
 A:Note: sequence extracted from NCBI backbone (NCBIP:140451)
 A:Note: this was designated clone 2
 A:Accession: A49655
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-15 <GRO>
 A:Experimental source: knee joint, synovial fluid lymphocytes
 A:Note: this was designated clone SF-1
 A:Note: sequence extracted from NCBI backbone (NCBIP:140445)
 C:Keywords: T-cell receptor

Query Match 60.0%; Score 18; DB 2; Length 15;
 Best Local Similarity 33.3%; Pred. No. 2.4e+02;
 Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 | | |
 Db 10 WTDTOY 15

RESULT 3
 S33245
 neuromodulatory peptide Wwamide-2 - giant African snail
 C:Species: Achatina fulica (giant African snail)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
 C:Accession: S33245
 R:Minakata, H.; Ikeda, T.; Muneoka, Y.; Kobayashi, M.; Nomoto, K.
 FEBS Lett. 323, 104-108, 1993
 A:Title: Wwamide-1, -2 and -3: novel neuromodulatory peptides isolated from ganglia o
 A:Reference number: S33244; MUID:93265912
 A:Accession: S33245
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <MIN>

Query Match 53.3%; Score 16; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
 | |
 Db 1 WR 2

RESULT 4
 B57444
 neuropeptide Grb-AST B2 - two-spotted cricket
 C:Species: Gryllus bimaculatus (two-spotted cricket)
 C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
 C:Accession: B57444
 R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
 J. Biol. Chem. 270, 21103-21108, 1995
 A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the
 A:Reference number: A57444; MUID:95403341
 A:Accession: B57444
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <LOR>

Query Match 53.3%; Score 16; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.4e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
 | |
 Db 2 WR 3

RESULT 5

C57444
neuropeptide Grb-AST B3 - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: C57444
J:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
R: Biol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cricket
A:Reference number: A57444; MUID:95403341
A:Accession: C57444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <LOR>

Query Match 53.3%; Score 16; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||
DB 2 WR 3

RESULT 6

Achatina cardio-excitatory peptide-1 - giant African snail
C:Species: Achatina fulica (giant African snail)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jul-1997
C:Accession: A34662
R:Fujimoto, K.; Ohta, N.; Yoshida, M.; Kubota, I.; Muneoka, Y.; Kobayashi, M.
Biochem. Biophys. Res. Commun. 167, 777-783, 1990
A:Title: A novel cardio-excitatory peptide isolated from the atria of the African giant snail
A:Reference number: A34662; MUID:90211261
A:Accession: A34662
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <FUJ>
C:Keywords: amidated carboxyl end
F:11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 53.3%; Score 16; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||
DB 5 WR 6

RESULT 7

B41946
T-cell receptor gamma chain (1t.57) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: B41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma gene
A:Reference number: A41946; MUID:92049316
A:Accession: B41946
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-11 <WHE>
C:Keywords: T-cell receptor

Query Match 53.3%; Score 16; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||
DB 5 WR 6

RESULT 8

A53709
alpha-conotoxin ImI - cone shell (Conus imperialis)
N:Alternate names: alpha-CTX-ImI
C:Species: Conus imperialis (imperial cone)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A53709
R:McIntosh, J.M.; Yoshitani, D.; Mahe, E.; Nielsen, D.B.; Rivier, J.E.; Gray, W.R.; O
J. Biol. Chem. 269, 16733-16739, 1994
A:Title: A nicotinic acetylcholine receptor ligand of unique specificity, alpha-conot
A:Reference number: A53709; MUID:94266889
A:Accession: A53709
A:Molecule type: protein
A:Residues: 1-12 <MC>
A:Note: structure confirmed by chemical synthesis
C:Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsyn
C:Superfamily: alpha-conotoxin
C:Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neu
F:2-8, 3-12/Disulfide bonds: #status experimental
F:12/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 53.3%; Score 16; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||
DB 10 WR 11

RESULT 9

S18362
aspartate transaminase (EC 2.6.1.1) - Sulfolobus solfataricus
N:Alternate names: aspartate aminotransferase
C:Species: Sulfolobus solfataricus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Aug-1997
C:Accession: S18362
R:Birol, L.; Arnone, M.I.; Cubellis, M.V.; Andreotti, G.; Nitti, G.; Marino, G.; San
Biochim. Biophys. Acta 1080, 198-204, 1991
A:Title: The active site of Sulfolobus solfataricus aspartate aminotransferase.
A:Reference number: S18362; MUID:92062695
A:Accession: S18362
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <BIR>
C:Keywords: aminotransferase

Query Match 53.3%; Score 16; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||
DB 10 WR 11

RESULT 10

S54344
glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C:Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 07-May-1999
C:Accession: S54344
R:Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.
Biochem. J. 306, 551-555, 1995
A:Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in g
A:Reference number: S54343; MUID:95194333

A:Accession: S54344
A:Molecule type: protein
A:Residues: 1-13 <OKA>
C:Keywords: oxidoreductase

Query Match 53.3%; Score 16; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||
Db 8 WR 9

RESULT 11

PC4391
Cysteine proteinase (EC 3.4.22.-) B - *Freesia refracta* ssp. 'Golden leader' (fragment)
C:Species: *Freesia refracta* ssp. 'Golden leader'
C:Date: 10-Nov-1997 #sequence_revision 10-Nov-1997 #text_change 07-May-1999
C:Accession: PC4391
R:Kaneda, M.; Yonezawa, H.; Uchikoba, T.
Biosci. Biotechnol. Biochem. 61, 1554-1559, 1997
A:Title: Purification and characterization of a cysteine protease from corms of *freesia*,
A:Reference number: PC4391; MUID:97480942
A:Accession: PC4391
A:Molecule type: protein
A:Residues: 1-13 <KAN>
A:Experimental source: corms
C:Comment: This enzyme plays many proteolytic functions in intracellular and extracellular
C:Keywords: cysteine proteinase; hydrolase

Query Match 53.3%; Score 16; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||
Db 8 WR 9

RESULT 12

LFECW
trp operon leader peptide - *Escherichia coli*
C:Species: *Escherichia coli*
C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 16-Jul-1999
C:Accession: A03589; S41637; D64874
R:Yanofsky, C.; Platt, T.; Crawford, I.P.; Nichols, B.P.; Christie, G.E.; Horowitz, H.;
Nucleic Acids Res. 9, 6647-6668, 1981
A:Title: The complete nucleotide sequence of the tryptophan operon of *Escherichia coli*.
A:Reference number: A03746; MUID:82150258
A:Accession: A03589
A:Molecule type: DNA
A:Residues: 1-14 <YAN>
A:Cross-references: GB:J01714; GB:M12471; GB:M12472; GB:M24865; GB:M25264; GB:M25593; GB:
R:Ramesh, V.
Nucleic Acids Res. 21, 5485-5488, 1993
A:Title: NMR evidence for the RNA stem-loop structure involved in the transcription atte
A:Reference number: S41637; MUID:94089403
A:Accession: S41637
A:Molecule type: DNA
A:Residues: 1-14 <RAM>
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: D64874
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-14 <BLAT>
A:Cross-references: GB:AE0000224; GB:U000096; NID:g1787509; PIDN:AAC74347.1; PID:g1787519;

A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: trpL; trpEe
A:Map position: 27 min
C:Function:
A:Description: involved in control of tryptophan operon transcription by attenuation
C:Superfamily: trp leader peptide

Query Match 53.3%; Score 16; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||
Db 11 WR 12

RESULT 13

LFEBWC
trp operon leader peptide - *Citrobacter freundii*
C:Species: *Citrobacter freundii*
C:Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 13-Nov-1998
C:Accession: A03592
R:Blumenberg, M.; Yanofsky, C.
J. Bacteriol. 152, 57-62, 1982
A:Title: Evolutionary divergence of the *Citrobacter freundii* tryptophan operon regula
A:Reference number: A91792; MUID:83007061
A:Accession: A03592
A:Molecule type: DNA
A:Residues: 1-14 <BLU>
C:Genetics:
A:Gene: trpL
C:Function:
A:Description: involved in control of tryptophan operon transcription by attenuation
C:Superfamily: trp leader peptide

Query Match 53.3%; Score 16; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||
Db 11 WR 12

RESULT 14

LFEBWT
trp operon leader peptide - *Salmonella typhimurium*
C:Species: *Salmonella typhimurium*
C:Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 13-Nov-1998
C:Accession: A03590
R:Lee, F.; Bertrand, K.; Bennett, G.; Yanofsky, C.
J. Mol. Biol. 121, 193-217, 1978
A:Title: Comparison of the nucleotide sequences of the initial transcribed regions of
A:Reference number: A92850; MUID:78196931
A:Accession: A03590
A:Molecule type: DNA
A:Residues: 1-14 <LEE>
C:Genetics:
A:Gene: trpL; trpEe
C:Function:
A:Description: involved in control of tryptophan operon transcription by attenuation
C:Superfamily: trp leader peptide

Query Match 53.3%; Score 16; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.6e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
||

Db 11 WR 12

RESULT 15

PT0026
calotropin DI - mudar (fragment)
C:Species: Calotropis gigantea (mudar, madar)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: PT0026
R:Shattacharya, D.; Sengupta, A.; Sinha, N.K.
Phytochemistry 26, 633-636, 1987
A:Title: Chemical modification and amino terminal sequence of calotropin DI from Calotropis gigantea
A:Reference number: PT0026
A:Accession: PT0026
A:Molecule type: protein
A:Residues: 1-14 <BHA>
C:Comment: This enzyme is classified as a plant cysteine protease.
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 53.3%; Score 16; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. NO. 6.6e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2

Db 8 WR 9

Search completed: May 2, 2000, 00:19:01
Job time: 109 sec

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GenCore version 4.5

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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:18:27 ; Search time 7.61 seconds
(without alignments)

23.547 Million cell updates/sec

Title: US-09-258-947-174

Perfect score: 30

Sequence: 1 WRXXEY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 1030

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	66.7	15	1	UC08_MAIZE
2	19	63.3	19	1	CAT3_FASHE
3	16	53.3	7	1	WMA1_ACHFU
4	16	53.3	11	1	CEPL_ACHFU
5	16	53.3	12	1	CXAL_CONIM
6	16	53.3	14	1	CALI_CALGI
7	16	53.3	14	1	KARA_BROPL
8	16	53.3	14	1	LPW_CITFR
9	16	53.3	14	1	LPW_ECOLI
10	16	53.3	14	1	LPW_SALTY
11	16	53.3	16	1	CAT9_FASHE
12	16	53.3	17	1	LPW_BRELA
13	16	53.3	18	1	GALS_SALTY
14	14	46.7	13	1	UVRD_SALTY
15	14	46.7	15	1	FKB7_PINPS
16	13	43.3	7	1	WMA2_ACHFU
17	13	43.3	7	1	WMA3_ACHFU
18	13	43.3	10	1	GONI_PETMA
19	13	43.3	10	1	GON3_PETMA
20	13	43.3	12	1	UR2A_CATCO
21	13	43.3	12	1	UR2B_CATCO
22	13	43.3	12	1	UR2B_CYPCA
23	13	43.3	12	1	UR2_GILMI
24	13	43.3	12	1	UR2_POLSP
25	13	43.3	12	1	UR2_SCYCA
26	13	43.3	13	1	UR2_RANKI
27	13	43.3	14	1	MAST_PARID
28	13	43.3	14	1	MAST_POLJA
29	13	43.3	14	1	MAST_VESXA
30	13	43.3	14	1	SMS1_MYOSC
31	13	43.3	14	1	SMS_ALLMI
32	13	43.3	15	1	MALT_BACTQ
33	13	43.3	17	1	GAST_MACMU
34	13	43.3	17	1	TPIS_PINPS

35	13	43.3	20	1	CAT4_FASHE	P08328 fasciola he
36	12	40.0	7	1	FAR2_ASCSU	P31890 ascaris suu
37	12	40.0	9	1	LITR_PHYRO	P08346 phyllomedus
38	12	40.0	9	1	LMIP_LOEMI	P31799 locusta mig
39	12	40.0	9	1	UHA2_HUMAN	P40929 homo sapien
40	12	40.0	10	1	GON2_CHICK	P37043 gallus gall
41	12	40.0	11	1	RANC_RANPI	P08951 rana pipien
42	12	40.0	11	1	NO40_LOTJA	O22426 lotus japon
43	12	40.0	12	1	NO40_SESRO	O24369 sesbania ro
44	12	40.0	13	1	NO40_PEA	P55959 pisum sativ
45	12	40.0	13	1	NO40_VICSA	P55961 vicia sativ
46	12	40.0	14	1	ECNM_PSECF	P19314 pseudomonas
47	12	40.0	15	1	ECDA_LYMDI	P80338 lymantria d
48	12	40.0	15	1	GLN2_PINPS	P81107 pinus pinas
49	12	40.0	15	1	PC20_BRANA	P81096 brassica na
50	12	40.0	15	1	UC16_MAIZE	P80622 zea mays (m
51	12	40.0	15	1	UC20_MAIZE	P80626 zea mays (m
52	12	40.0	15	1	UREL_WORMO	P17337 morganella
53	12	40.0	17	1	RANR_RANRU	P08952 rana rugosa
54	12	40.0	18	1	AL13_CARMA	P81512 carcinus ma
55	12	40.0	18	1	CYCH_MOUSE	O61458 mus musculu
56	12	40.0	18	1	SODM_MYCHA	P80582 mycobacteri
57	12	40.0	18	1	UC21_MAIZE	P80627 zea mays (m
58	12	40.0	19	1	ETFA_CLOPA	P81342 clostridium
59	12	40.0	19	1	FIBB_YULVU	P14482 vulpes vulp
60	12	40.0	19	1	OXLA_OPHHA	P81383 ophiophagus
61	12	40.0	20	1	CAOS_RAT	P19633 rattus norv
62	12	40.0	20	1	CISY_STRHY	P20903 streptomyce
63	12	40.0	20	1	COG4_CHIOP	P34156 chionocete
64	12	40.0	20	1	COXF_ONCMY	P80329 oncorhynch
65	12	40.0	20	1	ELAS_GADMO	P32197 gadus morhu
66	12	40.0	20	1	FIBR_PACLE	P81070 pacifastacu
67	12	40.0	20	1	KORA_METTM	P80904 methanobact
68	12	40.0	20	1	PSBH_SYNVU	P19052 synechococc
69	12	40.0	20	1	SUCB_CANFA	P99507 canis famill
70	12	40.0	20	1	VR90_BORPE	P99507 canis famill
71	12	36.7	5	1	BP97_BOTIN	P81549 bordetella
72	11	36.7	5	1	UF01_MOUSE	P38439 mus musculu
73	11	36.7	6	1	LOK1_LOEMI	P41491 locusta mig
74	11	36.7	8	1	ACT_THUAL	P18691 thunnus alb
75	11	36.7	8	1	AKHG_GRYBI	P14086 gryllus bim
76	11	36.7	8	1	AKH_LITBAU	P25418 libellula a
77	11	36.7	8	1	AKH_MELML	P25423 melolontha
78	11	36.7	8	1	AKH_TABAT	P14395 tabanus atr
79	11	36.7	8	1	CCRN_MACEU	P30369 macropus eu
80	11	36.7	8	1	HTF1_PERAM	P04548 periplaneta
81	11	36.7	8	1	HTF2_PERAM	P04549 periplaneta
82	11	36.7	8	1	HTF_TENNO	P25419 tenebrio mo
83	11	36.7	8	1	LCK1_LEUMA	P21140 leucophaea
84	11	36.7	8	1	LCK2_LEUMA	P21141 leucophaea
85	11	36.7	8	1	LCK3_LEUMA	P21142 leucophaea
86	11	36.7	8	1	LCK4_LEUMA	P21143 leucophaea
87	11	36.7	8	1	LCK5_LEUMA	P19987 leucophaea
88	11	36.7	8	1	LCK6_LEUMA	P19988 leucophaea
89	11	36.7	8	1	LCK7_LEUMA	P19989 leucophaea
90	11	36.7	8	1	LCK8_LEUMA	P19990 leucophaea
91	11	36.7	8	1	PLP_BRANA	P81707 brassica na
92	11	36.7	8	1	RPCH_PANBO	P08939 pandanus bo
93	11	36.7	9	1	DL_NEPNO	P24816 nephrops bo
94	11	36.7	9	1	DSIP_RABIT	P01158 oryctolagus
95	11	36.7	9	1	LITO_LITAU	P08945 litoria aur
96	11	36.7	9	1	NEF_HVIZ8	P12481 human immun
97	11	36.7	10	1	AKHX_LOEMI	P81626 locusta mig
98	11	36.7	10	1	APX_CAGPI	P80474 capnocytoph
99	11	36.7	10	1	BP92_BOTIN	P30422 bothrops in
100	11	36.7	10	1	BP92_BOTIN	P30422 bothrops in
101	11	36.7	10	1	BP98_BOTJA	P30426 bothrops in
102	11	36.7	10	1	BPP_VIPAS	P31351 vipera aspi
103	11	36.7	10	1	CAER_LITXA	P56364 litoria xan
104	11	36.7	10	1	GONI_ALLMI	P37041 alligator m
105	11	36.7	10	1	GONI_CHEPR	P80677 chelyosoma
106	11	36.7	10	1	GON2_CHEPR	P80678 chelyosoma
107	11	36.7	10	1	GON3_ONCKE	P23067 oncorhynch

108	11	36.7	10	1	GONL_SQUAC	P27429	squalus aca	181	11	36.7	20	1	CP35_PAPSP	P80056	papio sp. (
109	11	36.7	10	1	GRP_RANRI	P23260	rana ridibu	182	11	36.7	20	1	CPXX_RHORH	P31718	rhodococcus
110	11	36.7	10	1	HTF1_ROMMI	P18110	romalea mic	183	11	36.7	20	1	CRTC_SPIOL	P38060	spinaeol ol
111	11	36.7	10	1	HTF2_CARMO	P111385	carausius m	184	11	36.7	20	1	CS21_STRTR	P81621	streptococc
112	11	36.7	10	1	HTF_HELZE	P16353	heliethis z	185	11	36.7	20	1	DFTS_RAT	P07448	rattus norv
113	11	36.7	10	1	HTF_NAUCI	P10939	nauphoeta c	186	11	36.7	20	1	ERTU_MYCSY	P81407	mycoplasma
114	11	36.7	10	1	HTF_TABAT	P14596	tabanus atr	187	11	36.7	20	1	HGL1_FASHE	P80527	fasciola he
115	11	36.7	10	1	LABA_JATMU	P13270	jatropha mu	188	11	36.7	20	1	LEC1_ARTTN	P18671	artocarpus
116	11	36.7	10	1	MP2_MICOC	P81533	microplitis	189	11	36.7	20	1	LEC2_MACPO	P18676	maclura pom
117	11	36.7	10	1	NO40_TOBAC	P55962	nicotiana t	190	11	36.7	20	1	LEC3_ARTTN	P18673	artocarpus
118	11	36.7	10	1	TOPI_SALTY	P40686	salmonella	191	11	36.7	20	1	LEC3_MACPO	P18677	maclura pom
119	11	36.7	10	1	TPIS_NICPL	P19118	nicotiana p	192	10	33.3	9	1	LECA_STAAU	P36884	staphylococ
120	11	36.7	10	1	CH60_DROME	P35380	drosophilu	193	10	33.3	15	1	UC19_MAIZE	P80625	zea mays (m
121	11	36.7	11	1	CORZ_PERAM	P11496	periplaneta	194	10	33.3	20	1	AMP_FUSNU	P81207	fusobacteri
122	11	36.7	11	1	LPW_THETH	P05624	thermus aqu	195	9	30.0	8	1	AL17_CARMA	P81820	carcinus ma
123	11	36.7	11	1	MLG_THETS	P41989	thermomyz	196	9	30.0	9	1	AL11_CARMA	P81814	carcinus ma
124	11	36.7	12	1	RR2_CONAM	P42341	conopholis	197	9	30.0	9	1	NEUX_HUMAN	P04277	homo sapien
125	11	36.7	12	1	NO40_SOYBN	P55960	glycine max	198	9	30.0	9	1	NEUX_RAT	P11382	rattus norv
126	11	36.7	12	1	UP01_CAEEL	P55954	caenorhabdi	199	9	30.0	9	1	NSK1_SARBU	P41492	sarcophaga
127	11	36.7	13	1	BOML_PSEGU	P42991	pseudophryn	200	9	30.0	10	1	LSK2_LEUMA	P09039	leucophaea
128	11	36.7	13	1	BPF1_BOTJA	P01020	bothriops ja	201	9	30.0	10	1	RL16_ACHLA	P29221	acholeplasm
129	11	36.7	13	1	CPX1_CONTE	P81755	conus texti	202	9	30.0	10	1	TKU1_UREUN	P40751	urechis uni
130	11	36.7	13	1	IRBP_MOUSE	P49194	mus musculu	203	9	30.0	10	1	UH05_RAT	P56573	rattus norv
131	11	36.7	13	1	MLA_ANOCA	P41589	anolis caro	204	9	30.0	10	1	UP11_CAEEL	P55956	caenorhabdi
132	11	36.7	13	1	MLA_CAMDR	P01198	camelus dro	205	9	30.0	10	1	UPA9_HUMAN	P30095	homo sapien
133	11	36.7	13	1	MPI_MICOC	P81532	microplitis	206	9	30.0	11	1	LSK1_LEUMA	P04428	leucophaea
134	11	36.7	13	1	TP13_PHYRO	P04096	phyllomedus	207	9	30.0	11	1	LSKP_PERAM	P36885	periplaneta
135	11	36.7	13	1	YPNP_PHOLU	P41122	photorhabdu	208	9	30.0	12	1	LOSK_LOEMI	P47733	locusta miq
136	11	36.7	14	1	ALVT_ALYOB	P08944	alytes obst	209	9	30.0	12	1	NUDM_CANFA	P54713	canis fami
137	11	36.7	14	1	LPW_RHIME	P18854	rhizobium m	210	9	30.0	12	1	UKA2_HUMAN	P54714	homo sapien
138	11	36.7	14	1	MAST_VESBA	P21554	vespa basal	211	9	30.0	13	1	FIBB_RABIT	P14478	oryctolagus
139	11	36.7	14	1	NEU2_FASHE	P80526	fasciola he	212	9	30.0	13	1	SODM_CANFA	P54712	canis fami
140	11	36.7	14	1	RECT_SALTY	P28355	salmonella	213	9	30.0	14	1	CAT2_FASHE	P80342	fasciola he
141	11	36.7	15	1	HS11_PINPS	P81083	pinus pinas	214	9	30.0	14	1	DHSL_ANACY	P17874	anabaena cy
142	11	36.7	15	1	LCK_DROME	P81829	drosophila	215	9	30.0	14	1	NSK2_SARBU	P41493	sarcophaga
143	11	36.7	15	1	MK2A_PALPR	P80409	palomena pr	216	9	30.0	14	1	UHA2_CANFA	P99506	canis fami
144	11	36.7	15	1	RBS_PALPR	P80657	physcomitre	217	9	30.0	14	1	YMTF_XANCP	Q03397	xanthomonas
145	11	36.7	15	1	RM12_YEAST	P36322	saccharomyc	218	9	30.0	15	1	COXI_THUOB	P80978	thunnus obe
146	11	36.7	15	1	UC14_MAIZE	P80620	zea mays (m	219	9	30.0	15	1	DCMM_PSECH	P19920	pseudomonas
147	11	36.7	15	1	UC23_MAIZE	P80629	zea mays (m	220	9	30.0	15	1	DCMM_PSECH	P19917	pseudomonas
148	11	36.7	15	1	YAA3_RHOPA	Q02006	rhodopseudo	221	9	30.0	15	1	MK1_PALPR	P80408	palomena pr
149	11	36.7	16	1	AL11_CALVO	P41839	calliphora	222	9	30.0	15	1	PGTS_PELAC	P80564	pelobacter
150	11	36.7	16	1	LPK1_LOEMI	P20404	locusta miq	223	9	30.0	15	1	SODM_STRGR	P80733	streptomyce
151	11	36.7	16	1	MK2B_PALPR	P80410	palomena pr	224	9	30.0	15	1	UC01_MAIZE	P80607	zea mays (m
152	11	36.7	16	1	MK2B_PALPR	P80411	palomena pr	225	9	30.0	15	1	UC29_MAIZE	P80635	zea mays (m
153	11	36.7	16	1	MLB_SQUAC	P01207	squalus aca	226	9	30.0	16	1	CXAL_CONAL	P56639	conus aulic
154	11	36.7	16	1	VPR_HV1C4	P05953	human immun	227	9	30.0	16	1	CXAL_CONEP	P56638	conus episc
155	11	36.7	16	1	VPR_HV1S3	P19555	human immun	228	9	30.0	16	1	CXAA_CONPE	P50984	conus penna
156	11	36.7	17	1	LCK_RAT	Q01621	rattus norv	229	9	30.0	16	1	CXAB_CONPE	P50985	conus penna
157	11	36.7	17	1	LPW_AGOBR	P50871	azospirillu	230	9	30.0	16	1	FIBA_MELEME	P14456	meles meles
158	11	36.7	17	1	NEE_HV1J3	P12480	human immun	231	9	30.0	16	1	FIBA_MUSVI	P14458	mustela vis
159	11	36.7	17	1	TAC1_TACGI	P23684	tachypleus	232	9	30.0	16	1	RL6_VIBPR	Q56715	vibrio prot
160	11	36.7	17	1	TAC3_TACGI	P18252	tachypleus	233	9	30.0	18	1	FIBB_ANAPL	P12802	anas platyr
161	11	36.7	18	1	HEMH_THETS	P80155	theromyzon	234	9	30.0	18	1	RL23_HALCU	P03975	halobacteri
162	11	36.7	18	1	MLB_HORSE	P01202	equus cabal	235	9	30.0	19	1	FIBB_HORSE	P14471	equus cabal
163	11	36.7	18	1	MLB_SCYCA	P01206	scyllorhinu	236	9	30.0	19	1	FIBB_LAMGL	P14473	lama glama
164	11	36.7	18	1	NODD_RHILU	Q52838	rhizobium l	237	9	30.0	19	1	FIBB_PIG	P14477	sus scrofa
165	11	36.7	18	1	NPA_BOVIN	P15016	bos taurus	238	9	30.0	19	1	FIBB_TAPTE	P14539	tapirus ter
166	11	36.7	18	1	PM1_LIMPO	P14215	limulus pol	239	9	30.0	19	1	G6PI_LACIA	P81181	lactococcus
167	11	36.7	18	1	PM2_LIMPO	P14316	limulus pol	240	9	30.0	20	1	CAT1_FASHE	Q00993	fasciola he
168	11	36.7	18	1	TOP1_KLEAE	P46155	klebsiella	241	9	30.0	20	1	FIBB_ELENA	P14538	elephas max
169	11	36.7	18	1	YAA5_RHOPA	Q02005	rhodopseudo	242	9	30.0	20	1	FIBB_FELCA	P14469	felis silve
170	11	36.7	19	1	AL22_HORSE	P81217	equus cabal	243	9	30.0	20	1	FIBB_SHEPR	P14470	ovis aries
171	11	36.7	19	1	DCAM_ACACA	P34039	acanthamoeb	244	9	30.0	20	1	GR78_PHAVU	P80089	phaseolus v
172	11	36.7	19	1	DURC_STRGP	P36503	streptomyce	245	9	30.0	20	1	OAR_PROPY	P14803	photinus py
173	11	36.7	19	1	LANA_ACTLG	P56650	actinoplane	246	9	30.0	20	1	SODM_HORVU	P28524	hordemus vul
174	11	36.7	19	1	LANC_STRSQ	P38655	streptomyce	247	8	26.7	7	1	FAR1_ASCSU	P31889	ascaris suu
175	11	36.7	19	1	UC31_MAIZE	P80637	zea mays (m	248	8	26.7	7	1	FAR5_HIRME	P42564	hirundo medi
176	11	36.7	20	1	A1BG_EQUAS	P39090	equus asinu	249	8	26.7	7	1	MSCL_SALTY	P39446	salmonella
177	11	36.7	20	1	APAI_ERYPA	P18647	erythrocebu	250	8	26.7	9	1	COXE_THUOB	P80975	thunnus obe
178	11	36.7	20	1	COG1_CHIOP	P34153	chionocete	251	8	26.7	9	1	HUTU_KLEAE	P12381	klebsiella
179	11	36.7	20	1	COG1_PARC	P20731	paralithode	252	8	26.7	10	1	UHA6_CHLPR	P38007	chlamydia t
180	11	36.7	20	1	COXA_THUOB	P80972	thunnus obe	253	8	26.7	11	1	COXA_CANFA	P99501	canis fami

254	8	26.7	11	1	POOC_PSEFL	P55173	pseudomonas	327	7	23.3	8	1	ALL7_CARMA	P81809	carcinus ma
255	8	26.7	11	1	TKN1_PSEGU	P42986	pseudophryn	328	7	23.3	8	1	ALL8_CARMA	P81811	carcinus ma
256	8	26.7	11	1	TKN2_PSEGU	P42987	pseudophryn	329	7	23.3	8	1	ALL9_CARMA	P81812	carcinus ma
257	8	26.7	11	1	TKN3_PSEGU	P42988	pseudophryn	330	7	23.3	8	1	ANG2_BOTJA	Q10582	bothrops ja
258	8	26.7	11	1	TKN4_PSEGU	P42989	pseudophryn	331	7	23.3	8	1	B4K_PORGI	P81886	porphyromon
259	8	26.7	11	1	TKN5_PSEGU	P42990	pseudophryn	332	7	23.3	8	1	GLUR_HUMAN	P02729	homo sapien
260	8	26.7	11	1	UF05_MOUSE	P38643	mus musculus	333	7	23.3	8	1	UF06_MOUSE	P38644	mus musculus
261	8	26.7	11	1	UN05_CLOPA	P81350	clostridium	334	7	23.3	8	1	UPAA_HUMAN	P30096	homo sapien
262	8	26.7	12	1	CALM_TETTH	Q05055	tetrahymena	335	7	23.3	8	1	AL10_CARMA	P81813	carcinus ma
263	8	26.7	12	1	PA2B_VIPBO	P31859	vipera beru	336	7	23.3	9	1	BUR_CLOPA	P81337	clostridium
264	8	26.7	13	1	CXAL_CONST	P15471	conus stria	337	7	23.3	9	1	FARP_CALSI	P38495	callinectes
265	8	26.7	13	1	FIBA_CAVPO	P14445	salvia porce	338	7	23.3	9	1	FLA2_TREYA	P80159	treponema h
266	8	26.7	13	1	PRC_SALTY	P43669	salmonella	339	7	23.3	9	1	ISOT_CYPCA	P42993	cyprinus ca
267	8	26.7	14	1	FIBA_HORSE	P14452	equus caball	340	7	23.3	9	1	NEUU_CAVPO	P34966	cavia porce
268	8	26.7	14	1	HCYA_MEGCR	Q10583	megathura c	341	7	23.3	9	1	OXYA_SCYCA	P42996	scyllorhinu
269	8	26.7	14	1	LPF2_ECOLI	P05985	escherichia	342	7	23.3	9	1	OXYA_SCYCA	P42996	scyllorhinu
270	8	26.7	14	1	TKNM_RANMA	P40951	rana margar	343	7	23.3	9	1	OXYF_SCYCA	P42997	scyllorhinu
271	8	26.7	15	1	ATP2_PINPS	P81663	pinus pinas	344	7	23.3	9	1	OXYT_BUFRE	P42995	bufo regula
272	8	26.7	15	1	FIBA_SYNCA	P14463	syncerus ca	345	7	23.3	9	1	OXYT_CYPCA	P23879	cyprinus ca
273	8	26.7	15	1	MAOX_CHICK	Q92060	gallus gall	346	7	23.3	9	1	OXYT_OCTVU	P80027	octopus vul
274	8	26.7	15	1	OBPA_WAMBR	P81285	mamestra br	347	7	23.3	9	1	OXYT_RABIT	P32878	oryctolagus
275	8	26.7	15	1	UC13_MAIZE	P80619	zea mays (m	348	7	23.3	9	1	OXYT_RAJCL	P42994	raja clavet
276	8	26.7	15	1	UC27_MAIZE	P80633	zea mays (m	349	7	23.3	9	1	OXYV_SQUAC	P43000	squalus aca
277	8	26.7	16	1	CI4B_BACSU	P81094	bacillus su	350	7	23.3	9	1	PGLR_DIAAB	P81179	diaprepes a
278	8	26.7	16	1	FIBA_EQUAS	P14449	equus asinu	351	7	23.3	9	1	TLR3_PICJA	P17441	pichia jada
279	8	26.7	16	1	FIBA_FELCA	P14450	felis silve	352	7	23.3	9	1	TKC1_CALVO	P41517	calliphora
280	8	26.7	16	1	FIBA_HYLLA	P14453	hylobates l	353	7	23.3	9	1	TKL1_LOCM1	P16223	locusta mig
281	8	26.7	16	1	FIBA_OOHEE	P14459	odocoleus	354	7	23.3	9	1	ULAD_HUMAN	P31929	homo sapien
282	8	26.7	16	1	FIBA_TAPTE	P14536	tapirus ter	355	7	23.3	9	1	UPA7_HUMAN	P30093	homo sapien
283	8	26.7	16	1	YMOR_PSEPU	Q02210	pseudomonas	356	7	23.3	10	1	AL19_CARMA	P81822	carcinus ma
284	8	26.7	17	1	FIBA_PIG	P14460	sus scrofa	357	7	23.3	10	1	AMPN_HELAM	P81731	helicoverpa
285	8	26.7	17	1	PROP_SALTY	P40862	salmonella	358	7	23.3	10	1	ANG1_BOTJA	Q10581	bothrops ja
286	8	26.7	18	1	FIBA_CAMDR	P14444	cameus dro	359	7	23.3	10	1	ANGT_BOVIN	P01017	bos taurus
287	8	26.7	18	1	FIBA_LAMGL	P14454	lama glama	360	7	23.3	10	1	ANGT_CHICK	P01018	gallus gall
288	8	26.7	18	1	PHPT_PSESE	P25271	pseudaletia	361	7	23.3	10	1	COXO_RAT	P80432	rattus norv
289	8	26.7	19	1	AMY_DERPT	P49274	dermatophag	362	7	23.3	10	1	COXO_THUOB	P80982	thunnus obe
290	8	26.7	19	1	FIBA_BUBAR	P14443	bubalus arb	363	7	23.3	10	1	CO30_LOCM1	P81735	locusta mig
291	8	26.7	19	1	FIBA_BUBBU	P14442	bubalus bub	364	7	23.3	10	1	ESTA_SCHGA	P81012	schizaphis
292	8	26.7	19	1	FIBA_CERNI	P14447	cervus nipp	365	7	23.3	10	1	SP34_DICMU	P15545	dictyostell
293	8	26.7	19	1	FIBA_MUNMU	P14457	muntilacus m	366	7	23.3	10	1	TKL2_LOCM1	P16224	locusta mig
294	8	26.7	19	1	FIBA_RANTA	P14462	rangifer ta	367	7	23.3	10	1	TKL3_LOCM1	P30249	locusta mig
295	8	26.7	19	1	FIBA_SHEEP	P14451	ovis aries	368	7	23.3	10	1	TKN1_SCYCA	P08608	scyllorhinu
296	8	26.7	19	1	H3_NARPS	P80553	narcissus p	369	7	23.3	10	1	TKNB_RANCA	P22689	rana catesb
297	8	26.7	19	1	NS2_MYCTU	P81136	mycobacteri	370	7	23.3	10	1	RLA2_MOUSE	P99027	mus musculus
298	8	26.7	19	1	NU06_SOLTU	P80729	solanum tub	371	7	23.3	10	1	TKS1_AEDAE	P42634	aedes aegyp
299	8	26.7	19	1	RS19_SPICI	O31159	spiroplasma	372	7	23.3	10	1	TKS2_AEDAE	P42635	aedes aegyp
300	8	26.7	20	1	DPF4_BOVIN	P81425	bos taurus	373	7	23.3	10	1	TKNOF_AEDAE	P13425	aedes aegyp
301	8	26.7	20	1	LECB_IRIHO	P36231	iris hollan	374	7	23.3	10	1	UHA3_HUMAN	P40930	homo sapien
302	8	26.7	20	1	OXLA_AKGRH	P81382	agkistrodon	375	7	23.3	11	1	ANGT_CRIGE	P05037	crinia geor
303	8	26.7	20	1	THIO_CANFA	P99505	canis famli	376	7	23.3	11	1	MHI_KLEPN	P80580	klebsiella
304	8	26.7	20	1	UCRQ_SQUAR	P81247	equisetum a	377	7	23.3	11	1	NIFS_BRAJA	P37030	bradyrhizob
305	8	26.7	20	1	VI01_VACCV	P16714	vaccinia vi	378	7	23.3	11	1	TKN1_UPERU	P08612	proteus vul
306	7	23.3	4	1	FAR3_HIRME	P42562	hirudo medi	379	7	23.3	11	1	TKN2_UPERU	P08616	uperoleia r
307	7	23.3	4	1	FAR4_HIRME	P42563	hirudo medi	380	7	23.3	11	1	TKNA_CHICK	P08616	uperoleia r
308	7	23.3	5	1	AL14_CARMA	P81817	carcinus ma	381	7	23.3	11	1	TKNA_GADMO	P19850	gallus gall
309	7	23.3	5	1	FARP_ARTIR	P41853	artiopesthi	382	7	23.3	11	1	TKNA_CONCMY	P22498	gallus morthu
310	7	23.3	5	1	PRCT_PERAM	P01373	periplanethi	383	7	23.3	11	1	TKNA_RANCA	P22499	oncorhynch
311	7	23.3	6	1	OVN_LEPDE	P42985	leptinotars	384	7	23.3	11	1	TKNA_RANCA	P22688	rana catesb
312	7	23.3	7	1	ALL2_CARMA	P81805	carcinus ma	385	7	23.3	11	1	TKNA_SCYCA	P23207	rana ridibu
313	7	23.3	7	1	ALL3_CARMA	P81806	carcinus ma	386	7	23.3	11	1	TKNA_RANCA	P41333	scyllorhinu
314	7	23.3	7	1	ALL4_CARMA	P81807	carcinus ma	387	7	23.3	11	1	TKND_RANCA	P22691	rana catesb
315	7	23.3	7	1	ALL5_CARMA	P81808	carcinus ma	388	7	23.3	11	1	TKN1_PHYFU	P08615	physalaemus
316	7	23.3	7	1	FAR3_PANRE	P41874	panagrellus	389	7	23.3	12	1	GRAR_RANRU	P99013	saccharomyc
317	7	23.3	7	1	GERP_MOUSE	P99025	mus musculus	390	7	23.3	12	1	TKNA_RANCA	P40754	rana rugosa
318	7	23.3	7	1	HN7_PIG	P01153	sus scrofa	391	7	23.3	12	1	TKNA_SCYCA	P08662	physcomitre
319	7	23.3	7	1	MNP1_LEPDE	P42984	leptinotars	392	7	23.3	12	1	TKND_RANCA	P01371	tremella me
320	7	23.3	7	1	UN06_PINPS	P81675	pinus pinas	393	7	23.3	12	1	TKN1_PHYFU	P08614	kassina mac
321	7	23.3	8	1	ALL2_CARMA	P81815	carcinus ma	394	7	23.3	12	1	TKN2_YEAST	P81359	clostridium
322	7	23.3	8	1	ALL3_CARMA	P81818	carcinus ma	395	7	23.3	12	1	GRAR_RANRU	P22489	bos taurus
323	7	23.3	8	1	ALL4_CARMA	P81819	carcinus ma	396	7	23.3	12	1	TKNA_RANCA		
324	7	23.3	8	1	ALL5_CARMA	P81821	carcinus ma	397	7	23.3	12	1	TKNA_RANCA		
325	7	23.3	8	1	ALL6_CARMA	P41840	calliphora	398	7	23.3	12	1	TKN2_KASMA		
326	7	23.3	8	1	ALL4_CALVO	P41841	calliphora	399	7	23.3	13	1	CRTC_BOVIN		

400	1	CXAA_CONST	13	23.3	7	23.3	17	1	NU04M_TRIRU	Q36834	trichophyto
401	1	GER1_HORVU	13	23.3	7	23.3	17	1	RM35_YEAST	P36530	saccharomyc
402	1	GER2_HORVU	13	23.3	7	23.3	18	1	A2M_OCTVU	P30800	octopus vul
403	1	NEUT_CAVPO	13	23.3	7	23.3	18	1	AGI_EUPCH	P33888	euphorbia c
404	1	NEUT_CHICK	13	23.3	7	23.3	18	1	AGI_EUPMA	P33889	euphorbia m
405	1	NEUT_RANTE	13	23.3	7	23.3	18	1	CPAX_BOVIN	P22779	bos taurus
406	1	NEUT_TRIVU	13	23.3	7	23.3	18	1	CXAL_CONER	P50982	conus ermin
407	1	NP1_LYMST	13	23.3	7	23.3	18	1	FMF1_ECOLI	P20860	escherichia
408	1	NP2_LYMST	13	23.3	7	23.3	18	1	HEX_ADECU	P35985	canine aden
409	1	NP3_LYMST	13	23.3	7	23.3	18	1	HSTB_ECOLI	P01560	escherichia
410	1	PSAJ_PEA	13	23.3	7	23.3	18	1	MCRB_METTE	P22949	methanosarc
411	1	PSBP_PINPS	13	23.3	7	23.3	18	1	RS4_PSEAE	O52759	pseudomonas
412	1	UHAI_HUMAN	13	23.3	7	23.3	18	1	RS4_PSEAE	P81098	heliathus
413	1	UN02_PINPS	13	23.3	7	23.3	18	1	UC03_MAIZE	P80609	zea mays (m
414	1	UN12_CLOPA	13	23.3	7	23.3	19	1	ALI7_OLEEU	P81430	olea europa
415	1	UN41_CLOPA	13	23.3	7	23.3	19	1	CXRX_THUOB	P80984	thunus obe
416	1	ANGT_HORSE	14	23.3	7	23.3	19	1	CXRX_THUOB	P28879	conus stria
417	1	COCO_LIMPO	14	23.3	7	23.3	19	1	CXRX_THUOB	P80704	comamonas t
418	1	CXAL_CONMA	14	23.3	7	23.3	19	1	HMD_METWO	P32441	methanobact
419	1	ECDC_LYMDI	14	23.3	7	23.3	19	1	ITHA_PETMA	P10986	petromyzon
420	1	EFTU_CANFA	14	23.3	7	23.3	19	1	LCRP_PETMA	P13986	petriplaneta
421	1	H4_EUPCR	14	23.3	7	23.3	19	1	MDH_STAUA	P03063	staphylococ
422	1	HYL4_PIG	14	23.3	7	23.3	19	1	MDH_COMAC	P80539	comamonas a
423	1	MARI_ALTSP	14	23.3	7	23.3	19	1	PAJ5_HUMAN	P24606	homo sapien
424	1	PHI_PRUSE	14	23.3	7	23.3	19	1	PHLC_STAUA	P80924	staphylococ
425	1	PPBL_PSEAE	14	23.3	7	23.3	19	1	PSBN_SYNVU	P12313	synthocococ
426	1	SCK3_LEIQU	14	23.3	7	23.3	19	1	SCX6_TITBA	P56610	tityus bahi
427	1	SODN_STRCO	14	23.3	7	23.3	19	1	TX3_PHONI	P31010	phonetria
428	1	SODN_STRGR	14	23.3	7	23.3	20	1	ACPH_BOVIN	P80227	bos taurus
429	1	SODN_STRSQ	14	23.3	7	23.3	20	1	ANCR_AGRBI	P33588	agkistrodon
430	1	UN04_CLOPA	14	23.3	7	23.3	20	1	CHP_THICU	P80486	thiobacilli
431	1	UN37_CLOPA	14	23.3	7	23.3	20	1	COG2_CHIOP	P34154	chionocete
432	1	ACEA_ACICA	15	23.3	7	23.3	20	1	COG3_CHIOP	P34155	chionocete
433	1	ACT_PINPS	15	23.3	7	23.3	20	1	COGA_PARM	P20732	paralithode
434	1	ALLS_MANSE	15	23.3	7	23.3	20	1	COGB_PARM	P20733	paralithode
435	1	COGI_RAT	15	23.3	7	23.3	20	1	COGC_PARM	P20734	paralithode
436	1	COXJ_THUOB	15	23.3	7	23.3	20	1	COXM_THUOB	P80981	thunus obe
437	1	CXAL_CONGE	15	23.3	7	23.3	20	1	COXN_THUOB	P80980	thunus obe
438	1	CXA2_CONAL	15	23.3	7	23.3	20	1	CRP_MUSCA	P19094	musetelob ca
439	1	FGF1_CANFA	15	23.3	7	23.3	20	1	FLAW_AZOVI	P52964	azotobacter
440	1	KLOM_LUMTE	15	23.3	7	23.3	20	1	GTS2_ASCSU	P48429	ascaris suu
441	1	LEC3_AXIPO	15	23.3	7	23.3	20	1	ITRA_ALBUU	P24925	albizzia ju
442	1	METK_MAIZE	15	23.3	7	23.3	20	1	LPP2_HUMAN	P56642	homo sapien
443	1	MILT_ONCKE	15	23.3	7	23.3	20	1	LPP3_HUMAN	P56643	homo sapien
444	1	PH3_PRUSE	15	23.3	7	23.3	20	1	MCRG_METTE	P22950	methanosarc
445	1	SALC_ONCMY	15	23.3	7	23.3	20	1	MDH_KIBAR	P19978	kibdelospor
446	1	SCOT_RAT	15	23.3	7	23.3	20	1	MDH_MICGL	P19979	microtetras
447	1	SODM_ENTAE	15	23.3	7	23.3	20	1	NEUA_RAT	P29188	rattus norv
448	1	TERM_BPM2	15	23.3	7	23.3	20	1	OKI1_TRIOK	P20005	trimeresuru
449	1	UEI5_HORVU	15	23.3	7	23.3	20	1	OMP1_ACTAC	P20242	actinobacil
450	1	ALRX_PSEPU	16	23.3	7	23.3	20	1	PGK_CLOPA	P81346	clostridium
451	1	ARCD_PSEPU	16	23.3	7	23.3	20	1	PSAL_SYNVU	P25937	synthocococ
452	1	CERB_RAT	16	23.3	7	23.3	20	1	PRRR_PYPAP	P37362	pyrrocococ
453	1	CFAB_BOVIN	16	23.3	7	23.3	20	1	RIPX_CUCPE	P80750	cucurbita p
454	1	CXA2_CONMA	16	23.3	7	23.3	20	1	RLC1_HALMA	P12740	haloarculla
455	1	CXA3_CONAL	16	23.3	7	23.3	20	1	SODF_PASPI	P81527	pasteurella
456	1	FENR_STRGR	16	23.3	7	23.3	20	1	SVR_RAT	P40329	rattus norv
457	1	FOR2_MYRGU	16	23.3	7	23.3	20	1	UN05_PINPS	P81674	pinus pinas
458	1	HTPG_ACICA	16	23.3	7	23.3	20	1	FARP_WONEX	P41966	monieria ex
459	1	KPKX_THEAC	16	23.3	7	23.3	20	1	FARP_ASCSU	P43171	ascaris suu
460	1	KTRC_AREMA	16	23.3	7	23.3	20	1	FTBB_PAPAN	P19344	papio anubi
461	1	PA2_NAUSP	16	23.3	7	23.3	20	1	FARP_MYTED	P42560	mytilus edu
462	1	PH2_PRUSE	16	23.3	7	23.3	20	1	BRK_MEGFL	P12797	megascolia
463	1	PSAJ_SPIOL	16	23.3	7	23.3	20	1	TKN_KASSE	P08611	kassina sen
464	1	RIPX_TRIKI	16	23.3	7	23.3	20	1	BRK_PARID	P42717	parapolybia
465	1	TRYP_FELCA	16	23.3	7	23.3	20	1	MYI4_PHEVI	P46980	pheretima v
466	1	UPAB_HUMAN	16	23.3	7	23.3	20	1	CBPB_PROAT	P19628	protopterus
467	1	APID_BOMPA	17	23.3	7	23.3	20	1	LUXB_KRYAS	P13000	krystophana
468	1	ATPI_PAVLU	17	23.3	7	23.3	20	1	OBP_LYMDI	P34173	lymantria d
469	1	EFQ_THAQO	17	23.3	7	23.3	20	1	ALAT_PIG	P13191	sus scrofa
470	1	FLAW_AZOC	17	23.3	7	23.3	20	1	BULB_NARPS	P80554	narcissus p
471	1	GSHX_PINPS	17	23.3	7	23.3	20	1	DCMS_FSECF	P19915	pseudomonas
472	1	ITHB_HINNE	17	23.3	7	23.3	20	1	YOA4_KLEAE	P56506	klebsiella

546	5	16.7	4	1	EOSI_HUMAN	P02731	homo sapien	619	5	16.7	10	1	COXQ_RABIT	P80336	oryctolagus
547	5	16.7	4	1	FLRP_HIRME	P42561	hirudo medi	620	5	16.7	10	1	ESL_LACCA	P81758	lactobacill
548	5	16.7	4	1	FMRF_NACNI	P01162	macrocallis	621	5	16.7	10	1	FARC_CALVO	P41867	calliphora
549	5	16.7	4	1	TUFT_HUMAN	P01858	homo sapien	622	5	16.7	10	1	FARP_LOCMI	P38553	locusta mig
550	5	16.7	5	1	BI0B_SALRY	P13678	salmonella	623	5	16.7	10	1	FARB_MANSE	P18523	manduca sex
551	5	16.7	5	1	TRM3_ECOLI	P13973	escherichia	624	5	16.7	10	1	FIBB_CERSI	P14537	ceratotheri
552	5	16.7	5	1	UC22_MAIZE	P80628	zea mays (m	625	5	16.7	10	1	FARB_HUMAN	P01358	homo sapien
553	5	16.7	6	1	ACPH_RABIT	P25154	oryctolagus	626	5	16.7	10	1	GLEM_HUMAN	P02728	homo sapien
554	5	16.7	6	1	UN06_CLOPA	P81351	clostridium	627	5	16.7	10	1	LCMS_LEUMA	P21144	leucophaea
555	5	16.7	7	1	CARP_MYTE	P10420	mytilus edu	628	5	16.7	10	1	LPK2_LOCMI	P41488	locusta mig
556	5	16.7	7	1	CHOX_ALCSP	P16101	alcaligenes	629	5	16.7	10	1	MALE_KLEPN	Q05564	klebsiella
557	5	16.7	7	1	FAR1_HELTI	P41871	helicoma tr	630	5	16.7	10	1	NEWS_DROME	P41494	drosophila
558	5	16.7	7	1	FAR1_PROCL	P38499	procamburus	631	5	16.7	10	1	OPD2_BOVIN	P11180	bos taurus
559	5	16.7	7	1	FAR2_PROCL	P38498	procamburus	632	5	16.7	10	1	PAP1_PARNA	P81863	pardachirus
560	5	16.7	7	1	FAR4_PANRE	P41875	panagrellus	633	5	16.7	10	1	PNEU_HUMAN	P22103	homo sapien
561	5	16.7	7	1	FARB_CALVO	P41866	calliphora	634	5	16.7	10	1	PORB_METTM	P80901	methanobact
562	5	16.7	7	1	IGNO_DACDE	P06294	dactylium d	635	5	16.7	10	1	PSBF_CAPAN	Q03367	capsicum an
563	5	16.7	7	1	LANC_CARUI	P36960	carnobacter	636	5	16.7	10	1	Q2OG_COMTE	P80466	comamonas t
564	5	16.7	7	1	MYOM_APLCA	P15513	aplysia cal	637	5	16.7	10	1	RCA_PINPS	P81084	pinus pinas
565	5	16.7	7	1	UF03_MOUSE	P38641	mus musculus	638	5	16.7	10	1	SPL_HALRO	Q10997	halocynthia
566	5	16.7	7	1	UF04_MOUSE	P38642	mus musculus	639	5	16.7	10	1	SPRC_RABIT	P38233	oryctolagus
567	5	16.7	7	1	UH11_RAT	P56576	rattus norv	640	5	16.7	10	1	SYK_CAMUP	Q48464	campylobact
568	5	16.7	8	1	ACT_CARMA	P80709	carcinus ma	641	5	16.7	10	1	TKL4_LOCMI	P30250	locusta mig
569	5	16.7	8	1	CLP_THICU	P80488	thiobacillu	642	5	16.7	10	1	TKNK_PIG	P01292	sus scrofa
570	5	16.7	8	1	COXG_RAT	P80430	rattus norv	643	5	16.7	10	1	TKN_PHYBI	P08610	phyllomedus
571	5	16.7	8	1	FAR1_PANRE	P41872	panagrellus	644	5	16.7	10	1	TRU2_UREUN	P40752	urechis uni
572	5	16.7	8	1	FAR3_HOMAM	P41486	homarus ame	645	5	16.7	10	1	TRP5_LEUMA	P81737	leucophaea
573	5	16.7	8	1	FAR4_HOMAM	P41487	homarus ame	646	5	16.7	10	1	TRP6_LEUMA	P81738	leucophaea
574	5	16.7	8	1	FAR8_CALVO	P41863	calliphora	647	5	16.7	10	1	TRP7_LEUMA	P81739	leucophaea
575	5	16.7	8	1	LMT2_LOCMI	P22396	locusta mig	648	5	16.7	10	1	TRP8_LEUMA	P81740	leucophaea
576	5	16.7	8	1	LPK_LEUMA	P13049	leucophaea	649	5	16.7	10	1	TRP9_LEUMA	P81741	leucophaea
577	5	16.7	8	1	LPMS_STAEP	P22211	staphylococ	650	5	16.7	10	1	UPA4_HUMAN	P30090	homo sapien
578	5	16.7	8	1	NPB_BOVIN	P15507	bos taurus	651	5	16.7	10	1	UPA5_HUMAN	P30091	homo sapien
579	5	16.7	8	1	NS3_MYCTU	P81152	mycobacteri	652	5	16.7	10	1	URAI1_HUMAN	P32118	homo sapien
580	5	16.7	8	1	RS1_ERWCH	P37985	erwinia chr	653	5	16.7	10	1	URA6_HUMAN	P32080	homo sapien
581	5	16.7	8	1	RS7_MYCIT	P33564	mycobacteri	654	5	16.7	10	1	URA7_HUMAN	P34990	homo sapien
582	5	16.7	8	1	UC26_MAIZE	P80632	zea mays (m	655	5	16.7	10	1	URE3_MORNO	P17339	morganella
583	5	16.7	8	1	UH09_RAT	P56575	rattus norv	656	5	16.7	10	1	UXA1_CHLTR	P38002	chlamydia t
584	5	16.7	8	1	UPA1_HUMAN	P30087	homo sapien	657	5	16.7	10	1	UXA7_CHLTR	P38008	chlamydia t
585	5	16.7	9	1	CONO_CONGE	P05486	conus geogr	658	5	16.7	10	1	UXB1_YEAST	P93012	saccharomyc
586	5	16.7	9	1	CONO_CONST	P05487	conus stria	659	5	16.7	11	1	BPP3_BOTIN	P30423	bothrops in
587	5	16.7	9	1	DCML_PSECF	P19913	pseudomonas	660	5	16.7	11	1	BPP4_BOTIN	P30424	bothrops in
588	5	16.7	9	1	DNF1_LOCMI	P16339	locusta mig	661	5	16.7	11	1	BPPB_AKHA	P01021	agkistrodon
589	5	16.7	9	1	FAR1_CALVO	P41856	calliphora	662	5	16.7	11	1	BPPB_AKHP	P04562	agkistrodon
590	5	16.7	9	1	FAR2_CALVO	P41857	calliphora	663	5	16.7	11	1	CSI5_BACSU	P81095	bacillus su
591	5	16.7	9	1	FAR2_PANRE	P41873	panagrellus	664	5	16.7	11	1	ESI_RAT	P56571	rattus norv
592	5	16.7	9	1	FAR3_CALVO	P41858	calliphora	665	5	16.7	11	1	FAR9_CALVO	P41864	calliphora
593	5	16.7	9	1	FAR4_CALVO	P41859	calliphora	666	5	16.7	11	1	HS70_PINPS	P81672	pinus pinas
594	5	16.7	9	1	FAR5_ASCSU	P43170	ascaris suu	667	5	16.7	11	1	LADD_ONCMY	P81018	oncorhynch
595	5	16.7	9	1	FAR5_CALVO	P41860	calliphora	668	5	16.7	11	1	NUHM_CANFA	P49820	canis famill
596	5	16.7	9	1	FAR6_CALVO	P41861	calliphora	669	5	16.7	11	1	PVK_PERAM	P41837	periplaneta
597	5	16.7	9	1	FAR7_CALVO	P41862	calliphora	670	5	16.7	11	1	Q2OA_COMTE	P80464	comamonas t
598	5	16.7	9	1	FAR9_ASCSU	P43172	ascaris suu	671	5	16.7	11	1	RRPL_CHAV	P13179	chandiura
599	5	16.7	9	1	FARA_CALVO	P41865	calliphora	672	5	16.7	11	1	TKC2_CALVO	P41518	calliphora
600	5	16.7	9	1	FARD_CALVO	P41868	calliphora	673	5	16.7	11	1	TKNA_HORSE	P01290	equus cabal
601	5	16.7	9	1	FIBB_ERIPA	P19346	erythrocebu	674	5	16.7	11	1	ULAG_HUMAN	P31933	homo sapien
602	5	16.7	9	1	FIBB_MACFU	P19345	macaca fusc	675	5	16.7	12	1	DCML_PSECA	P19919	pseudomonas
603	5	16.7	9	1	FIBB_PAPHA	P19343	papio hamad	676	5	16.7	12	1	EFTU_PSEAE	P09591	pseudomonas
604	5	16.7	9	1	FIBB_THEGE	P19342	theropithec	677	5	16.7	12	1	FARI_CALVO	P41869	calliphora
605	5	16.7	9	1	LMT3_LOCMI	P41489	locusta mig	678	5	16.7	12	1	HCYB_MEGCR	Q10584	megathura c
606	5	16.7	9	1	OXYT_EISFO	P42998	eisenia foe	679	5	16.7	12	1	LMT1_LOCMI	P22395	locusta mig
607	5	16.7	9	1	SAP_STOVA	P24047	stomopneute	680	5	16.7	12	1	OPS3_DROVI	P17645	drosophila
608	5	16.7	9	1	TRP4_LEUMA	P81736	leucophaea	681	5	16.7	12	1	PAD1_MICFM	P25072	micrurus fu
609	5	16.7	9	1	UF02_MOUSE	P38640	mus musculus	682	5	16.7	12	1	PORD_METTM	P80903	methanobact
610	5	16.7	9	1	ULAE_HUMAN	P31931	homo sapien	683	5	16.7	12	1	POTB_SALTY	Q56060	salmonella
611	5	16.7	9	1	ULAH_HUMAN	P31934	homo sapien	684	5	16.7	12	1	RR16_GINBI	P36207	giakgo bilo
612	5	16.7	9	1	ULAK_MOUSE	P99031	mus musculus	685	5	16.7	12	1	SOIS_BACSU	P80863	bacillus su
613	5	16.7	9	1	UN19_CLOPA	P81355	clostridium	686	5	16.7	12	1	TKN1_KASMA	P08613	kassina mac
614	5	16.7	9	1	UPA3_HUMAN	P30089	homo sapien	687	5	16.7	12	1	TM2A_METNA	P08652	methanosarc
615	5	16.7	9	1	XYLA_STRSQ	P19149	streptomyce	688	5	16.7	12	1	UCRH_MOUSE	P99028	mus musculus
616	5	16.7	9	1	YBFR_AZOVI	P25825	azotobacter	689	5	16.7	12	1	Y2PY_ECOLI	P17776	escherichia
617	5	16.7	10	1	COX4_THUOB	P80971	thunus obe	690	5	16.7	13	1	ACT7_SOYBN	P15987	glycine max
618	5	16.7	10	1	COXA_ONCMY	P80328	oncorhynch	691	5	16.7	13	1	AH4_PRUSE	P29262	prunus sero

692	5	16.7	13	1	ATPB_ARATH	P19366	arabidopsis	765	5	16.7	15	1	NUO8_SOLITU	P80731	solanum tub
693	5	16.7	13	1	BP37_LEUMA	P81754	leucophaea	766	5	16.7	15	1	PDGB_PIG	P20034	sus scrofa
694	5	16.7	13	1	CR1_APLCA	Q10998	aplysia cal	767	5	16.7	15	1	PGKH_PHYPA	P80659	physcomitris
695	5	16.7	13	1	CRBL_VESCR	P01518	vespa crabr	768	5	16.7	15	1	PIAS_MICAE	P10625	microcystis
696	5	16.7	13	1	CXA2_CONGE	P01520	conus geogr	769	5	16.7	15	1	PRP_MYCBO	P80149	mycobacteri
697	5	16.7	13	1	ECDE_LYMDI	P80941	lymantria d	770	5	16.7	15	1	TAL_TREBR	P34070	tremella br
698	5	16.7	13	1	FARB_ASCSU	P34173	ascaris suu	771	5	16.7	15	1	THL_CLOPA	P81347	clostridium
699	5	16.7	13	1	FIBB_HYLLA	P14472	hylobates l	772	5	16.7	15	1	TRPA_LEUNA	P81753	leucophaea
700	5	16.7	13	1	IDHA_CANFA	P54836	canis famli	773	5	16.7	15	1	UBL1_MONDO	P50103	monodelphis
701	5	16.7	13	1	IDHC_PIG	P20304	sus scrofa	774	5	16.7	15	1	UC06_MAIZE	P80612	zea mays (m
702	5	16.7	13	1	IDHP_RAT	P56574	rattus norv	775	5	16.7	15	1	UC25_MAIZE	P80631	zea mays (m
703	5	16.7	13	1	ITB5_BOVIN	P80747	bos taurus	776	5	16.7	15	1	UC28_MAIZE	P80634	zea mays (m
704	5	16.7	13	1	LMAL_LOCFI	P38496	locusta mig	777	5	16.7	15	1	UN01_PINPS	P81106	pinus pinas
705	5	16.7	13	1	LMT4_LOCFI	P41490	locusta mig	778	5	16.7	15	1	UN04_PINPS	P81673	pinus pinas
706	5	16.7	13	1	NP4_LYMSI	P80181	lymnaea sta	779	5	16.7	15	1	VORA_METTM	P80907	methanobact
707	5	16.7	13	1	NP5_LYMSI	P80182	lymnaea sta	780	5	16.7	15	1	AH1_PRUSE	P29259	trichus sero
708	5	16.7	13	1	NUPM_HUMAN	P51970	homo sapien	781	5	16.7	15	1	ANP8_ELEGR	P11921	eleginus gr
709	5	16.7	13	1	ODPA_CANFA	P49823	canis famli	782	5	16.7	15	1	BAI1_EUBSP	P33771	eubacterium
710	5	16.7	13	1	ORCK_ORCLI	P37086	orconectes	783	5	16.7	15	1	DBH3_RHIDE	P80605	rhizobium l
711	5	16.7	13	1	P60_CANFA	P49818	canis famli	784	5	16.7	15	1	FIBA_CERSI	P14535	ceratotheri
712	5	16.7	13	1	PEDI_HYDAT	P80578	hydra atten	785	5	16.7	15	1	FIBA_MACFU	P12803	macaca fusc
713	5	16.7	13	1	PSAE_PEA	P20118	pisum sativ	786	5	16.7	15	1	FIBA_MANLE	P14455	mandrillus
714	5	16.7	13	1	RL30_SALTY	O54300	salmonella	787	5	16.7	15	1	FIBA_RABIT	P14461	oryctolagus
715	5	16.7	13	1	RPOC_MYCGA	P47716	mycoplasma	788	5	16.7	15	1	FOR1_MYRGU	P81438	myrmecia gu
716	5	16.7	13	1	TAL3_TREME	P01370	tremella me	789	5	16.7	15	1	H5_COTJA	P18638	coturnix co
717	5	16.7	13	1	UHA3_CANFA	P56535	canis famli	790	5	16.7	15	1	HP29_SARPE	P29184	sarcophaga
718	5	16.7	13	1	VG16_BACSU	P80867	bacillus su	791	5	16.7	15	1	IBP4_PIG	P24854	sus scrofa
719	5	16.7	13	1	YC1A_SALTY	P25944	salmonella	792	5	16.7	15	1	LPH1_ECOLI	P30358	escherichia
720	5	16.7	13	1	YPB2_LACLC	P42021	lactococcus	793	5	16.7	15	1	MDH_SYNYA	P80460	synechocyst
721	5	16.7	14	1	ATP6_SPIOL	P80086	spinacia ol	794	5	16.7	15	1	MMPX_SOLITU	P80501	solanum tub
722	5	16.7	14	1	BGAT_MOUSE	P38649	m histo-bio	795	5	16.7	15	1	ODO2_BOVIN	P11179	bos taurus
723	5	16.7	14	1	FIBB_WANLE	P14474	mandrillus	796	5	16.7	15	1	ODPB_SOLITU	P81419	solanum tub
724	5	16.7	14	1	GLGS_SPIOL	P55235	spinacia ol	797	5	16.7	15	1	PGK_VIBCH	P96154	vibrio chol
725	5	16.7	14	1	GLPK_STRGR	P25013	streptomyce	798	5	16.7	15	1	PGTL_PELAC	P80563	pelobacter
726	5	16.7	14	1	GR75_CANFA	P99502	canis famli	799	5	16.7	15	1	PX_RAT	P14630	rattus norv
727	5	16.7	14	1	IFG2_RAT	P81795	rattus norv	800	5	16.7	15	1	RBL_CAPAN	P27063	capsicum an
728	5	16.7	14	1	KPPL_SELMI	P25933	selenastrum	801	5	16.7	15	1	RBL_CUCSA	P27064	cucumis sat
729	5	16.7	14	1	LECB_PSOSC	P22584	psophocarpu	802	5	16.7	15	1	RBL_VIGSI	P27067	vigna sinen
730	5	16.7	14	1	LPBR_BACLI	Q04303	bacillus li	803	5	16.7	15	1	TL17_SPIOL	P81778	spinacia ol
731	5	16.7	14	1	MY14_EISFO	P46979	eisenia foe	804	5	16.7	15	1	UVSX_BPT6	Q06728	bacterioph
732	5	16.7	14	1	PSAG_CUCSA	P42049	cucumis sat	805	5	16.7	15	1	A45K_MYCBO	P80069	mycobacteri
733	5	16.7	14	1	SAP2_ARBPU	P11760	arabacia pun	806	5	16.7	15	1	ACT6_SOYBN	P15986	glycine max
734	5	16.7	14	1	TAT_HV1W2	P12509	human immun	807	5	16.7	15	1	ALYS_MYCPH	P81528	mycobacteri
735	5	16.7	14	1	TAT_HV1Z8	P12511	human immun	808	5	16.7	15	1	ARGD_SALTY	P40732	salmonella
736	5	16.7	14	1	UC04_MAIZE	P80610	zea mays (m	809	5	16.7	15	1	B29K_PORGI	P81784	porphyromon
737	5	16.7	14	1	UC15_MAIZE	P80621	zea mays (m	810	5	16.7	15	1	DNAK_MYCSM	P80692	mycobacteri
738	5	16.7	14	1	UC34_MAIZE	P80640	zea mays (m	811	5	16.7	15	1	JHBP_PLAVG	P56675	platyrepia
739	5	16.7	14	1	UHA1_CANFA	P99503	canis famli	812	5	16.7	15	1	MDH_ACIDE	P80540	acidovorax
740	5	16.7	14	1	ULA4_HUMAN	P30039	homo sapien	813	5	16.7	15	1	PC24_BRANA	P81097	brassica na
741	5	16.7	14	1	YGDH_THEAC	Q05213	thermoplas	814	5	16.7	15	1	PNOC_PIG	P55791	sus scrofa
742	5	16.7	15	1	48KD_BACCE	P80173	bacillus ce	815	5	16.7	15	1	SP51_BACLI	P12241	synechococc
743	5	16.7	15	1	AH2_PRUSE	P29260	prunus sero	816	5	16.7	15	1	SVY_URSAR	P27642	bacillus li
744	5	16.7	15	1	ALB2_TRASC	P81189	trachemys s	817	5	16.7	15	1	TRP2_LEUNA	P36396	ursus arcto
745	5	16.7	15	1	CLOA_RAT	P31720	rattus norv	818	5	16.7	15	1	UN15_CLOPA	P81733	leucophaea
746	5	16.7	15	1	CH11_PEA	P21225	pisum sativ	819	5	16.7	15	1	YALA_TRYB	P81354	clostridium
747	5	16.7	15	1	CYSK_CLOPA	P81340	clostridium	820	5	16.7	15	1	AROF_STREB	P17961	trypanosoma
748	5	16.7	15	1	CYST_SALTY	P41032	salmonella	821	5	16.7	15	1	DRPH_PANBO	P80575	streptomyce
749	5	16.7	15	1	EF1A_MICCR	P81266	microplitis	822	5	16.7	15	1	DRPH_UCAPU	P01209	pandalus bo
750	5	16.7	15	1	ESTB_SCHGA	P81011	schizaphis	823	5	16.7	15	1	FIXA_RHILE	P08871	uca pugilat
751	5	16.7	15	1	ESTJ_MANSE	P19985	manduca sex	824	5	16.7	15	1	OBP_HYACE	P14313	rhizobium l
752	5	16.7	15	1	FIBA_ANAPL	P12801	anas platyr	825	5	16.7	15	1	RL24_PROVU	P34172	hyalophora
753	5	16.7	15	1	GR78_HORSE	P16392	equus cabal	826	5	16.7	15	1	RL24_SALTY	P20032	proteus vul
754	5	16.7	15	1	GUAN_DIDMA	P55936	didelphis m	827	5	16.7	15	1	RL24_SERNA	P37438	salmonella
755	5	16.7	15	1	ITRB_ALBUJU	P24927	albizzia ju	828	5	16.7	15	1	YMDB_CHLUA	P49624	serratia ma
756	5	16.7	15	1	KP22_SELMI	P25934	selenastrum	829	5	16.7	15	1	ADC_CLOPA	Q45827	chloroflexu
757	5	16.7	15	1	LEC1_PSOSC	P22582	psophocarpu	830	5	16.7	15	1	ANP7_ELEGR	P81336	clostridium
758	5	16.7	15	1	LEC2_PSOSC	P22585	psophocarpu	831	5	16.7	15	1	ATPB_CANFA	P11920	eleginus gr
759	5	16.7	15	1	LEC3_PSOSC	P22583	psophocarpu	832	5	16.7	15	1	COOT_SARBU	P99504	canis famli
760	5	16.7	15	1	LEU3_SULS7	P50455	sulfolobus	833	5	16.7	15	1	COX4_ONCYH	Q09148	sarcophaga
761	5	16.7	15	1	LM22_LOCFI	P38497	locusta mig	834	5	16.7	15	1	DURB_STRGM	P80327	oncorhynch
762	5	16.7	15	1	LPL_TETH	P21234	thermus acu	835	5	16.7	15	1	FIBA_ANTAM	P36502	streptococ
763	5	16.7	15	1	MCR4_METTE	P22948	methanosarc	836	5	16.7	15	1	FIBA_ANTAM	P14440	antilocapra
764	5	16.7	15	1	NUO3_SOLITU	P80563	solanum tub	837	5	16.7	15	1	FIBA_BISBO	P14441	bison bonas

838	5	16.7	19	1	FIBA_CEREL	P14446	cervus elap	911	3	10.0	8	1	CPD1_ENTFA	P13269	enterococcu
839	5	16.7	19	1	FLA3_SPIAU	P21986	spirochaeta	912	3	10.0	9	1	CCAP_CARMA	P38556	carcinus ma
840	5	16.7	19	1	FWO1_CAVPO	P43328	cavia porce	913	3	10.0	9	1	MOSF_CLYUA	P19853	clypeaster
841	5	16.7	19	1	HB22_UROHA	P19992	uromastyx h	914	3	10.0	9	1	SAMP_MUSCA	P15095	msteilus ca
842	5	16.7	19	1	H170_RAT	P21794	rattus norv	915	3	10.0	10	1	COXM_RAT	P80431	rattus norv
843	5	16.7	19	1	LPGE_ECOLI	P33236	escherichia	916	3	10.0	10	1	GS15_BACSU	P80861	bacillus su
844	5	16.7	19	1	MIFH_TRISP	P81529	trichinella	917	3	10.0	10	1	SIAP_BACTG	P49325	bacillus th
845	5	16.7	19	1	PHSL_DESBN	P13066	desulfovibr	918	3	10.0	10	1	TKNB_ONCHY	P28500	oncorhynchu
846	5	16.7	19	1	PBBH_PSEAE	P35483	pseudomonas	919	3	10.0	10	1	TKNB_RANRI	P29135	rana ridibu
847	5	16.7	19	1	PSAE_CUCSA	P42047	cucumis sat	920	3	10.0	10	1	TKNC_RANCA	P22690	rana cateab
848	5	16.7	19	1	PSBM_SYNYU	P12312	synechococc	921	3	10.0	10	1	UXA2_CHLTR	P38003	chlamydia t
849	5	16.7	19	1	PTHP_STRSA	P24365	streptococc	922	3	10.0	10	1	UXA2_CHLTR	P38006	chlamydia t
850	5	16.7	19	1	PYRB_PSEFL	P56585	pseudomonas	923	3	10.0	11	1	D3H1_HUMAN	P31937	homo sapien
851	5	16.7	19	1	RECO_SALTY	P40724	salmonella	924	3	10.0	11	1	MORN_HUMAN	P01163	homo sapien
852	5	16.7	19	1	RL10_CITFR	P43448	citrobacter	925	3	10.0	12	1	TKN_ELEMO	P01293	eledone mos
853	5	16.7	19	1	RL35_LISMO	O53085	listeria mo	926	3	10.0	12	1	XYLA_STRVN	P14405	streptomyce
854	5	16.7	19	1	TPIS_CLOPA	P81348	clostridium	927	3	10.0	13	1	CRBL_ICASP	P17237	icaria sp.
855	5	16.7	19	1	TRP3_LEUMA	P81735	leucophaea	928	3	10.0	13	1	CRBL_VESAN	P17233	vespa anali
856	5	16.7	19	1	TRPB_KLEAE	P14552	klebsiella	929	3	10.0	13	1	CRBL_VESLE	P17235	vespula lew
857	5	16.7	19	1	UKAL_HUMAN	P31940	homo sapien	930	3	10.0	13	1	CRBL_VESMA	P17232	vespa manda
858	5	16.7	20	1	AROD_ARYME	P46380	amycolotops	931	3	10.0	13	1	CRBL_VESTR	P17231	vespa tropi
859	5	16.7	20	1	ATP4_SPIOL	P80085	spinacia ol	932	3	10.0	13	1	CRBL_VESXA	P17234	vespa xanth
860	5	16.7	20	1	CATA_ACIRA	P81422	acinetobact	933	3	10.0	13	1	CRTC_RANES	P31832	rana escul
861	5	16.7	20	1	CO4_SHEEP	P05542	ovis aries	934	3	10.0	13	1	HPB1_RANES	P32415	rana escul
862	5	16.7	20	1	COXB_THUOB	P80974	thunus obe	935	3	10.0	13	1	HPB9_RANES	P32416	rana escul
863	5	16.7	20	1	COXQ_ONCHY	P80335	oncorhynchu	936	3	10.0	13	1	LPAA_PORGI	P84411	porphyromon
864	5	16.7	20	1	COXQ_THUOB	P80983	thunus obe	937	3	10.0	13	1	UN10_CLOPA	P81345	clostridium
865	5	16.7	20	1	CPBX_CAVPO	P34033	cavia porce	938	3	10.0	14	1	CRBL_VESOR	P17236	vespa orien
866	5	16.7	20	1	CUDP_VERCH	P80406	verticilliliu	939	3	10.0	14	1	UC18_MAIZE	P80624	zea mays (m
867	5	16.7	20	1	DEF6_DERFA	P49276	dermatophag	940	3	10.0	14	1	UN46_CLOPA	P81362	clostridium
868	5	16.7	20	1	DER6_DERPT	P49277	dermatophag	941	3	10.0	15	1	CDN3_LITGL	P56248	litoria gil
869	5	16.7	20	1	DNAK_CLOPA	P81341	clostridium	942	3	10.0	15	1	IRBP_CRISP	P13665	cricketidae
870	5	16.7	20	1	DNAK_MYCAV	P80462	mycobacteri	943	3	10.0	15	1	LPF_ECOLI	P03057	escherichia
871	5	16.7	20	1	DNAK_THIFE	P29133	thiobacilli	944	3	10.0	15	1	PSAO_CUCSA	P42052	cucumis sat
872	5	16.7	20	1	EMA2_MOUSE	P31230	mus musculus	945	3	10.0	15	1	UC17_MAIZE	P80623	zea mays (m
873	5	16.7	20	1	FRHA_METRA	P80489	methanosarc	946	3	10.0	15	1	UC30_MAIZE	P80636	zea mays (m
874	5	16.7	20	1	HELT_HELBO	P46593	heloderma h	947	3	10.0	15	1	URE2_THUOR	P20016	thunus th
875	5	16.7	20	1	KORC_METTM	P80906	methanobact	948	3	10.0	16	1	DHE2_THUOR	P17338	morganelia
876	5	16.7	20	1	LPTR_BACST	P03658	bacillus st	949	3	10.0	17	1	BOL2_MEGPE	P07493	megabombus
877	5	16.7	20	1	LPTR_BACSU	P23053	bacillus su	950	3	10.0	17	1	BOL5_MEGPE	P07496	megabombus
878	5	16.7	20	1	LYC_FELCA	P37155	felis silve	951	3	10.0	17	1	CHH3_BOMBO	P20729	bombus mori
879	5	16.7	20	1	M117_BOVIN	P35451	bos taurus	952	3	10.0	18	1	AHD2_TETPY	P35430	tetrabympa
880	5	16.7	20	1	MIF_PIG	P80928	sus scrofa	953	3	10.0	18	1	PSAI_SPIOL	P17228	spinacia ol
881	5	16.7	20	1	PORC_METTM	P80902	methanobact	954	3	10.0	18	1	TAN2_SCYCA	P08609	scyllorhinu
882	5	16.7	20	1	PSAF_MAIZE	P13193	zea mays (m	955	3	10.0	19	1	DURA_STRGV	P26504	streptococc
883	5	16.7	20	1	PSAF_PEA	P20119	pisum sativ	956	3	10.0	19	1	IRBP_CAVPO	P17666	cavia porce
884	5	16.7	20	1	PSAF_PEA	P17226	pisum sativ	957	3	10.0	19	1	MIFH_TRIMR	P81530	trichuris m
885	5	16.7	20	1	PSBM_WHEAT	P55967	tritricum ae	958	3	10.0	19	1	TGBL_TRILO	P80070	trichoderma
886	5	16.7	20	1	PYR2_PSEFL	P58586	pseudomonas	959	3	10.0	20	1	FRE3_LITLO	P56249	litoria inf
887	5	16.7	20	1	RECK_AZOVI	P37863	azotobacter	960	3	10.0	20	1	STYA_STYCL	P81469	styla clav
888	5	16.7	20	1	RL10_PROVU	P51411	proteus vul	961	3	10.0	20	1	STYB_STYCL	P01157	homo sapien
889	5	16.7	20	1	RL7_NEIME	P80716	neisseria m	962	2	6.7	3	1	GRWM_HUMAN	P01157	homo sapien
890	5	16.7	20	1	SAMP_PLEPL	P20677	pleuronecte	963	2	6.7	3	1	LUXE_VIBFI	P24272	vibrio fisc
891	5	16.7	20	1	SUCD_PSEAE	O51567	pseudomonas	964	2	6.7	4	1	DCML_PSECH	P19916	pseudomonas
892	5	16.7	20	1	TENA_ACTTE	P30833	actinia ten	965	2	6.7	4	1	DCMS_PSECH	P19918	pseudomonas
893	5	16.7	20	1	TENB_ACTTE	P30834	actinia ten	966	2	6.7	5	1	BIOA_CITFR	P19918	pseudomonas
894	5	16.7	20	1	TPX_CLOPA	P81361	clostridium	967	2	6.7	5	1	BIOA_SALTY	P13677	salmonella
895	5	16.7	20	1	TRY8_ECOLI	P33789	escherichia	968	2	6.7	5	1	BIOD_CITFR	P12997	citrobacter
896	5	16.7	20	1	TRY8_STREX	P80420	streptomyce	969	2	6.7	5	1	UXA4_CHLTR	P12997	citrobacter
897	5	16.7	20	1	UC33_MAIZE	P80639	zea mays (m	970	2	6.7	6	1	THOF_SARBU	P41495	sarcophaga
898	5	16.7	20	1	YPRB_SERMA	P22581	serratia ma	971	2	6.7	6	1	TRPI_PSEPU	P36414	pseudomonas
899	4	13.3	3	1	THYL_PIG	P01151	sus scrofa	972	2	6.7	6	1	VP19_HSVIK	P23210	herpes simp
900	4	13.3	10	1	RNKD_PIG	P19851	gallus gall	973	2	6.7	7	1	UC24_MAIZE	P80630	zea mays (m
901	4	13.3	20	1	RNKD_PIG	P80551	sus scrofa	974	2	6.7	8	1	FUSS_FUSSO	P81010	fusarium so
902	3	10.0	4	1	ACH1_ACHFU	P35904	achatina fu	975	2	6.7	9	1	MOSH_CLYJA	P19852	clypeaster
903	3	10.0	5	1	PAP2_PARMA	P81864	pardachirus	976	2	6.7	9	1	TALL_PICJA	P17440	pichia jadi
904	3	10.0	5	1	SUGA_ACHDO	P19991	acheta dome	977	2	6.7	9	1	THYF_PIG	P01255	sus scrofa
905	3	10.0	5	1	TPIS_CANFA	P54714	canis fami	978	2	6.7	9	1	UPA6_HUMAN	P30092	homo sapien
906	3	10.0	6	1	CIP1_MYTED	P13736	mytilus edu	979	2	6.7	10	1	AH3_PRUSE	P29261	prunus sero
907	3	10.0	6	1	CIP2_MYTED	P13737	mytilus edu	980	2	6.7	10	1	COXK_ONCHY	P80332	oncorhynchu
908	3	10.0	7	1	CCF1_ENTFA	P20104	enterococcu	981	2	6.7	10	1	COXQ_SHEEP	P80337	ovis aries
909	3	10.0	7	1	CIA_ENTFA	P19332	enterococcu	982	2	6.7	10	1	MOSQ_CLYJA	P19962	clypeaster
910	3	10.0	8	1	CAD1_ENTFA	P13268	enterococcu	983	2	6.7	10	1	NS1_MYCTU	P81135	mycobacteri

984 2 6.7 10 1 RRPL_PHODV
 985 2 6.7 10 1 UPA2_HUMAN
 986 2 6.7 10 1 UPA8_HUMAN
 987 2 6.7 10 1 UXA3_CHLTR
 988 2 6.7 10 1 VEG6_BACSU
 989 2 6.7 10 1 XYNB_DICB4
 990 2 6.7 12 1 CD11_LITXA
 991 2 6.7 12 1 CD14_LITXA
 992 2 6.7 12 1 UH03_RAT
 993 2 6.7 12 1 ULAL_MOUSE
 994 2 6.7 13 1 BLAC_STRGR
 995 2 6.7 13 1 CHEP_PARID
 996 2 6.7 13 1 EP65_HUMAN
 997 2 6.7 13 1 LIGA_TRAVE
 998 2 6.7 13 1 LIGB_TRAVE
 999 2 6.7 14 1 MAST_VESCR
 1000 2 6.7 14 1 MAST_VESLE

ALIGNMENTS

RESULT 1
 UC08_MAIZE
 ID UC08_MAIZE STANDARD; PRT; 15 AA.
 AC P80614;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 159)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC eumhyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
 OC Poaceae; Zea.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=COLEOPTILE;
 RA TOUZET P., RICCARDI F., MORIN C., DAMERVAL C., HUET J.-C.,
 RA PERNOLET J.-C., ZIVY M., DE VIENNE D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program".
 RL Theor. Appl. Genet. 33:997-1005(1996).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.4, ITS MW IS: 38.8 KD.
 CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR MAIZE-2DPAGE; P80614; COLEOPTILE.
 DR MAIZEDB; 123934; -.
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1785 MW; AD659C49 CRC32;

Query Match 66.7%; Score 20; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 53;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 |||
 Db 3 WRNAMY 8

RESULT 2
 CAT3_FASHE
 ID CAT3_FASHE STANDARD; PRT; 19 AA.
 AC P80332;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE PUTATIVE CATHEPSIN L3 (EC 3.4.22.15) (NEWLY EXCYSTED JUVENILE PROTEIN
 DE 8) (FRAGMENT)
 OS Fasciola hepatica (Liver fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomatidae; Echinostomata; Fascioloidae;
 RN Fasciolidae; Fasciola.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 95366993.
 RA TKALCEVIC J., ASHMAN K., MEEUSEN E.;
 RT "Fasciola hepatica: rapid identification of newly excysted juvenile
 RT proteins".
 RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
 CC -!- FUNCTION: THIOLE PROTEASE.
 CC -!- SUBUNIT: DIMER OF AN HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
 CC BONDS (POTENTIAL).
 CC -!- SUBCELLULAR LOCATION: LYSOSOMAL (POTENTIAL).
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE NEWLY EXCYSTED JUVENILE
 CC STAGE.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
 CC PAPAIN FAMILY OF THIOLE PROTEASES.
 DR HSP; P25774; IBXF.
 DR PROSITE; PS00139; THIOLE PROTEASE_CYS; PARTIAL.
 DR PROSITE; PS00639; THIOLE PROTEASE_HIS; PARTIAL.
 DR PROSITE; PS00640; THIOLE PROTEASE_ASN; PARTIAL.
 DR PFAM; PF00112; Peptidase_C1; 1.
 KW Hydrolase; Thiole protease; Lysosome.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2242 MW; 363E4116 CRC32;

Query Match 63.3%; Score 19; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 11e+02;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 |||
 Db 8 WREYGY 13

RESULT 3
 WWAL_ACHFU
 ID WWAL_ACHFU STANDARD; PRT; 7 AA.
 AC P35919;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE WWAMIDE-1.
 OS Achatina fulica (Giant African snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
 OC Achatinacea; Achatinidae; Achatina.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=GANGLION;
 RX MEDLINE; 93265912.
 RA MINAKATA H., IKEDA T., MUNEOKA Y., KOBAYASHI M., NOMOTO K.;
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from
 RT ganglia of the African giant snail, Achatina fulica.";
 RL FEBS Lett. 323:104-108(1993).
 CC -!- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
 CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
 CC PIR; S33245; S33245.
 DR Neuropeptide; Amidation.
 KW MOD_RES 7 7
 FT MOD_RES 7 7
 SQ SEQUENCE 7 AA; 993 MW; 4BDEA7F1 CRC32;

Query Match 53.3%; Score 16; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
 ||
 Db 1 WR 2

RESULT 4
CEPL_ACHFU
ID CEPL_ACHFU STANDARD; PRT; 11 AA.
AC P22730;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE CARDIO-EXCITATORY PEPTIDE-1 (ACEP-1).
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
RN [1]
RP SEQUENCE.
RC STRAIN=PERUSSAC; TISSUE=HEART ATRIUM;
RX MEDLINE; 90211261.
RA FUJIMOTO K., OHTA N., YOSHIDA M., KUBOTA I., MUNOKA Y., KOBAYASHI M.;
RT "A novel cardio-excitatory peptide isolated from the atria of the
RT African giant snail, Achatina fulica.";
RL Biochem. Biophys. Res. Commun. 167:777-783(1990).
CC -1- FUNCTION: POTENTIATES THE BEAT OF THE VENTRICLE, AND HAS ALSO
CC EXCITATORY ACTIONS ON THE PENIS RETRACTOR MUSCLE, THE BUCCAL
CC MUSCLE AND THE IDENTIFIED NEURONS CONTROLLING THE BUCCAL MUSCLE
CC MOVEMENT OF ACHATINA.
CC -1- SIMILARITY: TO POSSIBLE PEPTIDE L5 FROM APLYSIA.
DR PIR; A34662; A34662.
KW Hormone; Amidation.
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1305 MW; 39B3D100 CRC32;
AMIDATION.

Query Match 53.3%; Score 16; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WR 2
DB 5 WR 6

RESULT 5
CXAL_CONIM
ID CXAL_CONIM STANDARD; PRT; 12 AA.
AC P50983;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-DEC-1998 (Rel. 37, Last annotation update)
DE ALPHA-CONOTOXIN IMI.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Prosobranchia;
OC Neogastropoda; Conoidea; Conidae; Conus.
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=VENOM;
RX MEDLINE; 94266889.
RA MCINTOSH J.M., YOSHIKAWI D., MAHE E., NIELSEN D.B., RIVIER J.E.,
RA GRAY W.R., OLIVERA B.M.;
RT "A nicotinic acetylcholine receptor ligand of unique specificity,
RT alpha-conotoxin Imi.";
RL J. Biol. Chem. 269:16733-16739(1994).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE; 95379776.
RA JOHNSON D.S., MARTINEZ-J., ELGOYEN A.B., HEINEMANN S.F.,
RA MCINTOSH J.M.;
RT "Alpha-conotoxin Imi exhibits subtype-specific nicotinic
RT acetylcholine receptor blockade: preferential inhibition of homomeric
RT alpha 7 and alpha 9 receptors.";
RL Mol. Pharmacol. 48:1194-1199(1995).
CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
CC INHIBIT THEM. IT IS HIGHLY ACTIVE AGAINST THE NEUROMUSCULAR
CC RECEPTOR IN FROG BUT NOT IN MICE. IN CONTRAST, IT INDUCES SEIZURES
CC WHEN INJECTED CENTRALLY IN MICE AND RATS. IT TARGET NEURONAL

CC NACHRS IN MAMMALS. BLOCKS HOMOMERIC ALPHA-7 NICOTINIC RECEPTORS
CC WITH THE HIGHEST APPARENT AFFINITY AND HOMOMERIC ALPHA-9 RECEPTORS
CC WITH 8-FOLD LOWER AFFINITY. HAS NO EFFECT ON RECEPTORS COMPOSED OF
CC ALPHA-2/BETA-2, ALPHA-3/BETA-2, ALPHA-4/BETA-2, ALPHA-2/BETA-4,
CC ALPHA-3/BETA-4, OR ALPHA-4/BETA-4 SUBUNIT COMBINATIONS.
KW Postsynaptic neurotoxin; Acetylcholine receptor inhibitor; Amidation;
KW Venom.
FT DISULFID 2 8
FT DISULFID 3 12
FT MOD_RES 12 12
SQ SEQUENCE 12 AA; 1357 MW; 4C3D5F45 CRC32;
AMIDATION.

Query Match 53.3%; Score 16; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WR 2
DB 10 WR 11

RESULT 6
CAL1_CALGI
ID CAL1_CALGI STANDARD; PRT; 14 AA.
AC P20728;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CALOTROPIN DI (EC 3.4.22.-) (FRAGMENT).
OS Calotropis gigantea (Madar) (Bowstring hemp).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids I; Gentianales; Asclepiadaceae;
OC Calotropis.
RN [1]
RP SEQUENCE.
RA BHATTACHARYA D., SENGUPTA A., SINHA N.K.;
RT "Chemical modification and amino terminal sequence of calotropin DI
RT from Calotropis gigantea.";
RL Phytochemistry 26:633-636(1987).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
CC PAPAIN FAMILY OF THIOL PROTEASES.
DR PIR; PT0026; PT0026.
DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
KW Hydrolase; Thiol protease.
FT MOD_RES 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1715 MW; A765B0FD CRC32;
PYRROLIDONE CARBOXYLIC ACID.

Query Match 53.3%; Score 16; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 WR 2
DB 8 WR 9

RESULT 7
KARA_BROPL
ID KARA_BROPL STANDARD; PRT; 14 AA.
AC P22442;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE KARASIN (EC 3.4.22.-) (FRAGMENT).
OS Bromelia plumieri (Karatas).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida;

OC unclassified Commelinidae; Bromeliaceae; Bromelia.
 [1]
 RN
 RP SEQUENCE.
 RX MEDLINE; 90344224.
 RA MONTES C., AMADOR M., CUEVAS D., CORDOBA F.;
 RT "Subunit structure of karatasein, the proteinase isolated from
 RT Bromelia plumbieri (karatas).";
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-MAY-1991 (Rel. 18, Last annotation update)
 DE TRP OPERON LEADER PEPTIDE.
 GN TRPL OR TRPEE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 82150258.
 RA YANOFSKY C., PLATT T., CRAWFORD I.P., NICHOLS B.P., CHRISTIE G.E.,
 RA HOROWITZ H., VAN CLEEMPUT M., WU A.M.;
 RT "The complete nucleotide sequence of the tryptophan operon of
 RT Escherichia coli.";
 RL Nucleic Acids Res. 9:6647-6668(1981).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 76240562.
 RA SQUIRES C., LEE F., BERTRAND K., SQUIRES C.L., BRONSON M.J.,
 RA YANOFSKY C.;
 RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
 RT Escherichia coli.";
 RL J. Mol. Biol. 103:351-381(1976).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 80101455.
 RA OXENDER D.L., ZURAWSKI G., YANOFSKY C.;
 RT "Attenuation in the Escherichia coli tryptophan operon: role of RNA
 RT secondary structure involving the tryptophan codon region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
 RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
 RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
 RA MAU B., SHAO Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
 OF TRYPTOPHAN.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; J01714; AAA57296.1; -;
 DR EMBL; A04494; CAA00361.1; -;
 DR EMBL; AE000224; AAC74347.1; -;
 DR PIR; A03589; LFECW.
 DR ECGENE; EG11274; TRPL.
 KW Tryptophan biosynthesis; Leader peptide.
 SQ SEQUENCE 14 AA; 1720 MW; F7E1A5D0 CRC32;
 Query Match 53.3%; Score 16; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WR 2
 DB 11 WR 12

OC unclassified Commelinidae; Bromeliaceae; Bromelia.
 [1]
 RN
 RP SEQUENCE.
 RX MEDLINE; 90344224.
 RA MONTES C., AMADOR M., CUEVAS D., CORDOBA F.;
 RT "Subunit structure of karatasein, the proteinase isolated from
 RT Bromelia plumbieri (karatas).";
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE TRP OPERON LEADER PEPTIDE.
 GN TRPL OR TRPEE.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 82150258.
 RA YANOFSKY C., PLATT T., CRAWFORD I.P., NICHOLS B.P., CHRISTIE G.E.,
 RA HOROWITZ H., VAN CLEEMPUT M., WU A.M.;
 RT "The complete nucleotide sequence of the tryptophan operon of
 RT Escherichia coli.";
 RL Nucleic Acids Res. 9:6647-6668(1981).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 76240562.
 RA SQUIRES C., LEE F., BERTRAND K., SQUIRES C.L., BRONSON M.J.,
 RA YANOFSKY C.;
 RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
 RT Escherichia coli.";
 RL J. Mol. Biol. 103:351-381(1976).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 80101455.
 RA OXENDER D.L., ZURAWSKI G., YANOFSKY C.;
 RT "Attenuation in the Escherichia coli tryptophan operon: role of RNA
 RT secondary structure involving the tryptophan codon region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
 RA RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
 RA GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
 RA MAU B., SHAO Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
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 CC -----
 DR EMBL; J01714; AAA57296.1; -;
 DR EMBL; A04494; CAA00361.1; -;
 DR EMBL; AE000224; AAC74347.1; -;
 DR PIR; A03589; LFECW.
 DR ECGENE; EG11274; TRPL.
 KW Tryptophan biosynthesis; Leader peptide.
 SQ SEQUENCE 14 AA; 1723 MW; A36B3681 CRC32;
 Query Match 53.3%; Score 16; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+02;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 WR 2
 DB 11 WR 12

```
RESULT 10
LPW_SALTY STANDARD; PRT; 14 AA.
AC P03054;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE TRP OPERON LEADER PEPTIDE.
GN TRPL OR TRPEE.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 78196931.
RA LEE F., BERTRAND K., BENNETT G.N., YANOFSKY C.;
RT "Comparison of the nucleotide sequences of the initial transcribed
RT regions of the tryptophan operons of Escherichia coli and Salmonella
RT typhimurium".
RL J. Mol. Biol. 121:193-217(1978).
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CC -----
CC EMBL; M24960; -; NOT ANNOTATED_CDS.
DR PIR; A03590; LFEBSWT.
DR STYGENE; SG10400; TRPL.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 14 AA; 1635 MW; 051FEC4E CRC32;

Query Match 53.3%; Score 16; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
DB 11 WR 12

RESULT 11
CAT9_FASHE STANDARD; PRT; 16 AA.
AC P80533;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PUTATIVE CATHEPSIN-LIKE ENZYME (EC 3.4.22.-) (NEWLY EXCYSTED JUVENILE
DE PROTEIN 9) (FRAGMENT).
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomatidae; Echinostomata; Fasciolidae;
OC Fasciolidae; Fasciola.
RN [1]
RP SEQUENCE.
RX MEDLINE; 95366993.
RA TKALCEVIC J., ASHMAN K., MEUSEN E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proleus.".
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE NEWLY EXCYSTED JUVENILE
CC STAGE.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
CC PAPAIN FAMILY OF THIOL PROTEASES.

DR PROSITE; PS00139; THIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOL_PROTEASE_ASN; PARTIAL.
KW Hydrolase; Thiol protease.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1966 MW; 1CA59D22 CRC32;

Query Match 53.3%; Score 16; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
DB 8 WR 9

RESULT 12
LPW_BRELA STANDARD; PRT; 17 AA.
AC P06556;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRP OPERON LEADER PEPTIDE.
GN TRPL.
OS Brevibacterium lactofermentum, and
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae.
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-B.LACTOFERMENTUM;
RX MEDLINE; 87117512.
RA MATSUI K., SANO K., OHTSUBO E.;
RT "Complete nucleotide and deduced amino acid sequences of the
RT Brevibacterium lactofermentum tryptophan operon.";
RL Nucleic Acids Res. 14:10113-10114(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-B.LACTOFERMENTUM;
RX MEDLINE; 88032866.
RA MATSUI K., MIWA K., SANO K.;
RT "Two single-base-pair substitutions causing desensitization to
RT tryptophan feedback inhibition of anthranilate synthase and enhanced
RT expression of tryptophan genes of Brevibacterium lactofermentum.";
RL J. Bacteriol. 169:5330-5332(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-B.LACTOFERMENTUM;
RX MEDLINE; 87277409.
RA SANO K., MATSUI K.;
RT "Structure and function of the trp operon control regions of
RL Brevibacterium lactofermentum, a glutamic-acid-producing bacterium.";
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-C.GLUTAMICUM; STRAIN-ATCC 13059 / AS019;
RX MEDLINE; 91088299.
RA HEERY D.M., DUNICAN L.K.;
RT "Nucleotide sequence of the Corynebacterium glutamicum trpE gene.";
RL Nucleic Acids Res. 18:7138-7138(1990).
CC -!- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
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DR EMBL: X04960; CAA28622.1; -;
 DR EMBL: M17892; AAB59110.1; -;
 DR EMBL: M16663; -; NOT_ANNOTATED_CDS.
 DR PIR: X55994; CAA39466.1; -;
 DR PIR: A29458; A29458.
 DR PIR: A29834; A29834.
 DR PIR: A24723; A24723.
 DR PIR: S13087; S13087.
 KW Trypophan biosynthesis; Leader peptide.
 SQ SEQUENCE 17 AA; 2112 MW; 4C1F82F2 CRC32;

Query Match 53.3%; Score 16; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 4.9e-02;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
 ||
 Db 14 WR 15

RESULT 13

GALS_SALTY STANDARD; PRT; 18 AA.
 ID GALS_SALTY
 AC P41030;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE MGL REPRESSOR AND GALACTOSE ULTRAINDUCTION FACTOR (FRAGMENT).
 GN GALS.
 OS Salmonella typhimurium.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LT2;
 RX MEDLINE: 89112167.
 RA BENNER-LUGER D., BOOS W.;
 RT "The mglB sequence of Salmonella typhimurium LT2; promoter analysis
 by gene fusions and evidence for a divergently oriented gene coding
 for the mgl repressor.";
 RL Mol. Gen. Genet. 214:579-587(1988).
 CC -1- FUNCTION: REPRESSOR OF THE MGL OPERON. BINDS GALACTOSE AND
 D-FUCOSE AS INDUCERS. GALS BINDS TO AN OPERATOR DNA SEQUENCE
 WITHIN ITS OWN CODING SEQUENCE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LACI FAMILY OF TRANSCRIPTIONAL
 REGULATORS.
 CC STYGENE: SG10521; GALS.
 DR PROSITE: PS00356; HTH_LACI_FAMILY; PARTIAL.
 KW Transcription regulation; DNA-binding; Repressor.
 FT NON_TER 1 1
 SQ SEQUENCE 18 AA; 2133 MW; A0CC0E54 CRC32;

Query Match 53.3%; Score 16; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5.2e-02;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
 ||
 Db 9 WR 10

RESULT 14

UVRD_SALTY STANDARD; PRT; 13 AA.
 ID UVRD_SALTY
 AC Q05311;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE DNA HELICASE II (EC 3.6.1.-) (FRAGMENT).
 GN UVRD.
 OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 93300795.
 RA SMITH R.L., BANKS J.L., SNAVELY M.D., MAGUIRE M.E.;
 RT "Sequence and topology of the Cora magnesium transport systems of
 Salmonella typhimurium and Escherichia coli. Identification of a new
 class of transport protein.";
 RL J. Biol. Chem. 268:14071-14080(1993).
 CC -1- FUNCTION: HAS BOTH ATPASE AND HELICASE ACTIVITIES. UNWINDS DNA
 DUPLEXES WITH 3' TO 5' POLARITY WITH RESPECT TO THE BOUND STRAND
 AND INITIATES UNWINDING MOST EFFECTIVELY WHEN A SINGLE-STRANDED
 REGION IS PRESENT. INVOLVED IN THE POSTINCISION EVENTS OF
 NUCLEOTIDE EXCISION REPAIR AND METHYL-DIRECTED MISMATCH REPAIR.
 CC -1- SIMILARITY: BELONGS TO THE UVRD SUBFAMILY OF HELICASES.
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 CC -----
 CC EMBL: L11043; AAA02965.1; -;
 DR STYGENE: SG10414; UVRD.
 KW DNA repair; DNA replication; SOS response; Helicase; ATP-binding;
 KW DNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1492 MW; 008C542C CRC32;

Query Match 46.7%; Score 14; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 1.1e-03;
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 WRXXEY 6
 | | |
 Db 2 WLVAAY 7

RESULT 15
 FKX7_PINPS
 ID FKX7_PINPS STANDARD; PRT; 15 AA.
 AC P81104;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE 70 KD PEPTIDYLPROLYL ISOMERASE (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS
 ISOMERASE) (CYCLOPHILIN) (PPIASE) (S1205-06) (FRAGMENT).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
 OC Pinus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=NEEDLE;
 RA PLOMON C., COSTA P., BAHRMAN N., FRIGERIO J.-M.;
 RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
 dominant and codominant protein markers assayed on diploid tissue, in
 a haploid-based genetic map.";
 RL Silvae Genetica 46:161-165(1997).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=NEEDLE;
 RX MEDLINE: 99274088.
 RA COSTA P., PIONNEAU C., BAUW G., DUBOS C., BAHRMAN N., KREMER A.,
 RA FRIGERIO J.-M., PLOMON C.;
 RT "Separation and characterization of needle and xylem maritime pine
 proteins.";
 RL Electrophoresis 20:1098-1108(1999).
 CC -1- FUNCTION: PPIASE THAT BINDS CALMODULIN (BY SIMILARITY).

CC -!- CATALYTIC ACTIVITY: PEPTIDYLPROLINE (OMEGA-180) -
CC PEPTIDYLPROLINE (OMEGA-0).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
CC 5.3, ITS MW IS: 72 KD.
CC -!- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
DR PROSITE: PS00453; FKBP_PPIASE_1; PARTIAL.
DR PROSITE: PS00454; FKBP_PPIASE_2; PARTIAL.
DR PROSITE: PS00059; FKBP_PPIASE_3; PARTIAL.
KW Isomerase; Rotamase; Repeat; Calmodulin-binding.
FT NON_TER 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1675 MW; 160E9FCD CRC32;

Query Match 46.7%; Score 14; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WRXXE 5
Db 5 WETPE 9

Search completed: May 2, 2000, 00:19:54
Job time: 87 sec

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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:17:52 ; Search time 14.58 Seconds
(without alignments)
28.533 Million cell updates/sec

Title: US-09-258-947-174
Perfect score: 30
Sequence: 1 WRXXEY 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 2017

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database :

SPTREMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	60.0	16	12	Q83960
2	17	56.7	16	11	Q82134
3	17	56.7	18	12	Q73549
4	17	56.7	18	12	Q73575
5	17	56.7	18	12	Q73577
6	17	56.7	18	12	Q73579
7	17	56.7	18	12	Q73593
8	17	56.7	18	12	Q73601
9	17	56.7	18	12	Q73609
10	16	53.3	8	11	Q62721
11	16	53.3	12	7	Q77919
12	16	53.3	14	2	Q54081
13	16	53.3	16	12	Q83967
14	16	53.3	16	12	Q84055
15	16	53.3	17	2	Q07270
16	16	53.3	17	2	P81526
17	16	53.3	17	2	Q45304
18	16	53.3	17	4	Q16228
19	16	53.3	17	6	Q9XSG1
20	16	53.3	17	12	Q72017

16	53.3	18	12	Q69185
16	53.3	18	12	Q84129
21	53.3	19	2	Q53311
22	53.3	19	12	Q83965
23	53.3	20	12	Q85636
24	53.3	20	12	Q85636
25	53.3	20	12	Q85636
26	53.3	20	12	Q85636
27	53.3	20	12	Q85636
28	53.3	20	12	Q85636
29	53.3	20	12	Q85636
30	53.3	20	12	Q85636
31	53.3	20	12	Q85636
32	53.3	20	12	Q85636
33	53.3	20	12	Q85636
34	53.3	20	12	Q85636
35	53.3	20	12	Q85636
36	53.3	20	12	Q85636
37	53.3	20	12	Q85636
38	53.3	20	12	Q85636
39	53.3	20	12	Q85636
40	53.3	20	12	Q85636
41	53.3	20	12	Q85636
42	53.3	20	12	Q85636
43	53.3	20	12	Q85636
44	53.3	20	12	Q85636
45	53.3	20	12	Q85636
46	53.3	20	12	Q85636
47	53.3	20	12	Q85636
48	53.3	20	12	Q85636
49	53.3	20	12	Q85636
50	53.3	20	12	Q85636
51	53.3	20	12	Q85636
52	53.3	20	12	Q85636
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76	53.3	20	12	Q85636
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79	53.3	20	12	Q85636
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84	53.3	20	12	Q85636
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87	53.3	20	12	Q85636
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91	53.3	20	12	Q85636
92	53.3	20	12	Q85636
93	53.3	20	12	Q85636

Q69185	human cytom
Q84129	influenza a
Q53311	streptococc
Q83965	influenza a
Q85636	moloney mur
Q90735	gallus gall
Q73605	human immu
Q73573	human immu
Q73583	human immu
Q73587	human immu
Q73603	human immu
Q73607	human immu
Q73613	human immu
Q73615	human immu
Q73629	human immu
Q73631	human immu
Q73639	human immu
Q73643	human immu
Q73645	human immu
Q73647	human immu
Q73649	human immu
Q73651	human immu
Q73653	human immu
Q73655	human immu
Q95945	saccharomyc
Q9XMB4	egilops sq
P97733	rattus norv
Q53580	rhodobacter
Q34699	heliathanus
O00595	homo sapien
Q96225	h1-isoaspa
Q73920	human immu
Q73921	human immu
P93689	podospira a
Q9YQ85	porcine cir
P70739	alcaligenes
P72423	saccharopol
O55051	rattus norv
Q73917	human immu
Q73918	human immu
Q15888	homo sapien
P70243	mus musculu
Q83332	murine hepa
Q47410	escherichia
P78484	homo sapien
Q85723	simian sarc
Q83978	influenza a
O77910	oreochromis
O77911	oreochromis
Q84068	mus musculu
Q9XNR6	pylaiella l
Q50038	mycobacteri
Q93824	candida tro
Q16392	homo sapien
Q86129	vesicular s
Q14342	homo sapien
Q9ZRS3	arabidopsis
Q16297	homo sapien
Q64100	cricketid
O64101	cricketid
Q06800	saccharomyc
Q13376	homo sapien
O18774	oryctolagus
Q62548	mus musculu
O88868	mus musculu
Q73442	human immu
Q87589	chimpanzee
Q87591	chimpanzee
Q87593	chimpanzee
Q47078	escherichia
Q47079	escherichia
Q36277	zea mays (m
Q92YV7	myrmecia fo

94	12	40.0	19	12	Q9WR37	Q9WR37 human immun	167	11	36.7	11	7	077898	077898 oreochromis
95	12	40.0	19	13	P87484	P87484 gallus gall	168	11	36.7	11	7	077906	077906 oreochromis
96	12	40.0	20	2	Q50089	Q50089 mycobacteri	169	11	36.7	11	7	077908	077908 oreochromis
97	12	40.0	20	3	Q13594	Q13594 saccharomyc	170	11	36.7	11	7	077913	077913 oreochromis
98	12	40.0	20	7	Q19726	Q19726 homo sapien	171	11	36.7	11	7	077914	077914 oreochromis
99	12	40.0	20	12	Q89700	Q89700 human immun	172	11	36.7	11	7	077918	077918 pseudotroph
100	11	36.7	7	10	Q49223	Q49223 glycine max	173	11	36.7	11	7	078118	078118 oreochromis
101	11	36.7	8	2	Q85406	Q85406 coxiella bu	174	11	36.7	11	7	078120	078120 oreochromis
102	11	36.7	8	4	Q15890	Q15890 homo sapien	175	11	36.7	11	8	079636	079636 laudakia hi
103	11	36.7	8	6	Q02831	Q02831 oryctolagus	176	11	36.7	11	8	079639	079639 laudakia le
104	11	36.7	8	11	Q35835	Q35835 rattus norv	177	11	36.7	11	8	079642	079642 laudakia mi
105	11	36.7	8	13	P79940	P79940 xenopus lae	178	11	36.7	11	8	079918	079918 physignathu
106	11	36.7	9	4	Q00610	Q00610 homo sapien	179	11	36.7	11	8	079921	079921 phrynocepha
107	11	36.7	9	4	Q16386	Q16386 homo sapien	180	11	36.7	11	8	079985	079985 laudakia ca
108	11	36.7	9	4	Q95953	Q95953 homo sapien	181	11	36.7	11	8	079986	079986 laudakia er
109	11	36.7	9	6	Q28121	Q28121 bos taurus	182	11	36.7	11	12	Q83410	Q83410 mouse mamma
110	11	36.7	9	9	Q38366	Q38366 bacterioph	183	11	36.7	11	12	Q84117	Q84117 influenza a
111	11	36.7	9	12	Q65711	Q65711 berne virus	184	11	36.7	11	12	Q86555	Q86555 tomato yell
112	11	36.7	9	12	Q89100	Q89100 herpes simp	185	11	36.7	12	2	Q46747	Q46747 escherichia
113	11	36.7	9	12	Q89491	Q89491 murine minu	186	11	36.7	12	2	Q47048	Q47048 escherichia
114	11	36.7	9	12	Q90350	Q90350 hepatitis g	187	11	36.7	12	2	Q53579	Q53579 rhodobacter
115	11	36.7	10	2	Q47561	Q47561 escherichia	188	11	36.7	12	2	Q54226	Q54226 saccharopol
116	11	36.7	10	4	Q15342	Q15342 homo sapien	189	11	36.7	12	4	Q16405	Q16405 homo sapien
117	11	36.7	10	5	Q25355	Q25355 locusta mig	190	11	36.7	12	4	Q13865	Q13865 homo sapien
118	11	36.7	10	5	Q23356	Q23356 locusta mig	191	11	36.7	12	4	Q60773	Q60773 homo sapien
119	11	36.7	10	8	P2616	P2616 cnemidophor	192	11	36.7	12	6	Q9XT42	Q9XT42 canis fami
120	11	36.7	10	8	P2632	P2632 eremias gra	193	11	36.7	12	7	077889	077889 oreochromis
121	11	36.7	10	8	P92707	P92707 platysauru	194	11	36.7	12	7	077890	077890 oreochromis
122	11	36.7	10	8	P92733	P92733 rana limnoc	195	11	36.7	12	7	077891	077891 oreochromis
123	11	36.7	10	8	P92758	P92758 teratocinc	196	11	36.7	12	7	077915	077915 oreochromis
124	11	36.7	10	8	P92762	P92762 uromastix a	197	11	36.7	12	7	077920	077920 pseudotroph
125	11	36.7	10	8	P92771	P92771 xenosaurus	198	11	36.7	12	7	Q07884	Q07884 pan troglod
126	11	36.7	10	8	P92648	P92648 lialis jica	199	11	36.7	12	8	Q36623	Q36623 picea abies
127	11	36.7	10	8	P92654	P92654 mabuya auru	200	11	36.7	12	8	Q36669	Q36669 pinus sylve
128	11	36.7	10	8	P92766	P92766 varanus gri	201	11	36.7	12	8	Q37790	Q37790 larix eurol
129	11	36.7	10	8	P92774	P92774 xantusia vi	202	11	36.7	12	8	P92454	P92454 cycas revol
130	11	36.7	10	8	Q79885	Q79885 anolis pace	203	11	36.7	12	8	P92457	P92457 ephedra sp.
131	11	36.7	10	8	Q79888	Q79888 basiliscus	204	11	36.7	12	8	Q03815	Q03815 abies alba
132	11	36.7	10	8	Q79891	Q79891 crotaphytus	205	11	36.7	12	8	Q03816	Q03816 metasequoia
133	11	36.7	10	8	Q79894	Q79894 gambelia wi	206	11	36.7	12	8	P92680	P92680 trimeresura
134	11	36.7	10	8	Q79897	Q79897 hoplocercus	207	11	36.7	12	10	Q92NT6	Q92NT6 oryza brach
135	11	36.7	10	8	Q79900	Q79900 liolaemus p	208	11	36.7	12	11	Q63579	Q63579 rattus norv
136	11	36.7	10	8	Q79903	Q79903 oplurus cuv	209	11	36.7	12	11	Q63579	Q63579 rattus norv
137	11	36.7	10	8	Q79906	Q79906 phrynosoma	210	11	36.7	12	11	Q64331	Q64331 rattus norv
138	11	36.7	10	8	Q79909	Q79909 saurornis	211	11	36.7	12	11	Q61331	Q61331 mus musculu
139	11	36.7	10	8	Q79912	Q79912 chamaeleo f	212	11	36.7	12	12	Q12088	Q12088 caprine art
140	11	36.7	10	8	Q79915	Q79915 leiolepis b	213	11	36.7	12	12	Q12074	Q12074 caprine art
141	11	36.7	10	8	Q79924	Q79924 elgaria pan	214	11	36.7	12	12	Q12076	Q12076 caprine art
142	11	36.7	10	8	Q92YV3	Q92YV3 dipsosaurus	215	11	36.7	12	12	Q12078	Q12078 caprine art
143	11	36.7	10	8	Q92YV0	Q92YV0 petrosaurus	216	11	36.7	12	12	Q12080	Q12080 caprine art
144	11	36.7	10	8	Q92YU7	Q92YU7 sator angus	217	11	36.7	12	12	Q12082	Q12082 caprine art
145	11	36.7	10	8	Q92YU4	Q92YU4 sceloporu	218	11	36.7	12	12	Q12084	Q12084 caprine art
146	11	36.7	10	8	Q92YU1	Q92YU1 uma scopari	219	11	36.7	12	12	Q12086	Q12086 caprine art
147	11	36.7	10	8	Q92YU8	Q92YU8 urosaurus g	220	11	36.7	12	12	Q12090	Q12090 caprine art
148	11	36.7	10	8	Q92YU5	Q92YU5 uta stansbu	221	11	36.7	12	12	Q12092	Q12092 caprine art
149	11	36.7	10	8	Q92YT2	Q92YT2 leiocephalu	222	11	36.7	12	12	Q12094	Q12094 caprine art
150	11	36.7	10	8	Q92YU9	Q92YU9 phymaturu	223	11	36.7	12	12	Q12106	Q12106 caprine art
151	11	36.7	10	8	Q92YU6	Q92YU6 stenocercus	224	11	36.7	12	12	Q12108	Q12108 caprine art
152	11	36.7	10	10	Q92YU3	Q92YU3 aegilops sq	225	11	36.7	12	12	Q12110	Q12110 caprine art
153	11	36.7	10	11	Q70580	Q70580 mus musculu	226	11	36.7	12	12	Q12112	Q12112 caprine art
154	11	36.7	10	12	Q64971	Q64971 alfalfa mos	227	11	36.7	12	12	Q12114	Q12114 caprine art
155	11	36.7	10	13	Q42355	Q42355 brachydanio	228	11	36.7	12	12	Q12116	Q12116 caprine art
156	11	36.7	11	2	Q47602	Q47602 escherichia	229	11	36.7	12	12	Q12118	Q12118 caprine art
157	11	36.7	11	2	Q56413	Q56413 escherichia	230	11	36.7	12	12	Q75729	Q75729 human immun
158	11	36.7	11	4	Q60842	Q60842 homo sapien	231	11	36.7	12	12	Q66202	Q66202 porcine tra
159	11	36.7	11	5	Q24227	Q24227 drosophila	232	11	36.7	12	12	Q12036	Q12036 caprine art
160	11	36.7	11	7	Q77884	Q77884 oreochromis	233	11	36.7	12	12	Q41611	Q41611 human immun
161	11	36.7	11	7	Q77885	Q77885 oreochromis	234	11	36.7	12	12	Q72765	Q72765 porcine tra
162	11	36.7	11	7	Q77892	Q77892 oreochromis	235	11	36.7	13	1	Q50831	Q50831 methanococc
163	11	36.7	11	7	Q77893	Q77893 oreochromis	236	11	36.7	13	2	Q49230	Q49230 mycoplasma
164	11	36.7	11	7	Q77894	Q77894 oreochromis	237	11	36.7	13	2	Q52920	Q52920 rhizobium m
165	11	36.7	11	7	Q77895	Q77895 oreochromis	238	11	36.7	13	2	Q53300	Q53300 escherichia
166	11	36.7	11	7	Q77896	Q77896 oreochromis	239	11	36.7	13	2	Q53313	Q53313 corynebacte

240	11	36.7	13	2	Q9X514	Q9x514 enterococcu	313	11	36.7	17	11	063233	Q63233 rattus norv
241	11	36.7	13	2	Q9W72	Q9w72 enterococcu	314	11	36.7	17	11	063995	Q63995 mus musculu
242	11	36.7	13	2	Q9W71	Q9w71 enterococcu	315	11	36.7	17	11	062436	Q62436 mus musculu
243	11	36.7	13	3	Q10721	Q10721 pseudalles	316	11	36.7	17	11	P97758	P97758 mus musculu
244	11	36.7	13	4	Q16406	Q16406 homo sapien	317	11	36.7	17	12	Q85004	Q85004 porcine res
245	11	36.7	13	6	Q18890	Q18890 ateles pani	318	11	36.7	17	12	Q69074	Q69074 human herpe
246	11	36.7	13	8	Q95808	Q95808 graciliarop	319	11	36.7	17	12	Q85463	Q85463 avian sarco
247	11	36.7	13	8	Q95925	Q95925 porphyra pu	320	11	36.7	17	12	Q85463	Q85463 avian sarco
248	11	36.7	13	8	P92460	P92460 taxus bacca	321	11	36.7	17	12	Q73531	Q73531 human immun
249	11	36.7	13	8	Q99188	Q99188 rivulus cau	322	11	36.7	17	12	Q73533	Q73533 human immun
250	11	36.7	13	8	Q99188	Q99188 caprimulgus	323	11	36.7	17	12	Q73535	Q73535 human immun
251	11	36.7	13	8	Q9X112	Q9x112 bemisia tab	324	11	36.7	17	12	Q73537	Q73537 human immun
252	11	36.7	13	10	Q43174	Q43174 solanum tub	325	11	36.7	17	12	Q73541	Q73541 human immun
253	11	36.7	13	11	Q63935	Q63935 rattus norv	326	11	36.7	17	12	Q73543	Q73543 human immun
254	11	36.7	13	11	Q88176	Q88176 mus musculu	327	11	36.7	17	12	Q73547	Q73547 human immun
255	11	36.7	13	12	Q85645	Q85645 mouse mamma	328	11	36.7	17	12	Q73547	Q73547 human immun
256	11	36.7	14	2	Q56945	Q56945 versinia ps	329	11	36.7	17	12	089807	089807 epiphyphas po
257	11	36.7	14	2	Q54861	Q54861 streptococ	330	11	36.7	18	2	006514	006514 escherichia
258	11	36.7	14	4	Q13022	Q13022 homo sapien	331	11	36.7	18	2	Q09053	Q09053 methylomona
259	11	36.7	14	4	Q99902	Q99902 homo sapien	332	11	36.7	18	2	Q30588	Q30588 streptomyce
260	11	36.7	14	5	Q18502	Q18502 schistosoma	333	11	36.7	18	2	Q68570	Q68570 streptomyce
261	11	36.7	14	5	Q10757	Q10757 theromyzon	334	11	36.7	18	2	Q44607	Q44607 buchnera ap
262	11	36.7	14	6	Q09061	Q09061 bos taurus	335	11	36.7	18	2	Q47246	Q47246 escherichia
263	11	36.7	14	6	Q9XSL4	Q9xsl4 capra hircu	336	11	36.7	18	2	Q92G65	Q92g65 chlamydia t
264	11	36.7	14	12	Q88400	Q88400 simian t-ce	337	11	36.7	18	3	Q06711	Q06711 saccharomyc
265	11	36.7	14	12	Q9818	Q9818 murine minu	338	11	36.7	18	4	Q12995	Q12995 homo sapien
266	11	36.7	15	2	Q54325	Q54325 staphylococ	339	11	36.7	18	8	Q34695	Q34695 homarus ame
267	11	36.7	15	2	Q05003	Q05003 rhizobium l	340	11	36.7	18	8	Q98674	Q98674 cabomba car
268	11	36.7	15	2	Q92F32	Q92f32 salmonella	341	11	36.7	18	8	Q92YX7	Q92yx7 perga conde
269	11	36.7	15	4	Q93046	Q93046 homo sapien	342	11	36.7	18	8	Q92YX0	Q92yx0 blacus sp.
270	11	36.7	15	8	Q95762	Q95762 ctenosaura	343	11	36.7	18	8	Q92YW9	Q92yw9 agathidella
271	11	36.7	15	8	Q99386	Q99386 sus scrofa	344	11	36.7	18	8	Q92YW6	Q92yw6 alelodes ap
272	11	36.7	15	8	Q78794	Q78794 pytalidella l	345	11	36.7	18	8	Q92YW4	Q92yw4 alelodes ap
273	11	36.7	15	9	Q38427	Q38427 bacterioph	346	11	36.7	18	8	Q92YV9	Q92yv9 opius kraus
274	11	36.7	15	9	Q93515	Q93515 arabidopsis	347	11	36.7	18	8	Q92YV8	Q92yv8 aspilota sp
275	11	36.7	15	10	Q42223	Q42223 arabidopsis	348	11	36.7	18	8	Q92YV6	Q92yv6 bethyridae
276	11	36.7	15	12	Q86576	Q86576 subterranea	349	11	36.7	18	8	Q92YX3	Q92yx3 xylocopa vi
277	11	36.7	15	12	Q86865	Q86865 lymphocytic	350	11	36.7	18	8	Q92YX2	Q92yx2 encarsia fo
278	11	36.7	15	12	Q86867	Q86867 lymphocytic	351	11	36.7	18	8	Q92YX1	Q92yx1 amitus sp.
279	11	36.7	15	12	Q86869	Q86869 lymphocytic	352	11	36.7	18	8	Q92YX0	Q92yx0 scelio fulg
280	11	36.7	15	12	Q86543	Q86543 human herpe	353	11	36.7	18	8	Q92Y79	Q92y79 idris sp. c
281	11	36.7	15	13	Q90594	Q90594 gallus gall	354	11	36.7	18	8	Q92Y78	Q92y78 gryon sp. c
282	11	36.7	16	2	Q45530	Q45530 bacillus su	355	11	36.7	18	8	Q92Y75	Q92y75 cenococius
283	11	36.7	16	2	Q44543	Q44543 anabaena va	356	11	36.7	18	9	Q9XJQ5	Q9xjq5 bacterioph
284	11	36.7	16	2	Q48417	Q48417 klebsiella	357	11	36.7	18	10	082675	082675 cryptoglena
285	11	36.7	16	3	Q94554	Q94554 schizosacch	358	11	36.7	18	11	Q62256	Q62256 mus musculu
286	11	36.7	16	4	Q14495	Q14495 homo sapien	359	11	36.7	18	11	Q63136	Q63136 rattus norv
287	11	36.7	16	4	Q15632	Q15632 homo sapien	360	11	36.7	18	11	Q63653	Q63653 rattus norv
288	11	36.7	16	6	Q62810	Q62810 equus cabal	361	11	36.7	18	11	P70649	P70649 mus musculu
289	11	36.7	16	8	Q95765	Q95765 cyclura nub	362	11	36.7	18	11	Q9W006	Q9wuq6 mus musculu
290	11	36.7	16	8	Q34374	Q34374 daphnia pul	363	11	36.7	18	12	Q87587	Q87587 chimpanzee
291	11	36.7	16	8	Q9XNP6	Q9xnp6 boophilus m	364	11	36.7	18	12	Q88290	Q88290 small round
292	11	36.7	16	9	Q21922	Q21922 streptococ	365	11	36.7	18	12	Q73461	Q73461 human immun
293	11	36.7	16	11	Q920J2	Q920j2 mus musculu	366	11	36.7	18	12	Q73487	Q73487 human immun
294	11	36.7	16	12	Q79456	Q79456 human immun	367	11	36.7	18	12	Q73557	Q73557 human immun
295	11	36.7	16	12	Q79459	Q79459 human immun	368	11	36.7	18	12	Q73483	Q73483 human immun
296	11	36.7	16	12	Q86717	Q86717 human immun	369	11	36.7	18	12	Q73465	Q73465 human immun
297	11	36.7	16	12	Q75710	Q75710 human immun	370	11	36.7	18	12	Q73467	Q73467 human immun
298	11	36.7	16	12	Q9YQ11	Q9yq11 porcine tra	371	11	36.7	18	12	Q73469	Q73469 human immun
299	11	36.7	17	2	Q45529	Q45529 bacillus su	372	11	36.7	18	12	Q73471	Q73471 human immun
300	11	36.7	17	2	P78199	P78199 escherichia	373	11	36.7	18	12	Q73473	Q73473 human immun
301	11	36.7	17	2	Q9X616	Q9x616 bacillus th	374	11	36.7	18	12	Q73475	Q73475 human immun
302	11	36.7	17	4	P78490	P78490 homo sapien	375	11	36.7	18	12	Q73477	Q73477 human immun
303	11	36.7	17	4	Q15276	Q15276 homo sapien	376	11	36.7	18	12	Q73479	Q73479 human immun
304	11	36.7	17	4	Q75289	Q75289 homo sapien	377	11	36.7	18	12	Q73481	Q73481 human immun
305	11	36.7	17	4	Q95794	Q95794 homo sapien	378	11	36.7	18	12	Q73483	Q73483 human immun
306	11	36.7	17	6	Q20395	Q20395 canis famill	379	11	36.7	18	12	Q73485	Q73485 human immun
307	11	36.7	17	7	Q30218	Q30218 homo sapien	380	11	36.7	18	12	Q73489	Q73489 human immun
308	11	36.7	17	7	Q12862	Q12862 homo sapien	381	11	36.7	18	12	Q73491	Q73491 human immun
309	11	36.7	17	8	Q92YX4	Q92yx4 xorides pra	382	11	36.7	18	12	Q73493	Q73493 human immun
310	11	36.7	17	8	Q92YX0	Q92yx0 betylobraco	383	11	36.7	18	12	Q73495	Q73495 human immun
311	11	36.7	17	8	Q92Y77	Q92y77 trissolcus	384	11	36.7	18	12	Q73497	Q73497 human immun
312	11	36.7	17	8	Q9XNQ1	Q9xng1 boophilus m	385	11	36.7	18	12	Q73499	Q73499 human immun

386	11	36.7	18	12	Q73501	Q73501 human immun	459	11	36.7	19	8	Q99755	Q99755 aptenodytes
387	11	36.7	18	12	Q73503	Q73503 human immun	460	11	36.7	19	8	Q99756	Q99756 bonasa umbe
388	11	36.7	18	12	Q73505	Q73505 human immun	461	11	36.7	19	8	Q99757	Q99757 burhinus oe
389	11	36.7	18	12	Q73507	Q73507 human immun	462	11	36.7	19	8	Q99758	Q99758 cacatus gof
390	11	36.7	18	12	Q73509	Q73509 human immun	463	11	36.7	19	8	Q99759	Q99759 cathartes m
391	11	36.7	18	12	Q73511	Q73511 human immun	464	11	36.7	19	8	Q99760	Q99760 cepphus col
392	11	36.7	18	12	Q73513	Q73513 human immun	465	11	36.7	19	8	Q99761	Q99761 chordelies
393	11	36.7	18	12	Q73515	Q73515 human immun	466	11	36.7	19	8	Q99762	Q99762 colaptes au
394	11	36.7	18	12	Q73517	Q73517 human immun	467	11	36.7	19	8	Q99763	Q99763 coccyzus er
395	11	36.7	18	12	Q73519	Q73519 human immun	468	11	36.7	19	8	Q99764	Q99764 colius stri
396	11	36.7	18	12	Q73521	Q73521 human immun	469	11	36.7	19	8	Q99765	Q99765 diomedea ni
397	11	36.7	18	12	Q73523	Q73523 human immun	470	11	36.7	19	8	Q99766	Q99766 euromia ei
398	11	36.7	18	12	Q73525	Q73525 human immun	471	11	36.7	19	8	Q99767	Q99767 fulica amer
399	11	36.7	18	12	Q73527	Q73527 human immun	472	11	36.7	19	8	Q99768	Q99768 gavia immer
400	11	36.7	18	12	Q73529	Q73529 human immun	473	11	36.7	19	8	Q99769	Q99769 grus canade
401	11	36.7	18	12	Q73531	Q73531 human immun	474	11	36.7	19	8	Q99770	Q99770 grus fulvus
402	11	36.7	18	12	Q73533	Q73533 human immun	475	11	36.7	19	8	Q99771	Q99771 meleagris g
403	11	36.7	18	12	Q73535	Q73535 human immun	476	11	36.7	19	8	Q99772	Q99772 mycteria am
404	11	36.7	18	12	Q73537	Q73537 human immun	477	11	36.7	19	8	Q99773	Q99773 nyctanassa
405	11	36.7	18	12	Q73539	Q73539 human immun	478	11	36.7	19	8	Q99774	Q99774 opisthocomu
406	11	36.7	18	12	Q73541	Q73541 human immun	479	11	36.7	19	8	Q99775	Q99775 otus asio.
407	11	36.7	18	12	Q73543	Q73543 human immun	480	11	36.7	19	8	Q99776	Q99776 pandion hal
408	11	36.7	18	12	Q73545	Q73545 human immun	481	11	36.7	19	8	Q99777	Q99777 phasianus c
409	11	36.7	18	12	Q73547	Q73547 human immun	482	11	36.7	19	8	Q99778	Q99778 phalacrocor
410	11	36.7	18	12	Q73549	Q73549 human immun	483	11	36.7	19	8	Q99779	Q99779 phoenicopte
411	11	36.7	18	12	Q73551	Q73551 human immun	484	11	36.7	19	8	Q99780	Q99780 podilymbus
412	11	36.7	18	12	Q73553	Q73553 human immun	485	11	36.7	19	8	Q99781	Q99781 sphyrapicus
413	11	36.7	18	12	Q73555	Q73555 human immun	486	11	36.7	19	8	Q99782	Q99782 gavia pacif
414	11	36.7	18	12	Q73557	Q73557 human immun	487	11	36.7	19	8	Q99784	Q99784 urocolius m
415	11	36.7	18	12	Q73559	Q73559 human immun	488	11	36.7	19	8	Q99785	Q99785 tauraco har
416	11	36.7	18	12	Q73561	Q73561 human immun	489	11	36.7	19	8	Q99786	Q99786 podiceps ni
417	11	36.7	18	12	Q73563	Q73563 human immun	490	11	36.7	19	8	Q99787	Q99787 cathartes a
418	11	36.7	18	12	Q73565	Q73565 human immun	491	11	36.7	19	8	Q99788	Q99788 tockus eryt
419	11	36.7	18	12	Q73567	Q73567 human immun	492	11	36.7	19	8	Q99789	Q99789 trogon curu
420	11	36.7	18	12	Q73569	Q73569 human immun	493	11	36.7	19	8	Q99790	Q99790 zenaida mac
421	11	36.7	18	12	Q73571	Q73571 human immun	494	11	36.7	19	8	Q99792	Q99792 centistes s
422	11	36.7	18	12	Q73573	Q73573 human immun	495	11	36.7	19	8	Q99794	Q99794 ichneutes b
423	11	36.7	18	12	Q73575	Q73575 human immun	496	11	36.7	19	8	Q99796	Q99796 aphidius ro
424	11	36.7	18	12	Q73577	Q73577 human immun	497	11	36.7	19	8	Q99798	Q99798 jarra phoro
425	11	36.7	18	12	Q73579	Q73579 human immun	498	11	36.7	19	8	Q99799	Q99799 gnaptodon
426	11	36.7	18	12	Q73581	Q73581 human immun	499	11	36.7	19	8	Q99800	Q99800 dolopsidea
427	11	36.7	18	12	Q73583	Q73583 human immun	500	11	36.7	19	8	Q99802	Q99802 histomeru
428	11	36.7	18	12	Q73585	Q73585 human immun	501	11	36.7	19	8	Q99804	Q99804 disognus ar
429	11	36.7	18	12	Q73587	Q73587 human immun	502	11	36.7	19	8	Q99806	Q99806 microplitis
430	11	36.7	18	12	Q73589	Q73589 human immun	503	11	36.7	19	8	Q99808	Q99808 heterospili
431	11	36.7	18	12	Q73591	Q73591 human immun	504	11	36.7	19	8	Q99810	Q99810 glycine soj
432	11	36.7	18	12	Q73593	Q73593 human immun	505	11	36.7	19	8	Q99812	Q99812 boophilus m
433	11	36.7	18	12	Q73595	Q73595 human immun	506	11	36.7	19	8	Q99814	Q99814 aegilops sq
434	11	36.7	18	12	Q73597	Q73597 human immun	507	11	36.7	19	10	Q99816	Q99816 d phosphogl
435	11	36.7	18	12	Q73599	Q73599 human immun	508	11	36.7	19	10	Q99818	Q99818 allium cepa
436	11	36.7	18	12	Q73601	Q73601 human immun	509	11	36.7	19	11	Q99820	Q99820 rattus norv
437	11	36.7	18	12	Q73603	Q73603 human immun	510	11	36.7	19	11	Q99822	Q99822 rattus norv
438	11	36.7	18	12	Q73605	Q73605 human immun	511	11	36.7	19	11	Q99824	Q99824 mus musculu
439	11	36.7	18	12	Q73607	Q73607 human immun	512	11	36.7	19	11	Q99826	Q99826 mus musculu
440	11	36.7	18	12	Q73609	Q73609 human immun	513	11	36.7	19	11	Q99828	Q99828 mus musculu
441	11	36.7	18	12	Q73611	Q73611 human immun	514	11	36.7	19	12	Q99830	Q99830 mus musculu
442	11	36.7	18	12	Q73613	Q73613 human immun	515	11	36.7	19	12	Q99832	Q99832 mus musculu
443	11	36.7	18	12	Q73615	Q73615 human immun	516	11	36.7	19	12	Q99834	Q99834 mus musculu
444	11	36.7	18	12	Q73617	Q73617 human immun	517	11	36.7	19	12	Q99836	Q99836 mus musculu
445	11	36.7	18	12	Q73619	Q73619 human immun	518	11	36.7	19	12	Q99838	Q99838 mus musculu
446	11	36.7	18	12	Q73621	Q73621 human immun	519	11	36.7	19	12	Q99840	Q99840 mus musculu
447	11	36.7	18	12	Q73623	Q73623 human immun	520	11	36.7	19	12	Q99842	Q99842 mus musculu
448	11	36.7	18	12	Q73625	Q73625 human immun	521	11	36.7	19	12	Q99844	Q99844 mus musculu
449	11	36.7	18	12	Q73627	Q73627 human immun	522	11	36.7	19	12	Q99846	Q99846 mus musculu
450	11	36.7	18	12	Q73629	Q73629 human immun	523	11	36.7	19	12	Q99848	Q99848 mus musculu
451	11	36.7	18	12	Q73631	Q73631 human immun	524	11	36.7	19	12	Q99850	Q99850 mus musculu
452	11	36.7	18	12	Q73633	Q73633 human immun	525	11	36.7	19	12	Q99852	Q99852 mus musculu
453	11	36.7	18	12	Q73635	Q73635 human immun	526	11	36.7	19	12	Q99854	Q99854 mus musculu
454	11	36.7	18	12	Q73637	Q73637 human immun	527	11	36.7	19	12	Q99856	Q99856 mus musculu
455	11	36.7	18	12	Q73639	Q73639 human immun	528	11	36.7	19	12	Q99858	Q99858 mus musculu
456	11	36.7	18	12	Q73641	Q73641 human immun	529	11	36.7	19	12	Q99860	Q99860 mus musculu
457	11	36.7	18	12	Q73643	Q73643 human immun	530	11	36.7	19	12	Q99862	Q99862 mus musculu
458	11	36.7	18	12	Q73645	Q73645 human immun	531	11	36.7	19	12	Q99864	Q99864 mus musculu

532	11	36.7	20	8	Q36127	Q36127 thyrophagus	605	8	26.7	9	4	Q00611	Q00611 homo sapien
533	11	36.7	20	8	Q32Y85	Q92Y85 bombus terr	606	8	26.7	9	4	Q16220	Q16220 homo sapien
534	11	36.7	20	8	Q32Y74	Q92Y74 mirax sp. c	607	8	26.7	9	4	Q95574	Q95574 homo sapien
535	11	36.7	20	8	Q32Y72	Q92Y72 sathon sp.	608	8	26.7	10	2	Q52762	Q52762 rhizobium s
536	11	36.7	20	10	Q82275	Q82275 arabidopsis	609	8	26.7	10	5	Q36093	Q36093 piasothera oc
537	11	36.7	20	11	Q97907	Q97907 mus musculu	610	8	26.7	10	5	Q96041	Q96041 piasothera b
538	11	36.7	20	11	Q61714	Q61714 mus musculu	611	8	26.7	10	4	Q47606	Q47606 escherichia
539	11	36.7	20	11	Q61871	Q61871 mus musculu	612	8	26.7	11	5	Q25916	Q25916 plasmodium
540	11	36.7	20	11	Q62546	Q62546 mus spretus	613	8	26.7	11	5	Q25916	Q25916 plasmodium
541	11	36.7	20	11	Q35353	Q35353 rattus norv	614	8	26.7	11	12	Q83083	Q83083 leucania se
542	11	36.7	20	11	Q9WVP3	Q9WVP3 mus musculu	615	8	26.7	11	12	Q84073	Q84073 influenza a
543	11	36.7	20	12	Q36978	Q36978 human papil	616	8	26.7	12	6	Q46664	Q46664 macropus ro
544	11	36.7	20	12	Q84861	Q84861 unidentified	617	8	26.7	12	12	Q89243	Q89243 woodchuck h
545	11	36.7	20	12	Q56842	Q56842 vibrio chol	618	8	26.7	13	2	Q9XBY0	Q9XBY0 nitrogeen-fi
546	10	33.3	14	2	Q34394	Q34394 streptomyce	619	8	26.7	13	10	Q9XIM6	Q9XIM6 oryza sativ
547	10	33.3	18	2	Q30888	Q30888 bradyrhizob	620	8	26.7	13	12	Q83171	Q83171 cauliflower
548	10	33.3	18	2	Q30602	Q30602 helicobacte	621	8	26.7	14	2	Q85576	Q85576 chlamydia t
549	10	33.3	19	2	Q33545	Q33545 shigella so	622	8	26.7	14	2	Q52638	Q52638 escherichia
550	10	33.3	19	2	Q47554	Q47554 escherichia	623	8	26.7	14	2	Q52636	Q52636 escherichia
551	10	33.3	20	5	Q25281	Q25281 leishmania	624	8	26.7	14	4	Q16118	Q16118 homo sapien
552	9	30.0	8	8	Q35792	Q35792 saccharomyc	625	8	26.7	14	4	Q75692	Q75692 homo sapien
553	9	30.0	9	12	Q82622	Q82622 avian infec	626	8	26.7	14	4	Q95179	Q95179 homo sapien
554	9	30.0	10	2	Q54217	Q54217 staphylococ	627	8	26.7	14	8	Q92076	Q92076 euhadra her
555	9	30.0	10	11	Q63056	Q63056 rattus norv	628	8	26.7	15	2	Q54298	Q54298 salmonella
556	9	30.0	11	2	Q96319	Q96319 desulfovibr	629	8	26.7	15	2	Q53290	Q53290 mycobacteri
557	9	30.0	11	2	Q15994	Q15994 drosophila	630	8	26.7	15	2	Q52304	Q52304 escherichia
558	9	30.0	11	10	Q41131	Q41131 lycopersico	631	8	26.7	15	5	Q97430	Q97430 drosophila
559	9	30.0	11	11	Q97755	Q97755 rattus norv	632	8	26.7	15	8	Q35188	Q35188 nicotiana t
560	9	30.0	11	12	Q89269	Q89269 xestia c-ni	633	8	26.7	15	11	Q35411	Q35411 mus musculu
561	9	30.0	12	2	Q30019	Q30019 mycobacteri	634	8	26.7	15	11	Q62531	Q62531 mus spretus
562	9	30.0	12	11	Q9WUX1	Q9WUX1 rattus norv	635	8	26.7	15	11	Q92114	Q92114 mus musculu
563	9	30.0	13	2	Q21605	Q21605 escherichia	636	8	26.7	16	12	Q86128	Q86128 vesicular s
564	9	30.0	13	12	Q64813	Q64813 autographa	637	8	26.7	16	2	Q51436	Q51436 pseudomonas
565	9	30.0	14	2	Q44172	Q44172 synechococc	638	8	26.7	16	3	Q79034	Q79034 emericella
566	9	30.0	14	2	P71199	P71199 escherichia	639	8	26.7	16	9	Q38671	Q38671 pichia past
567	9	30.0	14	2	Q96347	Q96347 helicobacte	640	8	26.7	16	12	Q79455	Q79455 human immun
568	9	30.0	14	2	Q50268	Q50268 phytoplasma	641	8	26.7	16	12	Q79461	Q79461 human immun
569	9	30.0	14	11	Q921H4	Q921H4 mus musculu	642	8	26.7	17	12	Q26G32	Q26G32 chlamydia t
570	9	30.0	14	12	P91578	P91578 choristoneu	643	8	26.7	17	4	Q14001	Q14001 homo sapien
571	9	30.0	15	2	P97249	P97249 nitrosolobu	644	8	26.7	17	5	Q61238	Q61238 onchocerca
572	9	30.0	15	2	Q05463	Q05463 nitrosolobu	645	8	26.7	17	6	Q27943	Q27943 arctoccephal
573	9	30.0	15	2	Q68430	Q68430 buchnera ap	646	8	26.7	17	6	Q28246	Q28246 canis famil
574	9	30.0	15	2	Q05991	Q05991 staphylococ	647	8	26.7	17	6	Q28445	Q28445 hydrurga le
575	9	30.0	15	3	Q14379	Q14379 schizosach	648	8	26.7	17	6	Q28455	Q28455 leptonychot
576	9	30.0	15	8	Q35921	Q35921 salmo salar	649	8	26.7	17	6	Q28459	Q28459 mirounga an
577	9	30.0	15	9	Q80277	Q80277 bacterioph	650	8	26.7	17	6	Q28817	Q28817 phoca vitul
578	9	30.0	15	10	P93516	P93516 arabidopsis	651	8	26.7	17	7	Q19716	Q19716 homo sapien
579	9	30.0	16	2	Q10748	Q10748 clostridium	652	8	26.7	17	8	Q9XON9	Q9XON9 sinapis alb
580	9	30.0	16	2	P76922	P76922 escherichia	653	8	26.7	17	10	Q24445	Q24445 ceratodon p
581	9	30.0	16	11	Q63039	Q63039 rattus norv	654	8	26.7	17	10	Q49225	Q49225 glycine max
582	9	30.0	16	12	Q66737	Q66737 equine infe	655	8	26.7	17	11	Q62437	Q62437 mus musculu
583	9	30.0	16	12	Q79453	Q79453 human immun	656	8	26.7	17	11	Q61932	Q61932 mus musculu
584	9	30.0	16	12	Q79454	Q79454 human immun	657	8	26.7	18	2	Q47337	Q47337 escherichia
585	9	30.0	16	12	Q79460	Q79460 human immun	658	8	26.7	18	2	Q53503	Q53503 lactobacill
586	9	30.0	17	12	Q79452	Q79452 human immun	659	8	26.7	18	2	Q52411	Q52411 thermophil
587	9	30.0	18	2	Q57323	Q57323 yersinia ps	660	8	26.7	18	2	Q92F30	Q92F30 salmonella
588	9	30.0	18	2	P72015	P72015 mycobacteri	661	8	26.7	18	12	Q41588	Q41588 human immun
589	9	30.0	18	2	P97166	P97166 streptococ	662	8	26.7	19	2	Q33502	Q33502 lactobacill
590	9	30.0	18	6	Q28069	Q28069 bos taurus	663	8	26.7	19	3	Q92321	Q92321 saccharomyc
591	9	30.0	18	8	Q78379	Q78379 theileria a	664	8	26.7	19	9	Q38021	Q38021 bacterioph
592	9	30.0	18	11	Q63506	Q63506 rattus norv	665	8	26.7	19	11	Q64134	Q64134 rattus norv
593	9	30.0	19	2	Q31278	Q31278 neisseria m	666	8	26.7	19	12	Q65747	Q65747 bluetongue
594	9	30.0	19	2	Q52316	Q52316 escherichia	667	8	26.7	19	12	Q86832	Q86832 human herpe
595	9	30.0	19	4	Q95598	Q95598 homo sapien	668	8	26.7	20	2	Q51558	Q51558 pseudomonas
596	9	30.0	19	10	Q04817	Q04817 sporobolus	669	8	26.7	20	2	Q34964	Q34964 ehlichia p
597	9	30.0	19	11	Q63857	Q63857 mus musculu	670	8	26.7	20	2	Q34190	Q34190 ehlichia e
598	9	30.0	19	12	Q85728	Q85728 spleen necr	671	8	26.7	20	2	Q34192	Q34192 ehlichia s
599	9	30.0	19	13	Q91983	Q91983 gallus gall	672	8	26.7	20	2	Q34193	Q34193 ehlichia c
600	9	30.0	20	2	Q52918	Q52918 rhizobium m	673	8	26.7	20	6	Q28734	Q28734 cryctolagus
601	9	30.0	20	2	Q56130	Q56130 salmonella	674	8	26.7	20	6	P79256	P79256 aotus trivi
602	9	30.0	20	2	Q37868	Q37868 bacterioph	675	8	26.7	20	7	Q30135	Q30135 homo sapien
603	9	30.0	20	13	Q42534	Q42534 brachydanio	676	8	26.7	20	8	Q33294	Q33294 zea mays (m
604	8	26.7	8	4	Q15901	Q15901 homo sapien	677	8	26.7	20	8	Q95947	Q95947 saccharomyc

678	8	26.7	20	8	098714	098714 euglena gra	751	7	23.3	11	7	077912	077912 oreochromis
679	8	26.7	20	8	098716	098716 euglena spi	752	7	23.3	11	7	077916	077916 oreochromis
680	8	26.7	20	9	Q38458	Q38458 bacterioph	753	7	23.3	11	7	077917	077917 oreochromis
681	8	26.7	20	10	Q42486	Q42486 solanum tub	754	7	23.3	11	7	077921	077921 pseudotroph
682	8	26.7	20	11	Q63667	Q63667 rattus norv	755	7	23.3	11	7	078119	078119 oreochromis
683	8	26.7	20	11	Q62435	Q62435 mus musculu	756	7	23.3	11	7	078121	078121 oreochromis
684	8	26.7	20	11	Q64080	Q64080 rattus norv	757	7	23.3	11	8	Q32704	Q32704 nicotiana t
685	8	26.7	20	12	Q41270	Q41270 spodoptera	758	7	23.3	11	11	Q61797	Q61797 mus musculu
686	7	23.3	7	2	Q50556	Q50556 actinobacil	759	7	23.3	11	12	Q86556	Q86556 tomato yell
687	7	23.3	7	8	Q99182	Q99182 pterolebias	760	7	23.3	11	12	Q86864	Q86864 lymphocytic
688	7	23.3	7	12	Q9YVE3	Q9YVE3 human adeno	761	7	23.3	11	12	Q86864	Q86864 lymphocytic
689	7	23.3	7	12	Q9YQ10	Q9YQ10 porcine tra	762	7	23.3	11	12	Q86866	Q86866 avian infec
690	7	23.3	7	12	Q9YIR0	Q9YIR0 human adeno	763	7	23.3	11	12	Q86866	Q86866 lymphocytic
691	7	23.3	7	12	Q9YIQ9	Q9YIQ9 human adeno	764	7	23.3	11	12	Q86868	Q86868 lymphocytic
692	7	23.3	8	2	Q09258	Q09258 synechococc	765	7	23.3	12	2	Q56947	Q56947 versinia ps
693	7	23.3	8	2	Q52062	Q52062 bacillus me	766	7	23.3	12	2	Q05328	Q05328 pseudomonas
694	7	23.3	8	2	P72221	P72221 pseudomonas	767	7	23.3	12	2	Q53183	Q53183 rhodococcus
695	7	23.3	8	3	P87225	P87225 saccharomyc	768	7	23.3	12	2	Q50959	Q50959 neisseria g
696	7	23.3	8	4	Q15898	Q15898 homo sapien	769	7	23.3	12	7	Q31006	Q31006 bos taurus
697	7	23.3	8	4	Q95213	Q95213 oryctolagus	770	7	23.3	12	10	Q38715	Q38715 arachis hyp
698	7	23.3	8	8	Q34909	Q34909 locusta mig	771	7	23.3	12	10	Q41856	Q41856 zea mays (m
699	7	23.3	8	8	Q9XNP8	Q9XNP8 boophilus m	772	7	23.3	12	10	Q02319	Q02319 pinus sylve
700	7	23.3	8	10	Q40530	Q40530 nicotiana t	773	7	23.3	12	11	Q02320	Q02320 pinus sylve
701	7	23.3	8	12	Q84156	Q84156 orf virus.	774	7	23.3	12	11	Q54370	Q54370 mus musculu
702	7	23.3	8	12	Q86617	Q86617 gallid herp	775	7	23.3	12	12	Q69232	Q69232 bovine herp
703	7	23.3	9	2	Q53914	Q53914 streptomyce	776	7	23.3	12	12	Q83139	Q83139 barley stri
704	7	23.3	9	4	Q15891	Q15891 homo sapien	777	7	23.3	12	12	Q88575	Q88575 theiller's e
705	7	23.3	9	4	Q16605	Q16605 homo sapien	778	7	23.3	12	12	Q88576	Q88576 theiller's e
706	7	23.3	9	6	Q28093	Q28093 bos taurus	779	7	23.3	12	12	Q88577	Q88577 theiller's e
707	7	23.3	9	6	Q9XSL0	Q9XSL0 capra hircu	780	7	23.3	12	12	Q88578	Q88578 theiller's e
708	7	23.3	9	8	Q31653	Q31653 anser caeru	781	7	23.3	12	12	Q88579	Q88579 theiller's e
709	7	23.3	9	11	Q25330	Q25330 mus spretus	782	7	23.3	12	12	Q88580	Q88580 theiller's e
710	7	23.3	9	12	Q69349	Q69349 herpes simp	783	7	23.3	12	12	Q88581	Q88581 theiller's e
711	7	23.3	9	12	Q88612	Q88612 middeiburg	784	7	23.3	12	12	Q88582	Q88582 theiller's e
712	7	23.3	10	2	Q48469	Q48469 klebsiella	785	7	23.3	13	2	Q48357	Q48357 escherichia
713	7	23.3	10	2	P96305	P96305 alteromonas	786	7	23.3	13	2	P74844	P74844 salmonella
714	7	23.3	10	2	P96421	P96421 neisseria g	787	7	23.3	13	2	P94878	P94878 lactococcus
715	7	23.3	10	2	P96423	P96423 pseudomonas	788	7	23.3	13	2	Q86260	Q86260 klebsiella
716	7	23.3	10	2	P96306	P96306 aeromonas s	789	7	23.3	13	2	Q55234	Q55234 synechocyst
717	7	23.3	10	2	P96321	P96321 escherichia	790	7	23.3	13	4	Q14890	Q14890 homo sapien
718	7	23.3	10	2	P96352	P96352 marinobacte	791	7	23.3	13	4	Q14462	Q14462 homo sapien
719	7	23.3	10	2	Q9Z1B1	Q9Z1B1 clostridium	792	7	23.3	13	4	Q15219	Q15219 homo sapien
720	7	23.3	10	2	Q9X534	Q9X534 leclercia a	793	7	23.3	13	4	Q14461	Q14461 homo sapien
721	7	23.3	10	2	Q9X533	Q9X533 escherichia	794	7	23.3	13	4	Q16141	Q16141 homo sapien
722	7	23.3	10	12	Q86324	Q86324 rous sarcom	795	7	23.3	13	5	Q24365	Q24365 drosophila
723	7	23.3	10	12	Q86325	Q86325 rous sarcom	796	7	23.3	13	5	Q97122	Q97122 toxoplasma
724	7	23.3	10	12	Q86326	Q86326 rous sarcom	797	7	23.3	13	8	Q35793	Q35793 saccharomyc
725	7	23.3	10	12	Q82625	Q82625 infectious	798	7	23.3	13	11	P97622	P97622 rattus norv
726	7	23.3	10	12	Q90349	Q90349 hepatitis g	799	7	23.3	13	11	Q63047	Q63047 rattus norv
727	7	23.3	11	2	Q85462	Q85462 avian sarco	800	7	23.3	13	12	P90442	P90442 spodoptera
728	7	23.3	11	2	Q47059	Q47059 escherichia	801	7	23.3	13	12	Q65331	Q65331 autographa
729	7	23.3	11	2	Q68237	Q68237 borrelia bu	802	7	23.3	14	2	Q45876	Q45876 clostridium
730	7	23.3	11	3	Q56972	Q56972 versinia pe	803	7	23.3	14	2	Q45872	Q45872 clostridium
731	7	23.3	11	3	Q43762	Q42762 aspergillus	804	7	23.3	14	2	Q52220	Q52220 salmonella
732	7	23.3	11	5	Q95292	Q99292 drosophila	805	7	23.3	14	5	Q26100	Q26100 pratylenchu
733	7	23.3	11	7	Q29831	Q29831 homo sapien	806	7	23.3	14	8	Q98696	Q98696 hordeum vul
734	7	23.3	11	7	Q77874	Q77874 oreochromis	807	7	23.3	14	9	Q38469	Q38469 bacterioph
735	7	23.3	11	7	Q77875	Q77875 oreochromis	808	7	23.3	14	11	Q70599	Q70599 rattus norv
736	7	23.3	11	7	Q77876	Q77876 oreochromis	809	7	23.3	14	11	Q63937	Q63937 mesocricetu
737	7	23.3	11	7	Q77880	Q77880 oreochromis	810	7	23.3	14	11	Q10734	Q10734 mus musculu
738	7	23.3	11	7	Q77883	Q77883 oreochromis	811	7	23.3	14	11	Q92065	Q92065 mus musculu
739	7	23.3	11	7	Q77886	Q77886 oreochromis	812	7	23.3	14	12	Q67112	Q67112 influenza a
740	7	23.3	11	7	Q77887	Q77887 oreochromis	813	7	23.3	14	12	Q86616	Q86616 turkey herp
741	7	23.3	11	7	Q77888	Q77888 oreochromis	814	7	23.3	14	12	Q86127	Q86127 porcine cir
742	7	23.3	11	7	Q77897	Q77897 oreochromis	815	7	23.3	14	12	Q93202	Q93202 porcine cir
743	7	23.3	11	7	Q77899	Q77899 oreochromis	816	7	23.3	14	12	Q9YJ34	Q9YJ34 porcine cir
744	7	23.3	11	7	Q77900	Q77900 oreochromis	817	7	23.3	14	12	Q86578	Q86578 sigma virus
745	7	23.3	11	7	Q77901	Q77901 oreochromis	818	7	23.3	14	13	Q91777	Q91777 xenopus lae
746	7	23.3	11	7	Q77902	Q77902 oreochromis	819	7	23.3	14	13	P70007	P70007 xenopus lae
747	7	23.3	11	7	Q77903	Q77903 oreochromis	820	7	23.3	15	2	Q44507	Q44507 anabaena va
748	7	23.3	11	7	Q77904	Q77904 oreochromis	821	7	23.3	15	2	Q69142	Q69142 streptococc
749	7	23.3	11	7	Q77905	Q77905 oreochromis	822	7	23.3	15	2	Q46963	Q46963 escherichia
750	7	23.3	11	7	Q77907	Q77907 oreochromis	823	7	23.3	15	2	Q47893	Q47893 fremyella d

824	7	23.3	15	2	Q47892	Q47892 fremyella d	897	7	23.3	18	2	Q00952	Q00952 actinobacil
825	7	23.3	15	2	Q52640	Q52640 pseudomonas	898	7	23.3	18	2	Q92642	Q92642 chlamydia t
826	7	23.3	15	2	Q52135	Q52135 enterococcu	899	7	23.3	18	2	P77033	P77033 escherichia
827	7	23.3	15	4	Q16158	Q16158 homo sapien	900	7	23.3	18	2	Q9X3E9	Q9X3E9 prochloroco
828	7	23.3	15	4	P78482	P78482 homo sapien	901	7	23.3	18	3	Q01672	Q01672 pneumocysti
829	7	23.3	15	4	Q08947	Q08947 homo sapien	902	7	23.3	18	3	Q13665	Q13665 homo sapien
830	7	23.3	15	4	Q60743	Q60743 homo sapien	903	7	23.3	18	4	Q13767	Q13767 homo sapien
831	7	23.3	15	8	Q95771	Q95771 ctenosaura	904	7	23.3	18	4	Q16028	Q16028 homo sapien
832	7	23.3	15	8	Q95773	Q95773 conolophus	905	7	23.3	18	4	Q16244	Q16244 homo sapien
833	7	23.3	15	8	Q95879	Q95879 phrynosoma	906	7	23.3	18	7	Q29820	Q29820 homo sapien
834	7	23.3	15	8	Q36727	Q36727 homo sapien	907	7	23.3	18	7	Q29817	Q29817 homo sapien
835	7	23.3	15	8	Q9X1J8	Q9X1J8 bugeranus l	908	7	23.3	18	7	Q29819	Q29819 homo sapien
836	7	23.3	15	10	Q41526	Q41526 triticum ae	909	7	23.3	18	7	Q30980	Q30980 pan troglod
837	7	23.3	15	10	Q65177	Q65177 mesembryant	910	7	23.3	18	7	Q77923	Q77923 oreochromis
838	7	23.3	15	10	Q9XGM5	Q9XGM5 arabidopsis	911	7	23.3	18	8	Q98365	Q98365 myosurus mi
839	7	23.3	15	11	Q63936	Q63936 mesocricetu	912	7	23.3	18	8	Q37852	Q37852 bacterioph
840	7	23.3	15	11	Q63938	Q63938 mesocricetu	913	7	23.3	18	9	Q38573	Q38573 bacterioph
841	7	23.3	15	11	Q62544	Q62544 mus spretus	914	7	23.3	18	10	Q41458	Q41458 solanum tub
842	7	23.3	15	12	Q66174	Q66174 human coron	915	7	23.3	18	10	Q96345	Q96345 brassica na
843	7	23.3	15	12	Q69353	Q69353 herpes simp	916	7	23.3	18	11	Q61840	Q61840 mus musculu
844	7	23.3	15	12	Q88881	Q88881 tobacco mos	917	7	23.3	18	13	Q91380	Q91380 gallus gall
845	7	23.3	16	2	Q45863	Q45863 bacillus su	918	7	23.3	19	2	Q44850	Q44850 borrelia bu
846	7	23.3	16	2	Q47603	Q47603 escherichia	919	7	23.3	19	2	Q07479	Q07479 streptococc
847	7	23.3	16	2	Q53399	Q53399 bacillus th	920	7	23.3	19	2	Q45558	Q45558 bacillus sp
848	7	23.3	16	2	Q50900	Q50900 shigella so	921	7	23.3	19	2	Q47895	Q47895 fremyella d
849	7	23.3	16	2	Q51950	Q51950 staphylococ	922	7	23.3	19	2	P74875	P74875 salmonella
850	7	23.3	16	2	Q99374	Q99374 staphylococ	923	7	23.3	19	2	Q33755	Q33755 streptococc
851	7	23.3	16	4	Q16183	Q16183 homo sapien	924	7	23.3	19	2	Q57012	Q57012 staphylococ
852	7	23.3	16	5	Q26101	Q26101 pratylenchu	925	7	23.3	19	2	Q57313	Q57313 staphylococ
853	7	23.3	16	6	P79137	P79137 cercopithe	926	7	23.3	19	4	Q14737	Q14737 homo sapien
854	7	23.3	16	7	Q77922	Q77922 oreochromis	927	7	23.3	19	4	Q76047	Q76047 homo sapien
855	7	23.3	16	8	P92070	P92070 euhadra her	928	7	23.3	19	4	Q95578	Q95578 homo sapien
856	7	23.3	16	8	Q33429	Q33429 anas platyr	929	7	23.3	19	4	Q9Y3R8	Q9Y3R8 homo sapien
857	7	23.3	16	8	Q35214	Q35214 oenothera b	930	7	23.3	19	5	Q26099	Q26099 pratylenchu
858	7	23.3	16	9	Q38407	Q38407 bacterioph	931	7	23.3	19	5	Q20438	Q20438 caenorhabdi
859	7	23.3	16	10	Q82402	Q82402 fragaria nu	932	7	23.3	19	8	Q07054	Q07054 crithidia f
860	7	23.3	16	10	Q82404	Q82404 fragaria ni	933	7	23.3	19	8	Q07054	Q07054 crithidia f
861	7	23.3	16	10	Q82405	Q82405 fragaria ii	934	7	23.3	19	11	P70322	P70322 mus musculu
862	7	23.3	16	10	Q82406	Q82406 fragaria mo	935	7	23.3	19	11	P97920	P97920 mus musculu
863	7	23.3	16	10	Q82407	Q82407 fragaria vi	936	7	23.3	19	12	Q73129	Q73129 human immun
864	7	23.3	16	10	Q82781	Q82781 fragaria ve	937	7	23.3	19	12	Q11338	Q11338 molluscum c
865	7	23.3	16	11	Q54894	Q54894 mus musculu	938	7	23.3	19	12	Q64977	Q64977 alfalfa mos
866	7	23.3	16	12	Q00340	Q00340 vaccinia vi	939	7	23.3	19	12	Q69345	Q69345 human herpe
867	7	23.3	16	12	Q79457	Q79457 human immun	940	7	23.3	19	12	Q69396	Q69396 pseudorabie
868	7	23.3	16	12	Q79458	Q79458 human immun	941	7	23.3	19	12	Q84863	Q84863 unidentifie
869	7	23.3	16	12	Q90049	Q90049 human cytom	942	7	23.3	19	12	Q84864	Q84864 unidentifie
870	7	23.3	16	12	Q9WMG6	Q9WMG6 sigma virus	943	7	23.3	19	12	Q65340	Q65340 autographa
871	7	23.3	17	2	Q34216	Q34216 pseudomonas	944	7	23.3	19	12	Q90622	Q90622 simian herp
872	7	23.3	17	2	Q52210	Q52210 staphylococ	945	7	23.3	19	12	Q90625	Q90625 simian herp
873	7	23.3	17	2	Q92F05	Q92F05 salmonella	946	7	23.3	19	12	Q90628	Q90628 simian herp
874	7	23.3	17	2	Q92E26	Q92E26 buchnera ap	947	7	23.3	19	12	Q90630	Q90630 baboon herp
875	7	23.3	17	2	Q06946	Q06946 salmonella	948	7	23.3	19	12	Q90633	Q90633 baboon herp
876	7	23.3	17	2	Q9X515	Q9X515 enterococcu	949	7	23.3	19	12	Q90635	Q90635 simian herp
877	7	23.3	17	2	Q9WM21	Q9WM21 enterococcu	950	7	23.3	19	12	Q84197	Q84197 human respi
878	7	23.3	17	2	Q9WM20	Q9WM20 enterococcu	951	7	23.3	19	12	Q9W9U1	Q9W9U1 simian herp
879	7	23.3	17	4	Q92727	Q92727 homo sapien	952	7	23.3	19	13	Q91433	Q91433 gallus gall
880	7	23.3	17	6	P79167	P79167 equus cabal	953	7	23.3	19	13	P87468	P87468 xenopus lae
881	7	23.3	17	6	Q46667	Q46667 macropus ro	954	7	23.3	20	2	Q46499	Q46499 desulfovibr
882	7	23.3	17	6	Q62645	Q62645 saguinus oe	955	7	23.3	20	2	Q49448	Q49448 mycoplasma
883	7	23.3	17	7	P79480	P79480 cervus elap	956	7	23.3	20	2	Q47614	Q47614 escherichia
884	7	23.3	17	7	Q78036	Q78036 mus musculu	957	7	23.3	20	2	Q53345	Q53345 pseudomonas
885	7	23.3	17	8	Q07055	Q07055 crithidia f	958	7	23.3	20	2	Q53346	Q53346 pseudomonas
886	7	23.3	17	9	Q92X12	Q92X12 bacterioph	959	7	23.3	20	2	Q47598	Q47598 escherichia
887	7	23.3	17	10	Q41400	Q41400 sesbania ro	960	7	23.3	20	2	Q53121	Q53121 rhodobacter
888	7	23.3	17	11	Q62547	Q62547 mus spretus	961	7	23.3	20	2	Q60696	Q60696 homo sapien
889	7	23.3	17	11	Q88173	Q88173 rattus norv	962	7	23.3	20	4	Q16129	Q16129 homo sapien
890	7	23.3	17	12	Q84098	Q84098 influenza a	963	7	23.3	20	4	Q16240	Q16240 homo sapien
891	7	23.3	17	12	Q85072	Q85072 pepper seve	964	7	23.3	20	5	Q46158	Q46158 lumbricus r
892	7	23.3	17	12	Q85479	Q85479 rous sarcom	965	7	23.3	20	6	Q62720	Q62720 cryetolagus
893	7	23.3	17	12	Q90122	Q90122 choristoneu	966	7	23.3	20	7	Q77859	Q77859 oreochromis
894	7	23.3	17	13	Q91352	Q91352 gallus gall	967	7	23.3	20	8	Q34694	Q34694 homarus ame
895	7	23.3	18	2	Q50076	Q50076 mycobacteri	968	7	23.3	20	9	Q37944	Q37944 lactococcus
896	7	23.3	18	2	Q49250	Q49250 mycoplasma	969	7	23.3	20	10	Q9X1W8	Q9X1W8 oryza sativ

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970 7 23.3 20 11 Q63967 rattus norv
971 7 23.3 20 11 Q64031 cricetidae
972 7 23.3 20 12 Q65705 bovine resp
973 7 23.3 20 12 Q83416 pseudorabie
974 7 23.3 20 12 Q83272 cucumber mo
975 7 23.3 20 12 Q83272 cucumber mo
976 7 23.3 20 12 Q9WLD2 simian herp
977 7 23.3 20 12 Q9W8E9 newcastl d
978 6 20.0 7 8 Q98866 spinacia ol
979 6 20.0 9 12 Q85599 moloney mur
980 6 20.0 9 12 Q88953 vaccinia vi
981 6 20.0 9 12 Q67605 squash leaf
982 6 20.0 10 2 Q9XBH3 bacillus ce
983 6 20.0 11 11 Q60807 mus musculu
984 6 20.0 12 2 Q53358 escherichia
985 6 20.0 12 5 Q61574 osteritagia
986 6 20.0 12 12 Q78845 human immun
987 6 20.0 13 4 Q99931 homo sapien
988 6 20.0 13 11 P97944 mus musculu
989 6 20.0 14 2 Q44160 prunus arne
990 6 20.0 14 2 Q46228 clover prol
991 6 20.0 14 2 Q46291 canadiah pe
992 6 20.0 14 2 Q48878 loofah witc
993 6 20.0 14 2 Q56750 western x p
994 6 20.0 14 2 Q60199 escherichia
995 6 20.0 14 2 Q921E1 acetobacter
996 6 20.0 14 11 Q06415 rattus norv
997 6 20.0 14 11 Q06414 rattus norv
998 6 20.0 14 12 Q86922 human cytom
999 6 20.0 14 12 P87540 barley mild
1000 6 20.0 15 9 Q38574 bacterioph

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ALIGNMENTS

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RESULT 1
Q83960 PRELIMINARY; PRT; 16 AA.
ID Q83960;
AC Q83960;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE INFLUENZA A/ANN ARBOR/6/60 (H2N2), NON-STRUCTURAL PROTEIN
DE (SEG 8), COOH TERMINUS OF NS1 (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83303830.
RA PARVIN J.D., YOUNG J.F., PALESE P.;
RT "Nonsense mutations affecting the lengths of the NS1 nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; R00962; AAA43516.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1811 MW; F515CA75 CRC32;

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Query Match 60.0%; Score 18; DB 12; Length 16;
Best Local Similarity 40.0%; Pred. No. 5.9e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 WRXXE 5
   |||
Db 2 WRSSD 6

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RESULT 2
Q92134 PRELIMINARY; PRT; 16 AA.
ID Q92134;
AC Q92134;

```

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DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE MNSC1 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99137020.
RA KUTSUWADA K., SATOH J., OHKI G., MUTO S., IMAI M., ARAKAWA M.,
RA SUZUKI M.;
RT "Cloning and characterization of 5'-flanking region of mouse non-
RT selective cation channel 1.";
RL Biochim. Biophys. Acta 1444:92-100(1999).
DR EMBL; AB015230; BAA34298.1; -.
FT NON_TER 16
SQ SEQUENCE 16 AA; 1907 MW; 4F76D5A5 CRC32;

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Query Match 56.7%; Score 17; DB 11; Length 16;
Best Local Similarity 40.0%; Pred. No. 9.7e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 WRXXE 5
   |||
Db 7 WRSGE 11

```

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RESULT 3
Q73549 PRELIMINARY; PRT; 18 AA.
ID Q73549;
AC Q73549;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrofird viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RT immunodeficiency virus type 1-infected patients.";
RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-PATIENT P74, PCR;
RA LEIGH BROWN A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBSJ databases.
DR EMBL; U45115; AAB04266.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

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Query Match 56.7%; Score 17; DB 12; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 WRXXEY 6
   |||
Db 3 WRWGFY 8

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RESULT 4
Q73575 PRELIMINARY; PRT; 18 AA.
ID Q73575;
AC Q73575;

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Db      3 WRWGFY 8

RESULT 6
Q73579 PRELIMINARY; PRT; 18 AA.
AC Q73579;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
OC [1]
RC SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RT immunodeficiency virus type 1-infected patients.";
RT J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RA LEIGH BROWN A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45145; AAB04296.1; -.
FW RNA-directed DNA polymerase.
KW NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

Query Match 56.7%; Score 17; DB 12; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0;

QY 1 WRXKEY 6
|||
Db 3 WRWGFY 8

RESULT 7
Q73593 PRELIMINARY; PRT; 18 AA.
AC Q73593;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
OC [1]
RC SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RT immunodeficiency virus type 1-infected patients.";
RT J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RA LEIGH BROWN A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45159; AAB04310.1; -.
FW RNA-directed DNA polymerase.
KW NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

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Query Match 56.7%; Score 17; DB 12; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
 || |
 Db 3 WRWGFY 8

RESULT 8
 Q73601 ID Q73601 PRELIMINARY; PRT; 18 AA.
 AC Q73601;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE REVERSE TRANSCRIPTASE (FRAGMENT).
 GN POL.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT P74, PCR;
 RX MEDLINE; 96242958.
 RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
 "Evolution of zidovudine resistance-associated genotypes in human
 immunodeficiency virus type 1-infected patients";
 J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT P74, PCR;
 RA LEIGH BROWN A.J.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U45167; AAB04318.1; -.
 KW RNA-directed DNA polymerase.
 FT NON_TER 1 18
 SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

Query Match 56.7%; Score 17; DB 12; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
 || |
 Db 3 WRWGFY 8

RESULT 9
 Q73609 ID Q73609 PRELIMINARY; PRT; 18 AA.
 AC Q73609;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE REVERSE TRANSCRIPTASE (FRAGMENT).
 GN POL.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT P74, PCR;
 RX MEDLINE; 96242958.
 RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
 "Evolution of zidovudine resistance-associated genotypes in human
 immunodeficiency virus type 1-infected patients";
 J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT P74, PCR;
 RA LEIGH BROWN A.J.;

RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U45175; AAB04326.1; -.
 KW RNA-directed DNA polymerase.
 FT NON_TER 1 18
 SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

Query Match 56.7%; Score 17; DB 12; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WRXXEY 6
 || |
 Db 3 WRWGFY 8

RESULT 10
 Q62721 ID Q62721 PRELIMINARY; PRT; 8 AA.
 AC Q62721;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE PROHIBITIN (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FISHER;
 RX MEDLINE; 95331633.
 RA ALTUS M.S., WOOD C.M., STEWART D.A., ROSKAMS A.I., FRIEDMAN V.,
 HENDERSON T., OWENS G.A., DANNER D.B., JUPE E.R., DELL'ORCO R.T.,
 MCCLUNG J.K.;
 RT "Regions of evolutionary conservation between the rat and human
 prohibitin-encoding genes";
 Gene 158:291-294(1995).
 RL EMBL; U17178; AAA86692.1; -.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1150 MW; 3A1A5BE2 CRC32;

Query Match 53.3%; Score 16; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WR 2
 ||
 Db 2 WR 3

RESULT 11
 Q77919 ID Q77919 PRELIMINARY; PRT; 12 AA.
 AC Q77919;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE MHC CLASS II B LOCUS 4 (FRAGMENT).
 OS Pseudotropheus sp. 'Pseudotropheus tropheops complex'.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
 OC Perciformes; Labroidae; Cichlidae; Pseudotropheus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98315113.
 RA MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNSKA Z.,
 RA SUELTSMANN H., FIGUEROA F., KLEIN J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid Mhc
 class II B loci";
 Genetics 145:1527-1547(1998).
 RL EMBL; AF050032; AAC41371.1; -.

KW MHC.
FT NON_TER 1
FT NON_TER 12
SQ SEQUENCE 12 AA; 1529 MW; 42B030F1 CRC32;

Query Match 53.3%; Score 16; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
Db 4 WR 5

RESULT 12
ID Q54081 PRELIMINARY; PRT; 14 AA.
AC Q54081;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE HYPOTHETICAL 1.8 KD PROTEIN.
OS Saccharopolyspora erythraea (Streptomyces erythraeus).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Pseudonocardineae; Pseudonocardaceae;
OC Saccharopolyspora.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90094240.
RA DONADIO S., SHAFIEE A., HUTCHINSON C.R.;
RT "Disruption of a rhodanese-like gene results in cysteine auxotrophy in
RT Saccharopolyspora erythraea.";
RL J. Bacteriol. 172:350-360(1990).
DR EMBL; M29612; AAA88532.1; -.
KW Hypothetical protein.
SQ SEQUENCE 14 AA; 1759 MW; 450C4BF2 CRC32;

Query Match 53.3%; Score 16; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
Db 12 WR 13

RESULT 13
ID Q83967 PRELIMINARY; PRT; 16 AA.
AC Q83967;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE INFLUENZA A/CAMERO/46 (H1N1), NON-STRUCTURAL PROTEIN
DE (SEG 8), COOH TERMINUS OF NSI (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83303830.
RA PARVIN J.D., YOUNG J.F., PALESE P.;
RT "Nonsense mutations affecting the lengths of the NSI nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; K00961; AAA43519.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1711 MW; 225C2198 CRC32;

Query Match 53.3%; Score 16; DB 12; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
Db 2 WR 3

RESULT 14
ID Q84055 PRELIMINARY; PRT; 16 AA.
AC Q84055;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE INFLUENZA A/NETHERLAND/84/68 (H2N2), NON-STRUCTURAL PROTEIN
DE (SEG 8), COOH TERMINUS OF NSI (FRAGMENT).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenza virus A and B group.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83303830.
RA PARVIN J.D., YOUNG J.F., PALESE P.;
RT "Nonsense mutations affecting the lengths of the NSI nonstructural
RT proteins of influenza A virus isolates.";
RL Virology 128:512-517(1983).
DR EMBL; K00963; AAA43527.1; -.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1810 MW; 17BA92F1 CRC32;

Query Match 53.3%; Score 16; DB 12; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
Db 2 WR 3

RESULT 15
ID O07270 PRELIMINARY; PRT; 17 AA.
AC O07270;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE HYPOTHETICAL 2.1 KD PROTEIN.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-2296207;
RX MEDLINE; 98086105.
RA SUPPLY P., MAGDALENA J., HIMPENS S., LOCHT C.;
RT "Identification of novel intergenic repetitive units in a
RT mycobacterial two-component system operon.";
RL Mol. Microbiol. 26:991-1003(1997).
DR EMBL; Y13628; CAAT73961.1; -.
KW Hypothetical protein.
SQ SEQUENCE 17 AA; 2058 MW; 04EDF870 CRC32;

Query Match 53.3%; Score 16; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WR 2
Db 16 WR 17

Search completed: May 2, 2000, 00:19:34
Job time: 102 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:20:33 ; Search time 13.09 seconds
(without alignments)
16.285 Million cell updates/sec

Title: US-09-258-947-38
Perfect score: 61
Sequence: 1 WNWRYREV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 91374

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	9	1 W15299	Human platelet gly
2	61	100.0	9	1 W17558	Mimotope capable o
3	61	100.0	10	1 W32624	Human platelet gly
4	61	100.0	10	1 W17152	Mimotope capable o
5	45	73.8	10	1 W32625	Human platelet gly
6	45	73.8	10	1 W17159	Mimotope capable o
7	38	62.3	10	1 W32627	Human platelet gly
8	38	62.3	10	1 W17154	Mimotope capable o
9	36	59.0	10	1 W32626	Human platelet gly
10	36	59.0	10	1 W17153	Mimotope capable o
11	35	57.4	15	1 W12276	Synthetic library
12	35	57.4	15	1 W17134	A glycolipid sugar
13	35	57.4	15	1 W94702	Lipoteichoic acid
14	35	57.4	19	1 W94729	Sequence 15mer 2nd
15	35	57.4	19	1 W94710	Sequence 15mer 2-8/
16	35	57.4	19	1 W94721	Sequence 15mer 2-19
17	35	57.4	19	1 W94705	Sequence 15mer 2-1/
18	35	57.4	19	1 W94709	Sequence 15mer 2-7/
19	34	55.7	6	1 W21070	Lipolytic enzyme o
20	34	55.7	6	1 W23193	Terminal peptide e
21	34	55.7	10	1 W32732	Human platelet gly
22	33	54.1	10	1 W41879	Peptide used in ra
23	33	54.1	11	1 W62116	Human MDW2 binding
24	33	54.1	15	1 W10062	Peptide #3 inhibit
25	33	54.1	20	1 R54387	RAE 29.1-1. Isolab
26	33	54.1	20	1 W02471	RAE 29.1-1. Isolab
27	32	52.5	10	1 W32628	Human platelet gly
28	32	52.5	10	1 W32629	Human platelet gly
29	32	52.5	10	1 W32714	Human platelet gly
30	32	52.5	10	1 W17155	Mimotope capable o
31	32	52.5	10	1 W17156	Mimotope capable o
32	32	52.5	16	1 W00311	Osteoblast prolif
33	32	52.5	16	1 W60019	Calcitonin recepto
34	31.5	51.6	20	1 W99246	Endothelin antag

35	30	49.2	10	1 W32630	Human platelet gly
36	30	49.2	10	1 W32736	Human platelet gly
37	30	49.2	10	1 W17160	Mimotope capable o
38	30	49.2	15	1 W18840	Human immunoglobul
39	30	49.2	15	1 W94854	Sequence of human
40	29	47.5	6	1 R90503	Hybridoma ATCC HB-
41	29	47.5	7	1 W48277	Human ninjurin pep
42	29	47.5	8	1 W57542	Molecular mimetic
43	29	47.5	9	1 W05103	N-terminally acyla
44	29	47.5	9	1 W05104	N-terminally acety
45	29	47.5	9	1 W03684	branched chain pol
46	29	47.5	9	1 W48276	Human ninjurin pep
47	29	47.5	10	1 P83021	Example of gonadol
48	29	47.5	10	1 W24770	Human immunoglobul
49	29	47.5	10	1 W62180	Heavy chain CDR3 p
50	29	47.5	11	1 R31357	Antimicrobial pept
51	29	47.5	11	1 R4843	Lactoferrin-relate
52	29	47.5	11	1 R48537	Lactoferrin-deriva
53	29	47.5	11	1 R57464	Lactoferrin-deriva
54	29	47.5	11	1 R80266	Anti-parasitic lac
55	29	47.5	11	1 R84701	Bovine lactoferrin
56	29	47.5	11	1 R84084	Bovine lactoferrin
57	29	47.5	11	1 R87611	Lactoferrin-deriva
58	29	47.5	11	1 R91854	Lactoferrin-deriva
59	29	47.5	11	1 W14038	Anti-parasitic pep
60	29	47.5	11	1 W26152	Lactoferrin-deriva
61	29	47.5	11	1 W41292	Apoptosis inducer
62	29	47.5	11	1 W53227	Lactoferrin hydrol
63	29	47.5	11	1 W70312	Thrombus formation
64	29	47.5	15	1 P90211	Antigenic peptide
65	29	47.5	18	1 R69354	Bovine lactoferrin
66	29	47.5	18	1 W10515	Lactoferrin-deriva
67	29	47.5	20	1 R21808	Anti microbial pep
68	29	47.5	20	1 R21809	Anti microbial pep
69	29	47.5	20	1 R48440	Lactoferrin-relate
70	29	47.5	20	1 R48528	Lactoferrin-deriva
71	29	47.5	20	1 R48529	Lactoferrin-deriva
72	29	47.5	20	1 R57460	Lactoferrin-deriva
73	29	47.5	20	1 R80261	Anti-parasitic lac
74	29	47.5	20	1 R80262	Anti-parasitic lac
75	29	47.5	20	1 R84696	Bovine lactoferrin
76	29	47.5	20	1 R84697	Bovine lactoferrin
77	29	47.5	20	1 R90606	Lactoferrin-deriva
78	29	47.5	20	1 R87619	Lactoferrin-deriva
79	29	47.5	20	1 R87620	Lactoferrin-deriva
80	29	47.5	20	1 R91851	Lactoferrin-deriva
81	29	47.5	20	1 W03044	Lactoferrin-deriva
82	29	47.5	20	1 R98552	Peptide for anti-u
83	29	47.5	20	1 W14035	Anti-parasitic pep
84	29	47.5	20	1 W26149	Lactoferrin-deriva
85	29	47.5	20	1 W41288	Apoptosis inducer
86	29	47.5	20	1 W41287	Apoptosis inducer
87	29	47.5	20	1 W53222	Lactoferrin hydrol
88	29	47.5	20	1 W53223	Lactoferrin hydrol
89	29	47.5	20	1 W70309	Thrombus formation
90	28	45.9	4	1 R64366	DP-178 homologue 3
91	28	45.9	4	1 R75599	gp120 binding fab
92	28	45.9	4	1 R75600	gp120 binding fab
93	28	45.9	4	1 R75596	gp120 binding fab
94	28	45.9	5	1 R64367	DP-178 homologue 3
95	28	45.9	6	1 R64368	DP-178 homologue 3
96	28	45.9	7	1 R64369	DP-178 homologue 3
97	28	45.9	8	1 R64370	DP-178 homologue 3
98	28	45.9	9	1 R64371	DP-178 homologue 4
99	28	45.9	10	1 R64372	DP-178 homologue 4
100	28	45.9	10	1 W32703	Human platelet gly
101	28	45.9	11	1 R64373	DP-178 homologue 4
102	28	45.9	12	1 R64374	DP-178 homologue 4
103	28	45.9	12	1 W99912	HIV-1 vaccine synt
104	28	45.9	13	1 R64375	DP-178 homologue 4
105	28	45.9	13	1 W12895	Antimicrobial cati
106	28	45.9	13	1 W66375	Cationic peptide o
107	28	45.9	14	1 P71141	Anti-HIV peptide 2

108	28	45.9	14	1	R64376	DP-178 homologue 4	181	26	42.6	10	1	W32721	Human platelet gly
109	28	45.9	15	1	P90238	Antigenic peptide	182	26	42.6	12	1	R75656	Cyclic guanosine m
110	28	45.9	15	1	R64377	DP-178 homologue 4	183	26	42.6	16	1	W12874	Antimicrobial cati
111	28	45.9	15	1	R68688	CLTB-96 B-cell epi	184	26	42.6	19	1	W78308	Fragment Of human
112	28	45.9	15	1	R68722	B cell epitope, gp	185	26	42.6	20	1	R12286	Parvovirus B19 epi
113	28	45.9	15	1	W5892	GpII peptide conta	186	26	42.6	20	1	R66566	Cyclic guanosine m
114	28	45.9	15	1	W5858	HIV-1 T/B cell epi	187	26	42.6	20	1	W42009	CGB-PDE peptide ge
115	28	45.9	15	1	W67408	HIV-1 gp41 peptide	188	25.5	41.8	15	1	W16151	Peptide containing
116	28	45.9	15	1	W67374	HIV-1 peptide epit	189	25.5	41.8	15	1	W58278	IL-1R1 binding pe
117	28	45.9	15	1	W99908	HIV-1 vaccine synt	190	25.5	41.8	15	1	W68791	Peptide binding in
118	28	45.9	15	1	W99910	HIV-1 vaccine synt	191	25.5	41.8	15	1	Y09924	Interleukin-1 type
119	28	45.9	16	1	R64378	DP-178 homologue 4	192	25	41.0	5	1	R12717	Pentapeptide paral
120	28	45.9	17	1	R64379	CLTB-97A B-cell ep	193	25	41.0	5	1	R51581	Mimotope peptide #
121	28	45.9	17	1	R68690	HIV-1 T/B cell epi	194	25	41.0	5	1	R69949	Pentameric mimotop
122	28	45.9	17	1	W25860	HIV-1 T/B cell epi	195	25	41.0	5	1	R98695	Peptide 75 from 88
123	28	45.9	17	1	W67376	HIV-1 peptide epit	196	25	41.0	5	1	W10087	Low density lipopr
124	28	45.9	17	1	W99909	HIV-1 vaccine synt	197	25	41.0	8	1	W21050	Lipolytic enzyme o
125	28	45.9	18	1	R64380	DP-178 homologue 4	198	25	41.0	8	1	W21087	Lipolytic enzyme o
126	28	45.9	18	1	R68686	CLTB-94 B-cell epi	199	25	41.0	8	1	W23213	Terminal peptide e
127	28	45.9	18	1	W5856	HIV-1 T/B cell epi	200	25	41.0	8	1	W23210	Terminal peptide e
128	28	45.9	18	1	W67372	HIV-1 peptide epit	201	25	41.0	8	1	W63177	Amino terminal seq
129	28	45.9	18	1	W99907	HIV-1 vaccine synt	202	25	41.0	9	1	R22649	LH-RH analogue (2)
130	28	45.9	19	1	R64381	DP-178 homologue 5	203	25	41.0	9	1	R49226	HLA-A1 WAGE 3 anti
131	28	45.9	20	1	R64382	CLTB-92A B-cell ep	204	25	41.0	9	1	R65137	MAGE 3 immunogeni
132	28	45.9	20	1	R68684	HIV peptide #51. D	205	25	41.0	9	1	R75948	Melanoma antigen (
133	28	45.9	20	1	W80666	gp41 peptide 53. D	206	25	41.0	9	1	W66382	Indolicidin analog
134	28	45.9	20	1	W79720	HIV-1 T/B cell epi	207	25	41.0	9	1	W66369	Indolicidin analog
135	28	45.9	20	1	W5854	HIV-1 T/B cell epi	208	25	41.0	9	1	Y00813	HLA-A24 antigenic
136	28	45.9	20	1	W67370	HIV-1 peptide epit	209	25	41.0	10	1	P10168	Sequence of lutein
137	28	45.9	20	1	W99905	HIV-1 vaccine synt	210	25	41.0	10	1	R75952	Melanoma antigen (
138	27	44.3	4	1	R27863	Antimicrobial pept	211	25	41.0	10	1	W10089	Low density lipopr
139	27	44.3	4	1	R48522	Lactoferrin derive	212	25	41.0	10	1	W32707	Human platelet gly
140	27	44.3	4	1	R57453	Lactoferrin derive	213	25	41.0	10	1	W66381	Indolicidin analog
141	27	44.3	4	1	R79760	Anti-parasitic lac	214	25	41.0	10	1	W66367	Indolicidin analog
142	27	44.3	4	1	R94690	Bovine lactoferrin	215	25	41.0	10	1	Y00814	HLA-A24 antigenic
143	27	44.3	4	1	R90600	Lactoferrin derive	216	25	41.0	11	1	W13805	Antimicrobial cati
144	27	44.3	4	1	R7614	Lactoferrin-derive	217	25	41.0	12	1	P90980	Fragment Inv10 of
145	27	44.3	4	1	R31847	Lactoferrin-derive	218	25	41.0	12	1	R78458	Indolicidin analog
146	27	44.3	4	1	R98546	Peptide for anti-u	219	25	41.0	12	1	W12877	Antimicrobial cati
147	27	44.3	4	1	W4031	Anti-parasitic pep	220	25	41.0	12	1	W41013	Anti-glutathione a
148	27	44.3	4	1	W26145	Lactoferrin deriva	221	25	41.0	12	1	W66364	Indolicidin analog
149	27	44.3	4	1	W41281	Apoptosis inducer	222	25	41.0	12	1	W66361	Indolicidin analog
150	27	44.3	4	1	W32216	Lactoferrin hydrol	223	25	41.0	13	1	R30970	Broad spectrum ant
151	27	44.3	4	1	W70307	Thrombus formation	224	25	41.0	13	1	R55726	T-cell epitope TCE
152	27	44.3	5	1	W94177	FG loop sequence o	225	25	41.0	13	1	R78459	Indolicidin analog
153	27	44.3	6	1	R31352	Antimicrobial pept	226	25	41.0	13	1	R78457	Indolicidin analog
154	27	44.3	6	1	W05105	C-terminally amida	227	25	41.0	13	1	W12873	Antimicrobial cati
155	27	44.3	6	1	W03683	Branched chain pol	228	25	41.0	13	1	W13807	Antimicrobial cati
156	27	44.3	10	1	P80546	Novel decapeptide	229	25	41.0	13	1	W27179	Antimicrobial cati
157	27	44.3	10	1	R49057	Infectious pancrea	230	25	41.0	13	1	W27179	Antimicrobial cati
158	27	44.3	10	1	W03708	Ac-D-Trp(1,3)-D-Cp	231	25	41.0	13	1	W12889	Antimicrobial cati
159	27	44.3	10	1	W12881	Antimicrobial cati	232	25	41.0	13	1	W12892	Antimicrobial cati
160	27	44.3	10	1	R49107	Sequence of peptid	233	25	41.0	13	1	W12893	Antimicrobial cati
161	27	44.3	11	1	R55114	Peptide p240 from	234	25	41.0	13	1	W12896	Antimicrobial cati
162	27	44.3	12	1	R49075	Infectious pancrea	235	25	41.0	13	1	W12897	Antimicrobial cati
163	27	44.3	12	1	R49085	Infectious pancrea	236	25	41.0	13	1	W66441	Cationic peptide 1
164	27	44.3	12	1	W12890	Antimicrobial cati	237	25	41.0	13	1	W66378	Cationic peptide o
165	27	44.3	12	1	R49125	Sequence of C-term	238	25	41.0	13	1	W71690	Cationic peptide M
166	27	44.3	13	1	R78454	Indolicidin analog	239	25	41.0	13	1	W87609	Antimicrobial pept
167	27	44.3	14	1	W13809	Antimicrobial cati	240	25	41.0	14	1	W12875	Antimicrobial cati
168	27	44.3	14	1	W12876	Antimicrobial cati	241	25	41.0	14	1	W66362	Indolicidin analog
169	27	44.3	15	1	R47672	HIV epitope #5. Ne	242	25	41.0	14	1	R67987	B lymphocyte antig
170	27	44.3	15	1	W13801	Antimicrobial cati	243	25	41.0	15	1	W12277	Human B lymphocyte
171	27	44.3	17	1	Y01808	Peptide SU2 derive	244	25	41.0	15	1	W08471	Human B lymphocyte
172	27	44.3	18	1	R28777	High endotoxin aff	245	25	41.0	15	1	W12878	Antimicrobial cati
173	27	44.3	18	1	W37582	Synergistic HIV en	246	25	41.0	15	1	W12879	Antimicrobial cati
174	26	42.6	18	1	W79843	Peptide sequence o	247	25	41.0	15	1	W12885	Antimicrobial cati
175	26	42.6	9	1	W50755	Peptide derivative	248	25	41.0	15	1	W13802	Antimicrobial cati
176	26	42.6	9	1	W05102	N-terminal acety	249	25	41.0	15	1	W66360	Indolicidin analog
177	26	42.6	9	1	W03685	Branched chain pol	250	25	41.0	16	1	W12882	Antimicrobial cati
178	26	42.6	10	1	P61443	Luteinising hormon	251	25	41.0	16	1	W12886	Antimicrobial cati
179	26	42.6	10	1	P61418	Luteinising hormone	252	25	41.0	16	1	W12899	Antimicrobial cati
180	26	42.6	10	1	W32773	Human platelet gly	253	25	41.0	17	1	R31523	N terminal sequenc

254	25	41.0	19	1	R97973	Antigenic fragment	327	23	37.7	5	1	R80762	Transition metal i
255	24.5	40.2	7	1	R25021	C-terminal residue	328	23	37.7	5	1	R98653	Peptide 33 from 88
256	24.5	40.2	10	1	R32631	Human platelet gly	329	23	37.7	5	1	R98656	Peptide 36 from 88
257	24.5	40.2	10	1	W71757	Mimotope capable o	330	23	37.7	5	1	R98676	Peptide 56 from 88
258	24.5	40.2	20	1	W44672	Mutant muscarinic	331	23	37.7	5	1	W22932	Low density lipopr
259	24	39.3	4	1	W22904	Low density lipopr	332	23	37.7	5	1	W87121	Peptide determined
260	24	39.3	5	1	W10098	Low density lipopr	333	23	37.7	5	1	W81154	Chelating peptide
261	24	39.3	5	1	W22906	Low density lipopr	334	23	37.7	6	1	R20441	Anti-b-endorphin m
262	24	39.3	6	1	P50103	Cyclic peptide wit	335	23	37.7	6	1	R24965	Phe-Arg contg. ant
263	24	39.3	6	1	W50756	Peptide derivative	336	23	37.7	6	1	R84897	ATPR2Ap peptide t
264	24	39.3	6	1	W50757	Peptide derivative	337	23	37.7	7	1	P71501	Growth hormone rel
265	24	39.3	10	1	R11844	Example of peptide	338	23	37.7	7	1	R35391	Human thrombospond
266	24	39.3	10	1	R57395	Peptide for treati	339	23	37.7	8	1	W57527	Molecular mimetic
267	24	39.3	10	1	W03396	H-D-Trp(1), Lys(ep	340	23	37.7	8	1	W65084	Neuronal NOS blind
268	24	39.3	10	1	W03397	Ac-D-Trp(1), D-Ala	341	23	37.7	8	1	W94115	VIF-derived HIV pr
269	24	39.3	10	1	W03398	H-D-Trp(1), D-Ala	342	23	37.7	9	1	R24496	[ps18-9 pseudo] No
270	24	39.3	10	1	W32771	Human platelet gly	343	23	37.7	9	1	R57389	Peptide for treati
271	24	39.3	10	1	W32759	Human platelet gly	344	23	37.7	9	1	R94941	Modified salmon go
272	24	39.3	10	1	W32709	Human platelet gly	345	23	37.7	9	1	W39603	Human melanoma ass
273	24	39.3	10	1	W71162	Peptide used in an	346	23	37.7	9	1	W96182	IKK-alpha polypept
274	24	39.3	12	1	W66380	Cationic peptide o	347	23	37.7	10	1	P60126	Cyclic analogue of
275	24	39.3	13	1	W43997	Human myelin oligo	348	23	37.7	10	1	P70925	Luteinising hormon
276	24	39.3	13	1	W43998	Human myelin oligo	349	23	37.7	10	1	P70927	Luteinising hormon
277	24	39.3	13	1	W43999	Human myelin oligo	350	23	37.7	10	1	R11848	Example of peptide
278	24	39.3	13	1	W44000	Human myelin oligo	351	23	37.7	10	1	P61442	Luteinising hormon
279	24	39.3	13	1	W66365	Indolicidin analog	352	23	37.7	10	1	P61415	Luteinising hormone
280	24	39.3	14	1	W12612	SH2 binding peptid	353	23	37.7	10	1	P50785	Sequence of new go
281	24	39.3	14	1	W07889	Concanavalin A int	354	23	37.7	10	1	P50786	Sequence of new go
282	24	39.3	15	1	R48600	Sequence of portio	355	23	37.7	10	1	P50788	Sequence of new go
283	24	39.3	15	1	W07991	gp120 peptide 115.	356	23	37.7	10	1	P50621	Sequence of peptid
284	24	39.3	15	1	W09260	Monoclonal antibod	357	23	37.7	10	1	P40152	Sequence of peptid
285	24	39.3	15	1	W76906	Fusion immunoglob	358	23	37.7	10	1	P30177	Sequence of peptid
286	24	39.3	15	1	W76905	Fusion immunoglob	359	23	37.7	10	1	P30190	Sequence of peptid
287	24	39.3	16	1	R79553	Randomly generated	360	23	37.7	10	1	R50912	Cyclic peptide inh
288	24	39.3	16	1	W63064	Human immunodefici	361	23	37.7	10	1	R57396	Peptide for treati
289	24	39.3	16	1	W68328	MHC binding peptid	362	23	37.7	10	1	W16738	p185 binding and e
290	24	39.3	17	1	R75822	Antimicrobial tach	363	23	37.7	10	1	W16739	p185 binding and e
291	24	39.3	17	1	W37571	Synergistic HIV en	364	23	37.7	10	1	W16740	p185 binding and e
292	24	39.3	17	1	W79832	Peptide sequence o	365	23	37.7	10	1	W16741	p185 binding and e
293	24	39.3	18	1	R22540	Anti-HIV polypepti	366	23	37.7	10	1	W16746	p185 binding and e
294	24	39.3	18	1	R28778	High endotoxin aff	367	23	37.7	10	1	W16747	p185 binding and e
295	24	39.3	18	1	W37572	Synergistic HIV en	368	23	37.7	10	1	W16748	p185 binding and e
296	24	39.3	18	1	W37583	Synergistic HIV en	369	23	37.7	10	1	W16749	p185 binding and e
297	24	39.3	18	1	W79844	Peptide sequence o	370	23	37.7	10	1	W32766	Human platelet gly
298	24	39.3	18	1	W79833	Peptide sequence o	371	23	37.7	10	1	W32770	Human platelet gly
299	24	39.3	19	1	P90815	Non-immunogenic am	372	23	37.7	11	1	P71045	Sequence of peptid
300	24	39.3	19	1	W94708	Sequence 15mer2-5/	373	23	37.7	11	1	R57408	Peptide for treati
301	24	39.3	20	1	R57297	Bovine EK tryptic	374	23	37.7	11	1	W16722	p185 binding and e
302	24	39.3	20	1	R95385	Residues 199-218 o	375	23	37.7	11	1	W16723	p185 binding and e
303	24	39.3	20	1	W08050	HIV peptide #35. D	376	23	37.7	11	1	W16724	p185 binding and e
304	24	39.3	20	1	W23875	HIV-1 strain MN pe	377	23	37.7	11	1	W16725	p185 binding and e
305	24	39.3	20	1	W37549	Human myelin oligo	378	23	37.7	11	1	W16730	p185 binding and e
306	24	39.3	20	1	W37517	Human myelin oligo	379	23	37.7	11	1	W16731	p185 binding and e
307	24	39.3	20	1	W42151	T-cell epitope pep	380	23	37.7	11	1	W16732	p185 binding and e
308	24	39.3	20	1	W42152	T-cell epitope pep	381	23	37.7	11	1	W16733	p185 binding and e
309	24	39.3	20	1	W76874	Fusion immunoglob	382	23	37.7	11	1	W39604	Human melanoma ass
310	24	39.3	20	1	W76877	Fusion immunoglob	383	23	37.7	11	1	W79785	Amino acids 300-31
311	24	39.3	20	1	W80508	Smooth muscle-spec	384	23	37.7	11	1	W94114	VIF-derived HIV pr
312	24	39.3	20	1	W92519	Human FEN-1 protei	385	23	37.7	12	1	P70592	Sequence of portio
313	24	39.3	20	1	W96856	Nucleic acid bindi	386	23	37.7	12	1	R33952	B72.3 VH domain le
314	23	37.7	4	1	W10094	Low density lipopr	387	23	37.7	12	1	R93675	HIV principal neu
315	23	37.7	5	1	R12675	Pentapeptide paral	388	23	37.7	12	1	R83387	Kbmi-binding rando
316	23	37.7	5	1	R12678	Pentapeptide paral	389	23	37.7	12	1	W76401	Monoclonal antibod
317	23	37.7	5	1	R12698	Pentapeptide paral	390	23	37.7	13	1	R57410	Peptide for treati
318	23	37.7	5	1	R25919	Chelating peptide	391	23	37.7	13	1	W69623	Ste2 agonist from
319	23	37.7	5	1	R48985	Atomic force micro	392	23	37.7	13	1	W69624	Ste2 agonist from
320	23	37.7	5	1	R51562	Mimotope peptide #	393	23	37.7	13	1	W69625	Ste2 agonist from
321	23	37.7	5	1	R51539	Mimotope peptide #	394	23	37.7	13	1	W69626	Ste2 agonist from
322	23	37.7	5	1	R51542	Mimotope peptide #	395	23	37.7	13	1	W69627	Ste2 agonist from
323	23	37.7	5	1	R65517	Endothelin antagom	396	23	37.7	13	1	W69628	Ste2 agonist from
324	23	37.7	5	1	R69907	Pentameric mimotop	397	23	37.7	13	1	W69629	Ste2 agonist from
325	23	37.7	5	1	R69910	Pentameric mimotop	398	23	37.7	13	1	W69630	Ste2 agonist from
326	23	37.7	5	1	R69930	Pentameric mimotop	399	23	37.7	13	1	W69631	Ste2 agonist from

400	23	37.7	13	1	W69621	Ste2 agonist from	473	23	37.7	17	1	W75267	Adenovirus type 5
401	23	37.7	13	1	W69622	Ste2 agonist from	474	23	37.7	18	1	W30174	Interleukin-5 rece
402	23	37.7	13	1	W69632	Ste2 receptor agon	475	23	37.7	18	1	W34432	IL-5 receptor bind
403	23	37.7	13	1	W69633	Ste2 receptor agon	476	23	37.7	18	1	W63099	Acetylcholin recep
404	23	37.7	13	1	W69634	Ste2 receptor agon	477	23	37.7	18	1	Y10941	Amino acid sequenc
405	23	37.7	13	1	W71004	Epitope from Masta	478	23	37.7	18	1	W99563	Immunoglobulin Igg
406	23	37.7	13	1	W75333	Adenovirus type 2	479	23	37.7	18	1	W99564	Immunoglobulin Igg
407	23	37.7	13	1	W74428	Ste2 agonist M9 pe	480	23	37.7	19	1	W19531	Signal peptide for
408	23	37.7	13	1	W74429	Ste2 agonist pepti	481	23	37.7	19	1	W46724	Secretion signal p
409	23	37.7	13	1	W74430	Ste2 agonist pepti	482	23	37.7	20	1	R37689	Synthetic epitope
410	23	37.7	13	1	W74431	Ste2 agonist pepti	483	23	37.7	20	1	R45539	HCV NSS region (19
411	23	37.7	13	1	W74432	Ste2 agonist M1 pe	484	23	37.7	20	1	R44540	HCV NSS region (19
412	23	37.7	13	1	W74421	Ste2 agonist M2 pe	485	23	37.7	20	1	R1259	Eukaryotic secreti
413	23	37.7	13	1	W74422	Ste2 agonist M3 pe	486	23	37.7	20	1	R89346	Cdk2-interacting p
414	23	37.7	13	1	W74423	Ste2 agonist M4 pe	487	23	37.7	20	1	W02261	Gingivalis adhesio
415	23	37.7	13	1	W74424	Ste2 agonist M4 pe	488	23	37.7	20	1	W32121	Interaction trap s
416	23	37.7	13	1	W74425	Ste2 agonist M6 pe	489	23	37.7	20	1	W45451	Cyclic lipopeptide
417	23	37.7	13	1	W74426	Ste2 agonist M7 pe	490	23	37.7	20	1	W6353	Peptide derived fr
418	23	37.7	13	1	W74427	Ste2 agonist M8 pe	491	23	37.7	20	1	W6354	Peptide derived fr
419	23	37.7	14	1	R30416	p107 peptide NT85.	492	23	37.7	20	1	W6357	Peptide MCF05 deri
420	23	37.7	14	1	R57409	Peptide for treati	493	23	37.7	20	1	W6358	Peptide MCF04 deri
421	23	37.7	14	1	R85736	Endotoxin-binding,	494	22.5	36.9	10	1	W10902	Polyclonal anti-HB
422	23	37.7	14	1	W16706	p185 binding and e	495	22.5	36.9	12	1	W61266	BCL1 immunoglobi
423	23	37.7	14	1	W16707	p185 binding and e	496	22.5	36.9	20	1	W4671	Mutant muscarinic
424	23	37.7	14	1	W16708	p185 binding and e	497	22.5	36.9	20	1	W4675	Muscarinic acetyl
425	23	37.7	14	1	W16709	p185 binding and e	498	22	36.1	4	1	R37183	Polymer of Glu-Trp
426	23	37.7	14	1	W16714	p185 binding and e	499	22	36.1	4	1	R75601	gp120 binding Fab
427	23	37.7	14	1	W16715	p185 binding and e	500	22	36.1	4	1	R75603	gp120 binding Fab
428	23	37.7	14	1	W16716	p185 binding and e	501	22	36.1	4	1	R75597	gp120 binding Fab
429	23	37.7	14	1	W16717	p185 binding and e	502	22	36.1	4	1	R75598	gp120 binding Fab
430	23	37.7	14	1	W16769	p185 binding and e	503	22	36.1	4	1	R9792	Melanotrophic rele
431	23	37.7	14	1	W16770	p185 binding and e	504	22	36.1	4	1	W05280	Tumour necrosis fa
432	23	37.7	14	1	W16771	p185 binding and e	505	22	36.1	4	1	W43229	Peptide #6 having
433	23	37.7	14	1	W16772	p185 binding and e	506	22	36.1	4	1	W70295	Thrombus formation
434	23	37.7	14	1	W16777	p185 binding and e	507	22	36.1	4	1	W78955	Antidepressant MIF
435	23	37.7	14	1	W16778	p185 binding and e	508	22	36.1	5	1	R12658	Pentapeptide paral
436	23	37.7	14	1	W16779	p185 binding and e	509	22	36.1	5	1	P50708	Hexapeptide somato
437	23	37.7	14	1	W16780	p185 binding and e	510	22	36.1	5	1	R27862	Antimicrobial pept
438	23	37.7	14	1	W37619	Synergistic HIV en	511	22	36.1	5	1	R44785	Sequence of peptid
439	23	37.7	14	1	W71003	Epitope from Masta	512	22	36.1	5	1	R48520	Lactoferrin deriva
440	23	37.7	14	1	W9880	Peptide sequence o	513	22	36.1	5	1	R51522	Minotope peptide #
441	23	37.7	14	1	W75332	Adenovirus type 5	514	22	36.1	5	1	R57451	Lactoferrin deriva
442	23	37.7	15	1	P90269	Antigenic peptide	515	22	36.1	5	1	R59890	Pentameric mimotop
443	23	37.7	15	1	R47704	HIV epitope #37. N	516	22	36.1	5	1	R79758	Anti-parasitic lac
444	23	37.7	15	1	R47036	Apolipoprotein B-1	517	22	36.1	5	1	R89826	Melanotrophic rele
445	23	37.7	15	1	R58518	Heavy chain CDR3 f	518	22	36.1	5	1	R89827	Melanotrophic rele
446	23	37.7	15	1	R93291	Heavy chain CDR3 o	519	22	36.1	5	1	R84688	Bovine lactoferrin
447	23	37.7	15	1	W12279	Synthetic library	520	22	36.1	5	1	R90598	Lactoferrin deriva
448	23	37.7	15	1	W16691	p185 binding and e	521	22	36.1	5	1	R87612	Lactoferrin-deriva
449	23	37.7	15	1	W16692	p185 binding and e	522	22	36.1	5	1	R91845	Lactoferrin-deriva
450	23	37.7	15	1	W16693	p185 binding and e	523	22	36.1	5	1	R98544	Peptide for anti-u
451	23	37.7	15	1	W16698	p185 binding and e	524	22	36.1	5	1	R98636	Peptide 16 from 88
452	23	37.7	15	1	W16699	p185 binding and e	525	22	36.1	5	1	W14029	Anti-parasitic pep
453	23	37.7	15	1	W16700	p185 binding and e	526	22	36.1	5	1	W22933	Low density lipopr
454	23	37.7	15	1	W16701	p185 binding and e	527	22	36.1	5	1	W22934	Low density lipopr
455	23	37.7	15	1	W16689	p185 binding and e	528	22	36.1	5	1	W26143	Lactoferrin deriva
456	23	37.7	15	1	W16754	p185 binding and e	529	22	36.1	5	1	W41279	Apoptosis inducer
457	23	37.7	15	1	W16755	p185 binding and e	530	22	36.1	5	1	W53214	Lactoferrin hydrol
458	23	37.7	15	1	W16756	p185 binding and e	531	22	36.1	5	1	W70306	Thrombus formation
459	23	37.7	15	1	W16761	p185 binding and e	532	22	36.1	5	1	W78986	Antidepressant MIF
460	23	37.7	15	1	W16762	p185 binding and e	533	22	36.1	5	1	W78987	Antidepressant MIF
461	23	37.7	15	1	W16763	p185 binding and e	534	22	36.1	5	1	W94151	BC loop sequence o
462	23	37.7	15	1	W16764	p185 binding and e	535	22	36.1	5	1	W94156	BC loop sequence o
463	23	37.7	15	1	W49171	Human leucocyte an	536	22	36.1	6	1	P61446	Luteinising hormon
464	23	37.7	15	1	W62173	Escherichia coli p	537	22	36.1	6	1	R20454	Anti-b-endorphin m
465	23	37.7	15	1	W62166	Agrobacterium faec	538	22	36.1	6	1	P40530	Sequence of substa
466	23	37.7	15	1	W71348	Glycolipid sugar c	539	22	36.1	6	1	R35028	Arg-Arg contg. ant
467	23	37.7	15	1	W71332	A glycolipid sugar	540	22	36.1	6	1	R44780	Sequence of peptid
468	23	37.7	15	1	W84122	Peptide reacting w	541	22	36.1	6	1	R44783	Sequence of peptid
469	23	37.7	15	1	W67631	Multiple sclerosis	542	22	36.1	6	1	R44784	Sequence of peptid
470	23	37.7	15	1	W94120	VIF-derived HIV pr	543	22	36.1	6	1	R66836	Hexapeptide having
471	23	37.7	16	1	R15707	Rev HIV-2rod 34-49	544	22	36.1	6	1	W24365	New peptide which
472	23	37.7	17	1	W75335	Adenovirus type 5	545	22	36.1	6	1	W29004	Opioid peptide. Ne

546	22	36.1	6	1	R67472	Mu opioid receptor	619	22	36.1	10	1	R50816	Cyclic peptide inh
547	22	36.1	6	1	R67454	Mu opioid receptor	620	22	36.1	10	1	R50817	Cyclic peptide inh
548	22	36.1	6	1	W43226	All D-amino acid p	621	22	36.1	10	1	R50818	Cyclic peptide inh
549	22	36.1	6	1	W6397	Monoclonal antibod	622	22	36.1	10	1	R50819	Cyclic peptide inh
550	22	36.1	7	1	R44781	Sequence of peptid	623	22	36.1	10	1	R50823	Cyclic peptide inh
551	22	36.1	7	1	R44782	Sequence of peptid	624	22	36.1	10	1	R50920	Cyclic peptide inh
552	22	36.1	7	1	R44786	Sequence of peptid	625	22	36.1	10	1	R50921	Cyclic peptide inh
553	22	36.1	7	1	R89851	Melanotrophic rele	626	22	36.1	10	1	R50922	Cyclic peptide inh
554	22	36.1	7	1	R89853	Melanotrophic rele	627	22	36.1	10	1	R50923	Cyclic peptide inh
555	22	36.1	7	1	R89856	Melanotrophic rele	628	22	36.1	10	1	R50924	Cyclic peptide inh
556	22	36.1	7	1	R2025	60K-CSF protein fr	629	22	36.1	10	1	R50928	Cyclic peptide inh
557	22	36.1	7	1	W21480	Collagenase (fibro	630	22	36.1	10	1	R50930	Cyclic peptide inh
558	22	36.1	7	1	W24352	New peptide which	631	22	36.1	10	1	R50930	Cyclic peptide inh
559	22	36.1	7	1	W28991	Opioid peptide. Ne	632	22	36.1	10	1	R50931	Cyclic peptide inh
560	22	36.1	7	1	W2786	Rat thymus 60K-CSF	633	22	36.1	10	1	R50904	Cyclic peptide inh
561	22	36.1	7	1	W59480	HIV-1 Rev protein	634	22	36.1	10	1	R50905	Cyclic peptide inh
562	22	36.1	7	1	W60351	Tumour homing pept	635	22	36.1	10	1	R50906	Cyclic peptide inh
563	22	36.1	7	1	W78995	Antidepressant MIF	636	22	36.1	10	1	R50907	Cyclic peptide inh
564	22	36.1	7	1	W78998	Antidepressant MIF	637	22	36.1	10	1	R50908	Cyclic peptide inh
565	22	36.1	7	1	W78993	Antidepressant MIF	638	22	36.1	10	1	R50909	Cyclic peptide inh
566	22	36.1	7	1	W4168	FG loop sequence o	639	22	36.1	10	1	R50911	Cyclic peptide inh
567	22	36.1	7	1	W93677	Human breast cance	640	22	36.1	10	1	R50915	Cyclic peptide inh
568	22	36.1	8	1	R50842	Cyclic peptide inh	641	22	36.1	10	1	R50916	Cyclic peptide inh
569	22	36.1	8	1	R50843	Cyclic peptide inh	642	22	36.1	10	1	R50917	Cyclic peptide inh
570	22	36.1	8	1	R57399	Peptide for treati	643	22	36.1	10	1	R50918	Cyclic peptide inh
571	22	36.1	8	1	R83930	Human megakaryobla	644	22	36.1	10	1	R50919	Cyclic peptide inh
572	22	36.1	8	1	W4104	VIF-derived HIV pr	645	22	36.1	10	1	R50890	Cyclic peptide inh
573	22	36.1	8	1	Y03899	Predicted binding	646	22	36.1	10	1	R50891	Cyclic peptide inh
574	22	36.1	9	1	R24483	[psi8-9 pseudo] No	647	22	36.1	10	1	R50893	Cyclic peptide inh
575	22	36.1	9	1	R24484	[psi8-9 pseudo] No	648	22	36.1	10	1	R50894	Cyclic peptide inh
576	22	36.1	9	1	R24485	[psi8-9 pseudo] No	649	22	36.1	10	1	R50895	Cyclic peptide inh
577	22	36.1	9	1	R24486	[psi8-9 pseudo] No	650	22	36.1	10	1	R50896	Cyclic peptide inh
578	22	36.1	9	1	R24492	[psi8-9 pseudo] No	651	22	36.1	10	1	R50897	Cyclic peptide inh
579	22	36.1	9	1	R24494	[psi8-9 pseudo] No	652	22	36.1	10	1	R50898	Cyclic peptide inh
580	22	36.1	9	1	R24495	[psi8-9 pseudo] No	653	22	36.1	10	1	R50899	Cyclic peptide inh
581	22	36.1	9	1	R28448	[psi8-9 pseudo] No	654	22	36.1	10	1	R50901	Cyclic peptide inh
582	22	36.1	9	1	R28449	[psi8-9 pseudo] No	655	22	36.1	10	1	R50902	Cyclic peptide inh
583	22	36.1	9	1	R28450	[psi8-9 pseudo] No	656	22	36.1	10	1	R50903	Cyclic peptide inh
584	22	36.1	9	1	R28454	[psi8-9 pseudo] No	657	22	36.1	10	1	R50873	Cyclic peptide inh
585	22	36.1	9	1	R28461	[psi8-9 pseudo] No	658	22	36.1	10	1	R50875	Cyclic peptide inh
586	22	36.1	9	1	R33649	Selectin binding i	659	22	36.1	10	1	R50876	Cyclic peptide inh
587	22	36.1	9	1	R50820	Cyclic peptide inh	660	22	36.1	10	1	R50877	Cyclic peptide inh
588	22	36.1	9	1	R50821	Cyclic peptide inh	661	22	36.1	10	1	R50878	Cyclic peptide inh
589	22	36.1	9	1	R50822	Cyclic peptide inh	662	22	36.1	10	1	R50879	Cyclic peptide inh
590	22	36.1	9	1	R50914	Cyclic peptide inh	663	22	36.1	10	1	R50880	Cyclic peptide inh
591	22	36.1	9	1	R50840	Cyclic peptide inh	664	22	36.1	10	1	R50881	Cyclic peptide inh
592	22	36.1	9	1	R50841	Cyclic peptide inh	665	22	36.1	10	1	R50882	Cyclic peptide inh
593	22	36.1	9	1	R50835	Cyclic peptide inh	666	22	36.1	10	1	R50883	Cyclic peptide inh
594	22	36.1	9	1	R57390	Peptide for treati	667	22	36.1	10	1	R50884	Cyclic peptide inh
595	22	36.1	9	1	R69368	Bombesin antagonist	668	22	36.1	10	1	R50885	Cyclic peptide inh
596	22	36.1	9	1	R4804	Modified MART-1 me	669	22	36.1	10	1	R50857	Cyclic peptide inh
597	22	36.1	9	1	W00309	Bombesin analogue	670	22	36.1	10	1	R50859	Cyclic peptide inh
598	22	36.1	9	1	W49532	Human leucocyte an	671	22	36.1	10	1	R50862	Cyclic peptide inh
599	22	36.1	9	1	W49533	Human leucocyte an	672	22	36.1	10	1	R50863	Cyclic peptide inh
600	22	36.1	9	1	W49538	Human leucocyte an	673	22	36.1	10	1	R50864	Cyclic peptide inh
601	22	36.1	9	1	W49539	Human leucocyte an	674	22	36.1	10	1	R50865	Cyclic peptide inh
602	22	36.1	9	1	W65527	Hepatitis B surfac	675	22	36.1	10	1	R50867	Cyclic peptide inh
603	22	36.1	10	1	R11846	Example of peptide	676	22	36.1	10	1	R50868	Cyclic peptide inh
604	22	36.1	10	1	P61444	Luteinising hormon	677	22	36.1	10	1	R50869	Cyclic peptide inh
605	22	36.1	10	1	P61445	Luteinising hormon	678	22	36.1	10	1	R50870	Cyclic peptide inh
606	22	36.1	10	1	R28672	TGF-beta heparin b	679	22	36.1	10	1	R50844	Cyclic peptide inh
607	22	36.1	10	1	R30159	MAB 1-3-1 variable	680	22	36.1	10	1	R50845	Cyclic peptide inh
608	22	36.1	10	1	R33828	Selectin binding i	681	22	36.1	10	1	R50846	Cyclic peptide inh
609	22	36.1	10	1	R33818	Selectin binding i	682	22	36.1	10	1	R50847	Cyclic peptide inh
610	22	36.1	10	1	R33821	Selectin binding i	683	22	36.1	10	1	R50848	Cyclic peptide inh
611	22	36.1	10	1	R33824	Selectin binding i	684	22	36.1	10	1	R50849	Cyclic peptide inh
612	22	36.1	10	1	R33825	Selectin binding i	685	22	36.1	10	1	R50850	Cyclic peptide inh
613	22	36.1	10	1	R33830	Selectin binding i	686	22	36.1	10	1	R50851	Cyclic peptide inh
614	22	36.1	10	1	R33831	Selectin binding i	687	22	36.1	10	1	R50852	Cyclic peptide inh
615	22	36.1	10	1	R33832	Selectin binding i	688	22	36.1	10	1	R50853	Cyclic peptide inh
616	22	36.1	10	1	R33833	Selectin binding i	689	22	36.1	10	1	R50854	Cyclic peptide inh
617	22	36.1	10	1	R33834	Selectin binding i	690	22	36.1	10	1	R50855	Cyclic peptide inh
618	22	36.1	10	1	R50815	Cyclic peptide inh	691	22	36.1	10	1	R50824	Cyclic peptide inh

838	22	36.1	17	1	W03204	TGF-beta-3 fragmen	911	21	34.4	10	1	W32730	Human platelet gly
839	22	36.1	17	1	W03202	TGF-beta-1 fragmen	912	21	34.4	10	1	W36827	Immunogenic peptid
840	22	36.1	17	1	W03203	TGF-beta-2 fragmen	913	21	34.4	10	1	W23884	HIV-1 peptide 1988
841	22	36.1	17	1	W47440	Antigenic peptide.	914	21	34.4	10	1	W50025	Peptide tag for st
842	22	36.1	17	1	W78305	Fragment of human	915	21	34.4	10	1	W50212	Sequence from the
843	22	36.1	17	1	Y02837	Fragment of human	916	21	34.4	10	1	W17161	Minotope capable o
844	22	36.1	18	1	R70718	New alpha Conotoxi	917	21	34.4	10	1	W17162	Minotope capable o
845	22	36.1	18	1	R86116	Anti-ELAM-1 bindin	918	21	34.4	11	1	P30141	Sequence of peptid
846	22	36.1	18	1	W26921	ELAM-1 binding pep	919	21	34.4	11	1	R52691	PASK46-pllIH encod
847	22	36.1	18	1	W12883	Antimicrobial cati	920	21	34.4	11	1	R52693	PASK46-pllXH encod
848	22	36.1	18	1	W55528	Hepatitis B surfac	921	21	34.4	11	1	R70589	HIV(B35)-8, human
849	22	36.1	18	1	W63926	ELAM-1 peptide mim	922	21	34.4	11	1	W62138	Haemophilus influe
850	22	36.1	18	1	W67536	IGF-1/IGFBP inhibi	923	21	34.4	11	1	W62136	Haemophilus influe
851	22	36.1	19	1	R21061	Sequence of residu	924	21	34.4	11	1	W82541	HIV-1 p24 epitope
852	22	36.1	19	1	R21069	Sequence of residu	925	21	34.4	11	1	Y05440	Bronchodilatory pe
853	22	36.1	19	1	R50214	Glycoprotein F bin	926	21	34.4	12	1	P91799	HIV-1 core p24 Oli
854	22	36.1	19	1	W38498	HIV-1 strain MN pe	927	21	34.4	12	1	R52696	PASK46-pllXL encod
855	22	36.1	20	1	R04983	Papilloma virus ty	928	21	34.4	12	1	R52697	PASK46-pllXL encod
856	22	36.1	20	1	R15591	Immunopeptide #1 d	929	21	34.4	12	1	R77291	Peptide EVK(EYA)3
857	22	36.1	20	1	R33487	Cytotoxic T-lympho	930	21	34.4	12	1	R81821	Streptavidin bindi
858	22	36.1	20	1	R35455	Delta TCR V-J junc	931	21	34.4	12	1	R83353	Kbml-binding rando
859	22	36.1	20	1	R32817	Selectin binding i	932	21	34.4	12	1	R77414	Extension peptide
860	22	36.1	20	1	R57412	Peptide for treati	933	21	34.4	12	1	W13489	Rat nucleoside dip
861	22	36.1	20	1	R86101	Anti-ELAM-1 bindin	934	21	34.4	12	1	W16170	Peptide containing
862	22	36.1	20	1	W67531	Recombinant murine	935	21	34.4	12	1	W58189	IL-1RTI binding pe
863	22	36.1	20	1	W08016	HIV peptide #1. De	936	21	34.4	12	1	W58297	IL-1RTI binding pe
864	22	36.1	20	1	W26916	ELAM-1 binding pep	937	21	34.4	12	1	W37915	FGF receptor modul
865	22	36.1	20	1	W32143	Candidate binding	938	21	34.4	12	1	W68810	Peptide binding in
866	22	36.1	20	1	W63911	ELAM-1 peptide mim	939	21	34.4	12	1	W68710	Peptide binding in
867	22	36.1	20	1	W67519	IGF-1/IGFBP inhibi	940	21	34.4	12	1	W78864	HER-1/neu protein
868	22	36.1	20	1	W67506	IGF-1/IGFBP inhibi	941	21	34.4	12	1	Y09943	Interleukin-1 type
869	22	36.1	20	1	Y07838	Human secreted pro	942	21	34.4	13	1	R49295	Pseudo HLA-A2 posi
870	21.5	35.2	7	1	R25025	Arg-Arg contg. ant	943	21	34.4	13	1	R49499	Pseudo HLA-A2 posi
871	21.5	35.2	8	1	R31598	SN-115T, a prollyl	944	21	34.4	13	1	R49500	Pseudo HLA-A2 posi
872	21	34.4	4	1	W22905	Low density lipopr	945	21	34.4	13	1	R57072	Fasciola hepatica
873	21	34.4	5	1	W10093	Low density lipopr	946	21	34.4	13	1	R85731	Endotoxin-binding,
874	21	34.4	5	1	W87123	Peptide determined	947	21	34.4	13	1	R85729	Endotoxin-binding,
875	21	34.4	6	1	P50349	Analgesic hexapept	948	21	34.4	13	1	R75821	Antimicrobial tach
876	21	34.4	6	1	R60023	Conserved region o	949	21	34.4	13	1	R83668	E. coli colonisati
877	21	34.4	6	1	R93745	New peptide which	950	21	34.4	13	1	W09603	Thrombopoietin rec
878	21	34.4	6	1	W33112	Cyclic somatostati	951	21	34.4	13	1	W36754	Thrombopoietin rec
879	21	34.4	6	1	W23094	Cyclic somatostati	952	21	34.4	13	1	W37612	Synergistic HIV en
880	21	34.4	6	1	W23097	Cyclic somatostati	953	21	34.4	13	1	W37614	Synergistic HIV en
881	21	34.4	6	1	W28887	Opioide peptide. Ne	954	21	34.4	13	1	W79873	Peptide sequence o
882	21	34.4	7	1	P30467	Sequence of polype	955	21	34.4	13	1	W79875	Peptide sequence o
883	21	34.4	7	1	W01005	19K apoptosis-regu	956	21	34.4	13	1	W83571	Sequence of tetrad
884	21	34.4	7	1	W40895	Leader sequence 14	957	21	34.4	14	1	P71545	Tumour necrosis fa
885	21	34.4	7	1	W94330	19K binding intera	958	21	34.4	14	1	R12152	HIV p24 core prote
886	21	34.4	7	1	W010195	Plant glycosyltran	959	21	34.4	14	1	R15705	Rev HIV-lbrn 37-50
887	21	34.4	8	1	W05009	Scrambled version	960	21	34.4	14	1	R32256	Linker peptide to
888	21	34.4	8	1	W24548	CDR #3 of r101-2 h	961	21	34.4	14	1	R49293	Pseudo HLA-A2 posi
889	21	34.4	8	1	W45504	Targeting ligand d	962	21	34.4	14	1	R49294	Pseudo HLA-A2 posi
890	21	34.4	9	1	R07638	Bombesin peptide a	963	21	34.4	14	1	R49498	Pseudo HLA-A2 posi
891	21	34.4	9	1	R47976	Lactobacillus brev	964	21	34.4	14	1	R62082	Porcine pty analog
892	21	34.4	9	1	R73068	Antigen fragment 1	965	21	34.4	14	1	R65553	Human CD44 variabl
893	21	34.4	9	1	R73851	Des-Asn 29 [D-Trp	966	21	34.4	14	1	R85730	Endotoxin-binding,
894	21	34.4	9	1	W03705	Lys(4), D-Phe(6)-h	967	21	34.4	14	1	R85730	Endotoxin-binding,
895	21	34.4	9	1	W32485	Strept-tag peptide.	968	21	34.4	14	1	R85728	Endotoxin-binding,
896	21	34.4	9	1	W44010	Strept peptide epit	969	21	34.4	14	1	R85741	Endotoxin-binding,
897	21	34.4	9	1	W40896	Leader sequence 15	970	21	34.4	14	1	R85737	Endotoxin-binding,
898	21	34.4	9	1	W59211	Streptavidin tagge	971	21	34.4	14	1	R85735	Endotoxin-binding,
899	21	34.4	9	1	W29216	Peptide sequence s	972	21	34.4	14	1	R85734	Endotoxin-binding,
900	21	34.4	9	1	Y06914	Strept-tag sequence	973	21	34.4	14	1	R85733	Endotoxin-binding,
901	21	34.4	10	1	R66446	Streptavidin bindi	974	21	34.4	14	1	R91596	Synthetic peptide
902	21	34.4	10	1	R61567	Peptide fragment (975	21	34.4	14	1	R12152	HIV-1 group O stra
903	21	34.4	10	1	R77850	[D-Ala 28, D-Trp 3	976	21	34.4	14	1	W01828	CD44 epitope. T ce
904	21	34.4	10	1	R90158	Cys-bounded LBP-(9	977	21	34.4	14	1	W24020	Variable exon v6 o
905	21	34.4	10	1	R37512	Cytotoxic T lympho	978	21	34.4	14	1	W37611	Synergistic HIV en
906	21	34.4	10	1	W37512	Lys(4), D-Trp(6)-h	979	21	34.4	14	1	W37613	Synergistic HIV en
907	21	34.4	10	1	W21275	Hydroxymethylgluta	980	21	34.4	14	1	W37615	Synergistic HIV en
908	21	34.4	10	1	W32776	Human platelet gly	981	21	34.4	14	1	W37616	Synergistic HIV en
909	21	34.4	10	1	W32632	Human platelet gly	982	21	34.4	14	1	W37617	Synergistic HIV en
910	21	34.4	10	1	W26633	Human platelet gly	983	21	34.4	14	1	W37618	Synergistic HIV en

984 21 34.4 14 1 W37620 Synergistic HIV en
 985 21 34.4 14 1 W37623 Synergistic HIV en
 986 21 34.4 14 1 W37624 Synergistic HIV en
 987 21 34.4 14 1 W37625 Synergistic HIV en
 988 21 34.4 14 1 W37626 Synergistic HIV en
 989 21 34.4 14 1 W37627 Synergistic HIV en
 990 21 34.4 14 1 W37628 Synergistic HIV en
 991 21 34.4 14 1 W37629 Synergistic HIV en
 992 21 34.4 14 1 W37630 Synergistic HIV en
 993 21 34.4 14 1 W37631 Synergistic HIV en
 994 21 34.4 14 1 W37632 Synergistic HIV en
 995 21 34.4 14 1 W37633 Synergistic HIV en
 996 21 34.4 14 1 W37634 Synergistic HIV en
 997 21 34.4 14 1 W37635 Synergistic HIV en
 998 21 34.4 14 1 W40568 Polypeptide transi
 999 21 34.4 14 1 W40569 Polypeptide transi
 1000 21 34.4 14 1 W40562 Polypeptide transi

ALIGNMENTS

RESULT 1
 W15299 ID W15299 standard; peptide; 9 AA.
 AC W15299;
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotopes consensus.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-NOV-1997; U17882.
 PF 08-NOV-1996; US-556597.
 PR 13-NOV-1995; US-556597.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 WPI: 97-289227/26.
 DR Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination
 PS Claim 4; Page 98; 115pp; English.
 CC The present sequence represents the consensus sequence for a mimotope
 CC which functionally mimics a binding site for a monoclonal antibody (Mab)
 CC which recognises an epitope within the human platelet glycoprotein (gp)
 CC Ib/IX complex. More specifically the Mab is C-34. The mimotope peptide
 CC can be used for raising antibodies, as probes to search for anti-
 CC mimotopes and to neutralise the inhibitory activity of those antibodies
 CC which recognise the epitope which is mimicked by the peptide. Anti-
 CC mimotopes can be used to modulate the adhesion, aggregation or
 CC agglutination of platelets by affecting von Willebrand factor
 CC interaction with the platelets through the gp Ib/IX receptor, e.g. as an
 CC anti-thrombotic drug which inhibits the ristocetin induced aggregation
 CC of platelets.
 SQ Sequence 9 AA;

Query Match 100.0%; Score 61; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 1.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
 Db 1 WNWRYREYV 9

RESULT 2
 W1758 ID W1758 standard; peptide; 9 AA.

AC W1758;
 DT 08-DEC-1998 (first entry)
 DE Mimotope capable of binding to monoclonal antibody C-34 #38.
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US9817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 WPI: 98-556458/47.
 DR Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PT Claim 1; Column 48; 26pp; English.
 PS The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W1752 to W1832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 9 AA;

Query Match 100.0%; Score 61; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 1.5e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
 Db 1 WNWRYREYV 9

RESULT 3
 W32624 ID W32624 standard; peptide; 10 AA.
 AC W32624;
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.
 PF 08-NOV-1996; U17882.
 PR 13-NOV-1995; US-556597.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 WPI: 97-289227/26.
 DR Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination
 PS Claim 3; Page 96; 115pp; English.
 CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (Mab) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More

CC specifically the Mab is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 61; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
 DB 2 WNWRYREYV 10
 |||||

RESULT 4

ID W71752 standard; peptide; 10 AA.
 AC W71752;

DE Mimotope capable of binding to monoclonal antibody C-34 #1.
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.

OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.

PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.

PA (UYNV) UNIV NEW YORK STATE RES FOUND.

PI Lyle VA, Miller JL;
 WPI: 98-556458/47;

DR Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PT aggregation-inhibiting antibody

PS Claim 1; Column 47; 26pp; English.

CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 100.0%; Score 61; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00026;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
 DB 2 WNWRYREYV 10
 |||||

RESULT 5

W32625

ID W32625 standard; peptide; 10 AA.
 AC W32625;

DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.
 PF 08-NOV-1996; U17882.
 PR 13-NOV-1995; US-556597.
 PA (UYNV) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 WPI: 97-289227/26.
 DR Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination
 PS Claim 3; Page 96; 115pp; English.
 CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (Mab) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the Mab is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 73.8%; Score 45; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 0.09;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNWRYREYV 9
 DB 2 WNWRYREYV 10
 |||||

RESULT 6

W71759
 ID W71759 standard; peptide; 10 AA.

AC W71759;

DE Mimotope capable of binding to monoclonal antibody C-34 #2.
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.

OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.

PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.

PA (UYNV) UNIV NEW YORK STATE RES FOUND.

PI Lyle VA, Miller JL;
 WPI: 98-556458/47;

DR Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PT aggregation-inhibiting antibody

PS Disclosure; Column 4; 26pp; English.

CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W71752 to W71832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic

CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 73.8%; Score 45; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 0.09;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNRVREYV 9
 |||| :|||
 Db 2 WNRNKKYV 10

RESULT 7
 W32627
 ID W32627 standard; peptide: 10 AA.
 AC W32627;
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.
 PF 08-NOV-1996; U17882.
 PR 13-NOV-1995; US-556597.
 PA (UNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 97-289227/26.
 PT Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination
 PS Claim 3; Page 96; 115pp; English.
 CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (Mab) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the Mab is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used
 CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp Ib/IX receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 62.3%; Score 38; DB 1; Length 10;
 Best Local Similarity 85.7%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
 |||| :|||
 Db 4 WRYSEV 10

RESULT 8
 W1754
 ID W1754 standard; peptide: 10 AA.
 AC W1754;
 DT 08-DEC-1998 (first entry)
 DE Mimotope capable of binding to monoclonal antibody C-34 #4.
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;

KW binding site; platelet epitope; neutralise; aggregation; inhibition;
 KW von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US5817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PA (UNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 98-556458/47;
 PT Peptides that mimic platelet epitope - and neutralise
 PT aggregation-inhibiting antibody
 PS Claim 1; Column 47; 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W1752 to W1832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 62.3%; Score 38; DB 1; Length 10;
 Best Local Similarity 85.7%; Pred. No. 1.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
 |||| :|||
 Db 4 WRYSEV 10

RESULT 9
 W32626
 ID W32626 standard; peptide: 10 AA.
 AC W32626;
 DT 30-JAN-1998 (first entry)
 DE Human platelet glycoprotein Ib/IX complex epitope mimotope.
 KW Human platelet glycoprotein Ib/IX complex epitope; mimotope; probe;
 KW monoclonal antibody C-34; anti mimotope; binding site; antibody;
 KW platelet adhesion; aggregation; agglutination; von Willebrand factor;
 KW anti thrombotic drug; ristocetin.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9718236-A1.
 PD 22-MAY-1997.
 PF 08-NOV-1996; U17882.
 PR 13-NOV-1995; US-556597.
 PA (UNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI: 97-289227/26.
 PT Peptide which mimics human platelet glycoprotein Ib/IX complex
 PT epitope - also anti-mimotope molecule capable of binding to the
 PT peptide and useful to modulate platelet adhesion, aggregation or
 PT agglutination
 PS Claim 3; Page 96; 115pp; English.
 CC The present sequence represents a mimotope which functionally mimics a
 CC binding site for a monoclonal antibody (Mab) which recognises an epitope
 CC within the human platelet glycoprotein (gp) Ib/IX complex. More
 CC specifically the Mab is C-34. The mimotope peptide can be used for
 CC raising antibodies, as probes to search for anti-mimotopes and to
 CC neutralise the inhibitory activity of those antibodies which recognise
 CC the epitope which is mimicked by the peptide. Anti-mimotopes can be used

CC to modulate the adhesion, aggregation or agglutination of platelets by
 CC affecting von Willebrand factor interaction with the platelets through
 CC the gp IIb/III receptor, e.g. as an anti-thrombotic drug which inhibits
 CC the ristocetin induced aggregation of platelets.
 SQ Sequence 10 AA;

Query Match 59.0%; Score 36; DB 1; Length 10;
 Best Local Similarity 85.7%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
 III III
 DB 4 WRYFEYV 10

RESULT 10
 W17153 ID W1753 standard; peptide; 10 AA.
 AC W1753;
 DT 08-DEC-1998 (first entry)
 DE Mimotope capable of binding to monoclonal antibody C-34 #3.
 KW Mimotope; monoclonal antibody C-34; human; glycoprotein Ib/IX complex;
 binding site; platelet epitope; neutralise; aggregation; inhibition;
 von Willebrand factor interaction; adhesion; agglutination.
 OS Synthetic.
 OS Homo sapiens.
 PN US817748-A.
 PD 06-OCT-1998.
 PF 17-MAR-1995; 406330.
 PR 17-MAR-1995; US-406330.
 PA (UNY) UNIV NEW YORK STATE RES FOUND.
 PI Lyle VA, Miller JL;
 DR WPI; 98-556458/47.
 PT Peptides that mimic platelet epitope - and neutralise

PT aggregation-inhibiting antibody
 PS Claim 1; Column 47; 26pp; English.
 CC The present invention provides peptides which functionally mimic a
 CC binding site for a monoclonal antibody, where the monoclonal antibody
 CC recognises an epitope within the human glycoprotein Ib/IX complex.
 CC Peptides W1752 to W1832 are mimotopes which are capable of binding
 CC to monoclonal antibody C-34. The invention also provides an isolated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesised molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion,
 CC aggregation, or agglutination of platelets, where the method comprises
 CC selecting platelets and exposing them to an anti-mimotope molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein Ib/IX receptor, which modulates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.
 SQ Sequence 10 AA;

Query Match 59.0%; Score 36; DB 1; Length 10;
 Best Local Similarity 85.7%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
 III III
 DB 4 WRYFEYV 10

RESULT 11
 W12276 ID W12276 standard; peptide; 15 AA.
 AC W12276;
 DT 15-APR-1997 (first entry)
 DE Synthetic library peptide #1 which binds anti-T. gondii p30 antibody.
 KW Toxoplasma gondii; surface protein; antibody; screening; peptide library;
 diagnostic assay; immunisation; phage; fusion protein; envelop.

OS Synthetic.
 PN EP-724016-A1.
 PD 31-JUL-1996.
 PF 29-JAN-1996; 420030.
 PR 30-JAN-1995; FR-001297.
 PA (JOLI/) JOLIVET-REYNAUD C.
 PA (INMR) BIO MERIEUX.
 PI Jolivet-Reynaud C;
 DR WPI; 96-34331/35.
 PT New polypeptide reactive with anti-p30 antibodies against Toxoplasma
 PT gondii - useful for diagnosis or immunisation, also new nucleic
 PT acid, vectors and transformed cells
 PS Example 2: Page 7; 33pp; French.
 CC The invention relates to novel peptides which bind to antibodies which
 CC recognise the Toxoplasma gondii p30 envelop protein. A peptide library
 CC was generated to express pentadecapeptides on the surface of a
 CC filamentous phage as a fusion protein with the p30 protein. The library
 CC was screened with immobilised anti-T. gondii p30 protein antibody 1E1E7.
 CC Phages which bind this antibody were recovered and amplified by one round
 CC of infection in E. coli. The resultant phages were rescreened with the
 CC immobilised antibody and the second round screen isolated 38 bacterial
 CC colonies infected with phage. Of the 38 colonies, phage DNA from 30
 CC colonies was isolated and sequenced to determine the sequence of the
 CC pentadecapeptide encoded. The peptide sequences W12276-86 were
 CC identified. Of the 30 colonies studied, this peptide sequence was
 CC encoded 11 times. A template peptide sequence (W12287) corresponding to
 CC the sequence across the phage pIII sequence and putative pentadecapeptide
 CC was used to generate a series of overlapping pentadecapeptides. These
 CC peptides were used to determine the best peptide sequence which binds the
 CC 1E1E7 antibody. Peptides W03367-75 were isolated. The new peptides can
 CC then be used in diagnostic assays to detect T. gondii antibodies in a
 CC sample or to purify anti-p30 antibodies or for active immunisation
 CC against T. gondii.
 SQ Sequence 15 AA;

Query Match 57.4%; Score 35; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 5.2;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYR 6
 I::I
 DB 1 WHWRHR 6

RESULT 12
 W11334 ID W11334 standard; peptide; 15 AA.
 AC W11334;
 DT 25-NOV-1998 (first entry)
 DE A glycolipid sugar chain peptide.
 KW Glycolipid sugar chain; inhibit; adhesion; metastasis; cancer cell.
 OS Synthetic.
 PN J10237099-A.
 PD 08-SEP-1998.
 PF 26-FEB-1997; 042311.
 PR 26-FEB-1997; JP-042311.
 PA (IMMO) IMMUNO JAPAN INC.
 DR WPI; 98-537488/46.
 PT New peptide which reacts specifically with antibody against
 PT glyco-lipid sugar chains - useful for inhibition of cancer
 PT metastasis
 PS Claim 8; Page 3; 7pp; Japanese.
 CC W11332-36 represent glycolipid sugar chain replica peptides. They
 CC react specifically with an antibody against glycolipid sugar chains
 CC and inhibit adhesion and metastasis of cancer cells to a target cell.
 CC The peptides can be used to prevent cancer metastasis.
 SQ Sequence 15 AA;

Query Match 57.4%; Score 35; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 5.2;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 WNWRYR 6
Db 1 WHWRHR 6

RESULT 13
W94702
ID W94702 standard; peptide; 15 AA.
AC W94702;
DT 22-APR-1999 (first entry)
DE Lipoteichoic acid epitope peptide mimic for Mab 96-110.
KW Monoclonal antibody; MAB; lipoteichoic acid; gram positive; bacteria;
KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KW Mab 96-110.
OS Staphylococcus sp.
PN W09857994-A2.
PD 23-DEC-1998.
PF 16-JUN-1998; U12402.
PR 16-JUN-1997; US-049871.
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
DR WPI: 99-095329/08.
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
PS Claim 16; Page 120; 150pp; English.
CC The invention relates to a monoclonal antibody (MAB) to lipoteichoic acid
CC of gram positive bacteria, where the MAB is a chimeric immunoglobulin
CC comprising at least part of a human immunoglobulin constant region and
CC at least part of a non-human immunoglobulin variable region having
CC specificity to lipoteichoic acid of gram positive bacteria. The
CC antibodies bind to whole bacteria and enhance phagocytosis and killing of
CC the bacteria and enhance protection from lethal infection. The antibodies
CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic
CC acid antibody or characterised by amino acids corresponding to one or
CC more of the complementarity determining regions (CDRs) of the variable
CC region of the antibody) can be used for treating or preventing infections
CC caused by gram positive bacteria. They can also be used for the diagnosis
CC of gram positive bacterial infections. The present sequence represents a
CC specifically claimed lipoteichoic acid epitope peptide mimic that can be
CC bound by the antibody of the invention (Mab 96-110).
SQ Sequence 15 AA;

Query Match 57.4%; Score 35; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.2;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYR 6
Db 1 WHWRHR 6

RESULT 14
W94729
ID W94729 standard; Protein; 19 AA.
AC W94729;
DT 22-APR-1999 (first entry)
DE Sequence 15mer 2nd.1 resulting from library panning experiments.
KW Monoclonal antibody; MAB; lipoteichoic acid; gram positive; bacteria;
KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KW Mab 96-110; panning.
OS Staphylococcus sp.
PN W09857994-A2.
PD 23-DEC-1998.
PF 16-JUN-1998; U12402.
PR 16-JUN-1997; US-049871.
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
DR WPI: 99-095329/08.
DR N-PSDB; X05555.
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
PS Example 5; Fig 6A-B; 150pp; English.
CC The invention relates to a monoclonal antibody (MAB) to lipoteichoic acid
CC of gram positive bacteria, where the MAB is a chimeric immunoglobulin
CC comprising at least part of a human immunoglobulin constant region and
CC at least part of a non-human immunoglobulin variable region having
CC specificity to lipoteichoic acid of gram positive bacteria. The
CC antibodies bind to whole bacteria and enhance phagocytosis and killing of
CC the bacteria and enhance protection from lethal infection. The antibodies
CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic
CC acid antibody or characterised by amino acids corresponding to one or
CC more of the complementarity determining regions (CDRs) of the variable
CC region of the antibody) can be used for treating or preventing infections
CC caused by gram positive bacteria. They can also be used for the diagnosis
CC of gram positive bacterial infections. The present sequence represents a
CC specifically claimed lipoteichoic acid epitope peptide mimic that can be
CC bound by the antibody of the invention (Mab 96-110).
SQ Sequence 15 AA;

Query Match 57.4%; Score 35; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.2;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYR 6
Db 1 WHWRHR 6

RESULT 15
W94710
ID W94710 standard; Protein; 19 AA.
AC W94710;
DT 22-APR-1999 (first entry)
DE Sequence 15mer 2-8/0 resulting from 15mer library panning experiment.
KW Monoclonal antibody; MAB; lipoteichoic acid; gram positive; bacteria;
KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KW Mab 96-110; panning.
OS Staphylococcus sp.
PN W09857994-A2.
PD 23-DEC-1998.
PF 16-JUN-1998; U12402.
PR 16-JUN-1997; US-049871.
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
DR WPI: 99-095329/08.
DR N-PSDB; X05536.
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
PS Example 5; Fig 6A-B; 150pp; English.
CC The invention relates to a monoclonal antibody (MAB) to lipoteichoic acid
CC of gram positive bacteria, where the MAB is a chimeric immunoglobulin
CC comprising at least part of a human immunoglobulin constant region and
CC at least part of a non-human immunoglobulin variable region having
CC specificity to lipoteichoic acid of gram positive bacteria. The
CC antibodies bind to whole bacteria and enhance phagocytosis and killing of
CC the bacteria and enhance protection from lethal infection. The antibodies
CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic
CC acid antibody or characterised by amino acids corresponding to one or
CC more of the complementarity determining regions (CDRs) of the variable
CC region of the antibody) can be used for treating or preventing infections
CC caused by gram positive bacteria. They can also be used for the diagnosis
CC of gram positive bacterial infections. Sequences W94726-34 represent
CC three series of panning experiments were conducted to identify peptide
CC sequences to which antibody of the invention (Mab 96-110) bound strongly.
CC The translated sequences provide lipoteichoic acid epitope peptide mimics
CC to which Mab96-110 bound.
SQ Sequence 19 AA;

Query Match 57.4%; Score 35; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. No. 6.6;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYR 6
Db 3 WHWRHR 8

RESULT 15
W94710
ID W94710 standard; Protein; 19 AA.
AC W94710;
DT 22-APR-1999 (first entry)
DE Sequence 15mer 2-8/0 resulting from 15mer library panning experiment.
KW Monoclonal antibody; MAB; lipoteichoic acid; gram positive; bacteria;
KW immunoglobulin; phagocytosis; infection; epitope; peptide mimic;
KW Mab 96-110; panning.
OS Staphylococcus sp.
PN W09857994-A2.
PD 23-DEC-1998.
PF 16-JUN-1998; U12402.
PR 16-JUN-1997; US-049871.
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
PI Fischer GW, Schuman RF, Stinson JL, Wong H;
DR WPI: 99-095329/08.
DR N-PSDB; X05536.
PT New antibodies to lipoteichoic acid of gram positive bacteria - used
PT to develop products for the diagnosis, prevention and treatment of
PT infections caused by gram positive bacteria
PS Example 5; Fig 6A-B; 150pp; English.
CC The invention relates to a monoclonal antibody (MAB) to lipoteichoic acid
CC of gram positive bacteria, where the MAB is a chimeric immunoglobulin
CC comprising at least part of a human immunoglobulin constant region and
CC at least part of a non-human immunoglobulin variable region having
CC specificity to lipoteichoic acid of gram positive bacteria. The
CC antibodies bind to whole bacteria and enhance phagocytosis and killing of
CC the bacteria and enhance protection from lethal infection. The antibodies
CC or peptides (encoded by a DNA of the variable region of anti-lipoteichoic
CC acid antibody or characterised by amino acids corresponding to one or
CC more of the complementarity determining regions (CDRs) of the variable
CC region of the antibody) can be used for treating or preventing infections
CC caused by gram positive bacteria. They can also be used for the diagnosis
CC of gram positive bacterial infections. Sequences W94705-22 represent
CC three series of panning experiments were conducted to identify peptide
CC sequences to which antibody of the invention (Mab 96-110) bound strongly.
CC The translated sequences provide lipoteichoic acid epitope peptide mimics
CC to which Mab96-110 bound.
SQ Sequence 19 AA;

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SQ Sequence 19 AA;

Query Match 57.4%; Score 35; DB 1; Length 19;
Best Local Similarity 66.7%; Pred. NO. 6.6;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYR 6
|:|:|:
Db 3 WHWRHR 8

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OM protein - protein search, using sw model

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Title: US-09-258-947-38
Perfect score: 61
Sequence: 1 WNWRYREYV 9

Scoring table: BLOSUM62
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Searched: 133990 seqs, 13297546 residues

Total number of hits satisfying chosen parameters: 72966

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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5	45	73.8	10	2	US-08-406-330-2
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10	36	59.0	10	2	US-08-556-597-3
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123	28	45.9	20	2	US-08-462-507A-55	Sequence 55, Appl	196	24	39.3	16	4	PCT-US94-01238-49	Sequence 49, Appl
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151	25	41.0	9	1	US-08-186-266-15	Sequence 15, Appl	224	23	37.7	6	1	US-08-433-318A-12	Sequence 12, Appl
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161	25	41.0	19	2	US-09-174-060-20	Sequence 20, Appl	234	23	37.7	6	2	US-08-922-048-13	Sequence 13, Appl
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164	24.5	40.2	10	2	US-08-556-597-8	Sequence 8, Appl	237	23	37.7	6	4	PCT-US95-02708-9	Sequence 9, Appl
165	24.5	40.2	20	1	US-08-273-669-9	Sequence 9, Appl	238	23	37.7	6	4	PCT-US96-06270-3	Sequence 3, Appl
166	24.5	40.2	20	2	US-08-954-724-9	Sequence 9, Appl	239	23	37.7	6	4	PCT-US96-06270-2	Sequence 2, Appl
167	24.5	40.2	20	2	US-08-965-947-9	Sequence 9, Appl	240	23	37.7	6	4	PCT-US96-06270-4	Sequence 4, Appl
168	24	39.3	7	2	US-08-934-741A-38	Sequence 38, Appl	241	23	37.7	6	4	PCT-US96-06270-5	Sequence 5, Appl
169	24	39.3	8	1	US-08-382-013A-53	Sequence 53, Appl	242	23	37.7	6	4	PCT-US96-06270-10	Sequence 10, Appl
170	24	39.3	10	1	US-08-382-013A-55	Sequence 55, Appl	243	23	37.7	6	4	PCT-US96-06270-11	Sequence 11, Appl
171	24	39.3	10	1	US-08-397-101-2	Sequence 2, Appl	244	23	37.7	6	4	PCT-US96-06270-12	Sequence 12, Appl
172	24	39.3	10	2	US-08-556-597-89	Sequence 89, Appl	245	23	37.7	6	4	PCT-US96-06270-13	Sequence 13, Appl
173	24	39.3	10	2	US-08-556-597-154	Sequence 154, App	246	23	37.7	6	5	5217891-1	Patent No. 5217891
174	24	39.3	10	2	US-08-556-597-160	Sequence 160, App	247	23	37.7	7	1	US-07-801-812A-24	Sequence 24, Appl
175	24	39.3	10	4	PCT-US93-08436-2	Sequence 2, Appl	248	23	37.7	7	1	US-08-260-202A-31	Sequence 31, Appl

249	23	37.7	7	1	US-08-487-568-24	Sequence 24, Appl	322	23	37.7	13	2	US-08-461-598-51	Sequence 51, Appl
250	23	37.7	9	1	US-08-242-678D-10	Sequence 10, Appl	323	23	37.7	13	2	US-08-461-598-92	Sequence 92, Appl
251	23	37.7	9	2	US-08-751-767A-65	Sequence 65, Appl	323	23	37.7	13	2	US-08-461-598-94	Sequence 94, Appl
252	23	37.7	10	1	US-08-433-318A-134	Sequence 134, Appl	324	23	37.7	13	2	US-08-461-598-96	Sequence 96, Appl
253	23	37.7	10	1	US-08-433-318A-135	Sequence 135, Appl	325	23	37.7	13	2	US-08-461-598-98	Sequence 98, Appl
254	23	37.7	10	1	US-08-433-318A-136	Sequence 136, Appl	326	23	37.7	13	2	US-08-461-598-100	Sequence 100, Appl
255	23	37.7	10	1	US-08-433-318A-137	Sequence 137, Appl	327	23	37.7	13	2	US-08-461-598-102	Sequence 102, Appl
256	23	37.7	10	1	US-08-433-318A-142	Sequence 142, Appl	328	23	37.7	13	2	US-08-461-598-104	Sequence 104, Appl
257	23	37.7	10	1	US-08-433-318A-143	Sequence 143, Appl	329	23	37.7	13	2	US-08-461-598-106	Sequence 106, Appl
258	23	37.7	10	1	US-08-433-318A-144	Sequence 144, Appl	330	23	37.7	13	2	US-08-461-598-108	Sequence 108, Appl
259	23	37.7	10	1	US-08-433-318A-145	Sequence 145, Appl	331	23	37.7	13	2	US-08-461-598-110	Sequence 110, Appl
260	23	37.7	10	2	US-08-556-597-98	Sequence 98, Appl	332	23	37.7	13	2	US-08-461-598-112	Sequence 112, Appl
261	23	37.7	10	2	US-08-556-597-159	Sequence 159, Appl	333	23	37.7	13	2	US-08-747-137-148	Sequence 148, Appl
262	23	37.7	10	2	US-08-922-048-134	Sequence 134, Appl	334	23	37.7	13	2	US-08-747-137-149	Sequence 149, Appl
263	23	37.7	10	2	US-08-922-048-135	Sequence 135, Appl	335	23	37.7	14	1	US-08-433-318A-102	Sequence 102, Appl
264	23	37.7	10	2	US-08-922-048-136	Sequence 136, Appl	336	23	37.7	14	1	US-08-433-318A-103	Sequence 103, Appl
265	23	37.7	10	2	US-08-922-048-137	Sequence 137, Appl	337	23	37.7	14	1	US-08-433-318A-104	Sequence 104, Appl
266	23	37.7	10	2	US-08-922-048-142	Sequence 142, Appl	338	23	37.7	14	1	US-08-433-318A-105	Sequence 105, Appl
267	23	37.7	10	2	US-08-922-048-143	Sequence 143, Appl	339	23	37.7	14	1	US-08-433-318A-110	Sequence 110, Appl
268	23	37.7	10	2	US-08-922-048-144	Sequence 144, Appl	340	23	37.7	14	1	US-08-433-318A-111	Sequence 111, Appl
269	23	37.7	10	2	US-08-922-048-145	Sequence 145, Appl	341	23	37.7	14	1	US-08-433-318A-112	Sequence 112, Appl
270	23	37.7	10	4	PCT-US91-02942-61	Sequence 61, Appl	342	23	37.7	14	1	US-08-433-318A-113	Sequence 113, Appl
271	23	37.7	10	4	PCT-US96-06270-134	Sequence 134, Appl	343	23	37.7	14	1	US-08-433-318A-165	Sequence 165, Appl
272	23	37.7	10	4	PCT-US96-06270-135	Sequence 135, Appl	344	23	37.7	14	1	US-08-433-318A-166	Sequence 166, Appl
273	23	37.7	10	4	PCT-US96-06270-136	Sequence 136, Appl	345	23	37.7	14	1	US-08-433-318A-167	Sequence 167, Appl
274	23	37.7	10	4	PCT-US96-06270-137	Sequence 137, Appl	346	23	37.7	14	1	US-08-433-318A-168	Sequence 168, Appl
275	23	37.7	10	4	PCT-US96-06270-142	Sequence 142, Appl	347	23	37.7	14	1	US-08-433-318A-173	Sequence 173, Appl
276	23	37.7	10	4	PCT-US96-06270-143	Sequence 143, Appl	348	23	37.7	14	1	US-08-433-318A-174	Sequence 174, Appl
277	23	37.7	10	4	PCT-US96-06270-144	Sequence 144, Appl	349	23	37.7	14	1	US-08-433-318A-175	Sequence 175, Appl
278	23	37.7	10	4	PCT-US96-06270-145	Sequence 145, Appl	350	23	37.7	14	1	US-08-922-048-102	Sequence 102, Appl
279	23	37.7	10	5	5217891-20	Patent No. 5217891	351	23	37.7	14	2	US-08-922-048-103	Sequence 103, Appl
280	23	37.7	11	1	US-08-433-318A-118	Sequence 118, Appl	352	23	37.7	14	2	US-08-922-048-104	Sequence 104, Appl
281	23	37.7	11	1	US-08-433-318A-119	Sequence 119, Appl	353	23	37.7	14	2	US-08-922-048-105	Sequence 105, Appl
282	23	37.7	11	1	US-08-433-318A-120	Sequence 120, Appl	354	23	37.7	14	2	US-08-922-048-110	Sequence 110, Appl
283	23	37.7	11	1	US-08-433-318A-121	Sequence 121, Appl	355	23	37.7	14	2	US-08-922-048-111	Sequence 111, Appl
284	23	37.7	11	1	US-08-433-318A-126	Sequence 126, Appl	356	23	37.7	14	2	US-08-922-048-112	Sequence 112, Appl
285	23	37.7	11	1	US-08-433-318A-127	Sequence 127, Appl	357	23	37.7	14	2	US-08-922-048-113	Sequence 113, Appl
286	23	37.7	11	1	US-08-433-318A-128	Sequence 128, Appl	358	23	37.7	14	2	US-08-922-048-165	Sequence 165, Appl
287	23	37.7	11	1	US-08-433-318A-129	Sequence 129, Appl	359	23	37.7	14	2	US-08-922-048-166	Sequence 166, Appl
288	23	37.7	11	2	US-08-922-048-118	Sequence 118, Appl	360	23	37.7	14	2	US-08-922-048-167	Sequence 167, Appl
289	23	37.7	11	2	US-08-922-048-119	Sequence 119, Appl	361	23	37.7	14	2	US-08-922-048-168	Sequence 168, Appl
290	23	37.7	11	2	US-08-922-048-120	Sequence 120, Appl	362	23	37.7	14	2	US-08-922-048-173	Sequence 173, Appl
291	23	37.7	11	2	US-08-922-048-121	Sequence 121, Appl	363	23	37.7	14	2	US-08-922-048-174	Sequence 174, Appl
292	23	37.7	11	2	US-08-922-048-126	Sequence 126, Appl	364	23	37.7	14	2	US-08-922-048-175	Sequence 175, Appl
293	23	37.7	11	2	US-08-922-048-127	Sequence 127, Appl	365	23	37.7	14	2	US-08-922-048-176	Sequence 176, Appl
294	23	37.7	11	2	US-08-922-048-128	Sequence 128, Appl	366	23	37.7	14	2	US-08-922-048-176	Sequence 176, Appl
295	23	37.7	11	2	US-08-922-048-129	Sequence 129, Appl	367	23	37.7	14	2	US-08-152-721B-4	Sequence 4, Appl
296	23	37.7	11	4	PCT-US96-06270-118	Sequence 118, Appl	368	23	37.7	14	4	PCT-US96-06270-102	Sequence 102, Appl
297	23	37.7	11	4	PCT-US96-06270-119	Sequence 119, Appl	369	23	37.7	14	4	PCT-US96-06270-103	Sequence 103, Appl
298	23	37.7	11	4	PCT-US96-06270-120	Sequence 120, Appl	370	23	37.7	14	4	PCT-US96-06270-104	Sequence 104, Appl
299	23	37.7	11	4	PCT-US96-06270-121	Sequence 121, Appl	371	23	37.7	14	4	PCT-US96-06270-105	Sequence 105, Appl
300	23	37.7	11	4	PCT-US96-06270-126	Sequence 126, Appl	372	23	37.7	14	4	PCT-US96-06270-110	Sequence 110, Appl
301	23	37.7	11	4	PCT-US96-06270-127	Sequence 127, Appl	373	23	37.7	14	4	PCT-US96-06270-111	Sequence 111, Appl
302	23	37.7	11	4	PCT-US96-06270-128	Sequence 128, Appl	374	23	37.7	14	4	PCT-US96-06270-112	Sequence 112, Appl
303	23	37.7	11	4	PCT-US96-06270-129	Sequence 129, Appl	375	23	37.7	14	4	PCT-US96-06270-113	Sequence 113, Appl
304	23	37.7	12	2	US-08-602-725-5	Sequence 5, Appl	376	23	37.7	14	4	PCT-US96-06270-165	Sequence 165, Appl
305	23	37.7	13	1	US-08-464-531-43	Sequence 43, Appl	377	23	37.7	14	4	PCT-US96-06270-166	Sequence 166, Appl
306	23	37.7	13	1	US-08-464-531-47	Sequence 47, Appl	378	23	37.7	14	4	PCT-US96-06270-167	Sequence 167, Appl
307	23	37.7	13	1	US-08-464-531-49	Sequence 49, Appl	379	23	37.7	14	4	PCT-US96-06270-168	Sequence 168, Appl
308	23	37.7	13	1	US-08-464-531-51	Sequence 51, Appl	380	23	37.7	14	4	PCT-US96-06270-173	Sequence 173, Appl
309	23	37.7	13	1	US-08-464-531-92	Sequence 92, Appl	381	23	37.7	14	4	PCT-US96-06270-174	Sequence 174, Appl
310	23	37.7	13	1	US-08-464-531-94	Sequence 94, Appl	382	23	37.7	14	4	PCT-US96-06270-175	Sequence 175, Appl
311	23	37.7	13	1	US-08-464-531-96	Sequence 96, Appl	383	23	37.7	14	4	PCT-US96-06270-176	Sequence 176, Appl
312	23	37.7	13	1	US-08-464-531-98	Sequence 98, Appl	384	23	37.7	15	1	US-08-433-318A-85	Sequence 85, Appl
313	23	37.7	13	1	US-08-464-531-100	Sequence 100, Appl	385	23	37.7	15	1	US-08-433-318A-88	Sequence 88, Appl
314	23	37.7	13	1	US-08-464-531-102	Sequence 102, Appl	386	23	37.7	15	1	US-08-433-318A-89	Sequence 89, Appl
315	23	37.7	13	1	US-08-464-531-104	Sequence 104, Appl	387	23	37.7	15	1	US-08-433-318A-94	Sequence 94, Appl
316	23	37.7	13	1	US-08-464-531-106	Sequence 106, Appl	388	23	37.7	15	1	US-08-433-318A-95	Sequence 95, Appl
317	23	37.7	13	1	US-08-464-531-108	Sequence 108, Appl	389	23	37.7	15	1	US-08-433-318A-96	Sequence 96, Appl
318	23	37.7	13	1	US-08-464-531-110	Sequence 110, Appl	390	23	37.7	15	1	US-08-433-318A-97	Sequence 97, Appl
319	23	37.7	13	2	US-08-461-598-43	Sequence 43, Appl	391	23	37.7	15	1	US-08-433-318A-150	Sequence 150, Appl
320	23	37.7	13	2	US-08-461-598-47	Sequence 47, Appl	392	23	37.7	15	1	US-08-433-318A-151	Sequence 151, Appl
321	23	37.7	13	2	US-08-461-598-49	Sequence 49, Appl	393	23	37.7	15	1	US-08-433-318A-152	Sequence 152, Appl

395	23	37.7	15	1	US-08-433-318A-157	Sequence 157, App	468	22	36.1	6	1	US-08-089-994A-12	Sequence 12, Appl
396	23	37.7	15	1	US-08-433-318A-158	Sequence 158, App	469	22	36.1	6	1	US-07-851-941-17	Sequence 17, Appl
397	23	37.7	15	1	US-08-433-318A-159	Sequence 159, App	470	22	36.1	6	1	US-08-384-680-1	Sequence 1, Appl1
398	23	37.7	15	1	US-08-433-318A-160	Sequence 160, App	471	22	36.1	6	1	US-08-384-680-6	Sequence 6, Appl1
399	23	37.7	15	1	US-08-300-386A-35	Sequence 35, Appl1	472	22	36.1	6	1	US-08-384-680-9	Sequence 9, Appl1
400	23	37.7	15	2	US-08-480-190-271	Sequence 271, App	473	22	36.1	6	1	US-08-253-854-84	Sequence 84, Appl
401	23	37.7	15	2	US-08-592-646A-30	Sequence 30, Appl1	474	22	36.1	6	1	US-08-487-006-134	Sequence 134, App
402	23	37.7	15	2	US-08-592-646A-51	Sequence 51, Appl1	475	22	36.1	6	1	US-08-433-318A-6	Sequence 6, Appl1
403	23	37.7	15	2	US-08-750-856A-10	Sequence 10, Appl1	476	22	36.1	6	1	US-08-433-318A-7	Sequence 7, Appl1
404	23	37.7	15	2	US-08-488-379-271	Sequence 871, App	477	22	36.1	6	1	US-08-433-318A-8	Sequence 8, Appl1
405	23	37.7	15	2	US-08-922-048-85	Sequence 85, Appl1	478	22	36.1	6	1	US-08-433-318A-9	Sequence 9, Appl1
406	23	37.7	15	2	US-08-922-048-87	Sequence 87, Appl1	479	22	36.1	6	1	US-08-433-318A-14	Sequence 14, Appl1
407	23	37.7	15	2	US-08-922-048-88	Sequence 88, Appl1	480	22	36.1	6	1	US-08-433-318A-15	Sequence 15, Appl1
408	23	37.7	15	2	US-08-922-048-89	Sequence 89, Appl1	481	22	36.1	6	1	US-08-433-318A-16	Sequence 16, Appl1
409	23	37.7	15	2	US-08-922-048-94	Sequence 94, Appl1	482	22	36.1	6	1	US-08-433-318A-17	Sequence 17, Appl1
410	23	37.7	15	2	US-08-922-048-95	Sequence 95, Appl1	483	22	36.1	6	1	US-08-922-048-6	Sequence 6, Appl1
411	23	37.7	15	2	US-08-922-048-96	Sequence 96, Appl1	484	22	36.1	6	2	US-08-922-048-7	Sequence 7, Appl1
412	23	37.7	15	2	US-08-922-048-97	Sequence 97, Appl1	485	22	36.1	6	2	US-08-922-048-8	Sequence 8, Appl1
413	23	37.7	15	2	US-08-922-048-150	Sequence 150, App	486	22	36.1	6	2	US-08-922-048-9	Sequence 9, Appl1
414	23	37.7	15	2	US-08-922-048-151	Sequence 151, App	487	22	36.1	6	2	US-08-922-048-14	Sequence 14, Appl1
415	23	37.7	15	2	US-08-922-048-152	Sequence 152, App	488	22	36.1	6	2	US-08-922-048-15	Sequence 15, Appl1
416	23	37.7	15	2	US-08-922-048-157	Sequence 157, App	489	22	36.1	6	2	US-08-922-048-16	Sequence 16, Appl1
417	23	37.7	15	2	US-08-922-048-158	Sequence 158, App	490	22	36.1	6	2	US-08-922-048-17	Sequence 17, Appl1
418	23	37.7	15	2	US-08-922-048-159	Sequence 159, App	491	22	36.1	6	2	US-08-488-659A-134	Sequence 134, App
419	23	37.7	15	2	US-08-922-048-160	Sequence 160, App	492	22	36.1	6	2	US-09-127-574-9	Sequence 9, Appl1
420	23	37.7	15	4	PCT-US93-06751-37	Sequence 37, Appl1	493	22	36.1	6	4	PCT-US94-07605-12	Sequence 12, Appl1
421	23	37.7	15	4	PCT-US93-07545-271	Sequence 271, App	494	22	36.1	6	4	PCT-US96-06270-6	Sequence 6, Appl1
422	23	37.7	15	4	PCT-US94-01258-35	Sequence 35, Appl1	495	22	36.1	6	4	PCT-US96-06270-7	Sequence 7, Appl1
423	23	37.7	15	4	PCT-US95-11235-35	Sequence 35, Appl1	496	22	36.1	6	4	PCT-US96-06270-8	Sequence 8, Appl1
424	23	37.7	15	4	PCT-US96-06270-85	Sequence 85, Appl1	497	22	36.1	6	4	PCT-US96-06270-9	Sequence 9, Appl1
425	23	37.7	15	4	PCT-US96-06270-87	Sequence 87, Appl1	498	22	36.1	6	4	PCT-US96-06270-14	Sequence 14, Appl1
426	23	37.7	15	4	PCT-US96-06270-88	Sequence 88, Appl1	499	22	36.1	6	4	PCT-US96-06270-15	Sequence 15, Appl1
427	23	37.7	15	4	PCT-US96-06270-89	Sequence 89, Appl1	500	22	36.1	6	4	PCT-US96-06270-16	Sequence 16, Appl1
428	23	37.7	15	4	PCT-US96-06270-94	Sequence 94, Appl1	501	22	36.1	6	4	PCT-US96-06270-17	Sequence 17, Appl1
429	23	37.7	15	4	PCT-US96-06270-95	Sequence 95, Appl1	502	22	36.1	7	1	US-08-384-680-2	Sequence 2, Appl1
430	23	37.7	15	4	PCT-US96-06270-96	Sequence 96, Appl1	503	22	36.1	7	1	US-08-384-680-5	Sequence 5, Appl1
431	23	37.7	15	4	PCT-US96-06270-97	Sequence 97, Appl1	504	22	36.1	7	1	US-08-384-680-12	Sequence 12, Appl1
432	23	37.7	15	4	PCT-US96-06270-150	Sequence 150, App	505	22	36.1	7	1	US-08-487-006-121	Sequence 121, App
433	23	37.7	15	4	PCT-US96-06270-151	Sequence 151, App	506	22	36.1	7	2	US-08-488-659A-121	Sequence 121, App
434	23	37.7	15	4	PCT-US96-06270-152	Sequence 152, App	507	22	36.1	7	5	5221620-12	Patent No. 5221620
435	23	37.7	15	4	PCT-US96-06270-157	Sequence 157, App	508	22	36.1	8	1	US-08-397-101-16	Sequence 16, Appl1
436	23	37.7	15	4	PCT-US96-06270-158	Sequence 158, App	509	22	36.1	8	1	PCT-US93-08436-16	Sequence 16, Appl1
437	23	37.7	15	4	PCT-US96-06270-159	Sequence 159, App	510	22	36.1	8	5	5190919-29	Patent No. 5190919
438	23	37.7	15	4	PCT-US96-06270-160	Sequence 160, App	511	22	36.1	9	1	US-07-619-747B-9	Sequence 9, Appl1
439	23	37.7	16	5	5459238-2	Patent No. 5459238	512	22	36.1	9	1	US-08-397-101-9	Sequence 9, Appl1
440	23	37.7	18	1	US-08-478-312-34	Sequence 34, Appl1	513	22	36.1	9	1	US-08-397-101-10	Sequence 10, Appl1
441	23	37.7	18	1	US-08-485-302-34	Sequence 41, Appl1	514	22	36.1	9	1	US-08-397-101-15	Sequence 15, Appl1
442	23	37.7	18	1	US-08-487-568-41	Sequence 25, Appl1	515	22	36.1	9	2	PCT-US93-08436-9	Sequence 9, Appl1
443	23	37.7	19	2	US-08-471-033-25	Sequence 25, Appl1	516	22	36.1	9	4	PCT-US93-08436-10	Sequence 10, Appl1
444	23	37.7	19	2	US-08-471-044-25	Sequence 25, Appl1	517	22	36.1	9	4	PCT-US93-08436-15	Sequence 15, Appl1
445	23	37.7	19	2	US-08-463-483A-25	Sequence 25, Appl1	518	22	36.1	9	4	US-08-433-318A-138	Sequence 138, App
446	23	37.7	19	2	US-08-471-046A-25	Sequence 25, Appl1	519	22	36.1	10	1	US-08-433-318A-139	Sequence 139, App
447	23	37.7	19	2	US-08-470-568B-25	Sequence 25, Appl1	520	22	36.1	10	1	US-08-433-318A-140	Sequence 140, App
448	23	37.7	20	2	US-08-469-334-25	Sequence 25, Appl1	521	22	36.1	10	1	US-08-433-318A-141	Sequence 141, App
449	23	37.7	20	2	US-07-994-277A-3	Sequence 3, Appl1	522	22	36.1	10	1	US-08-433-318A-146	Sequence 146, App
450	23	37.7	20	2	US-08-637-759B-112	Sequence 112, App	523	22	36.1	10	1	US-08-433-318A-147	Sequence 147, App
451	23	37.7	20	2	US-08-934-915-149	Sequence 149, App	524	22	36.1	10	1	US-08-433-318A-148	Sequence 148, App
452	23	37.7	20	2	US-07-894-063A-5	Sequence 5, Appl1	525	22	36.1	10	1	US-08-433-318A-149	Sequence 149, App
453	23	37.7	20	2	US-07-894-063A-6	Sequence 6, Appl1	526	22	36.1	10	1	US-08-397-101-1	Sequence 1, Appl1
454	23	37.7	20	4	PCT-US95-09307-12	Sequence 12, Appl1	527	22	36.1	10	1	US-08-397-101-3	Sequence 3, Appl1
455	22.5	36.9	20	1	US-08-273-669-8	Sequence 8, Appl1	528	22	36.1	10	1	US-08-397-101-4	Sequence 4, Appl1
456	22.5	36.9	20	1	US-08-273-669-12	Sequence 12, Appl1	529	22	36.1	10	1	US-08-397-101-5	Sequence 5, Appl1
457	22.5	36.9	20	2	US-08-954-724-8	Sequence 8, Appl1	530	22	36.1	10	1	US-08-397-101-6	Sequence 6, Appl1
458	22.5	36.9	20	2	US-08-954-724-12	Sequence 12, Appl1	531	22	36.1	10	1	US-08-397-101-7	Sequence 7, Appl1
459	22.5	36.9	20	2	US-08-965-947-8	Sequence 8, Appl1	532	22	36.1	10	1	US-08-397-101-8	Sequence 8, Appl1
460	22.5	36.9	20	2	US-08-965-947-12	Sequence 12, Appl1	533	22	36.1	10	1	US-08-397-101-11	Sequence 11, Appl1
461	22	36.1	5	1	US-08-165-545-5	Sequence 5, Appl1	534	22	36.1	10	1	US-08-397-101-12	Sequence 12, Appl1
462	22	36.1	5	1	US-07-851-941-16	Sequence 16, Appl1	535	22	36.1	10	1	US-08-397-101-13	Sequence 13, Appl1
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464	22	36.1	5	1	US-08-384-680-8	Sequence 8, Appl1	537	22	36.1	10	1	US-08-397-101-17	Sequence 17, Appl1
465	22	36.1	5	1	US-08-256-771-14	Sequence 14, Appl1	538	22	36.1	10	1	US-08-397-101-18	Sequence 18, Appl1
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543	22	36.1	10	2	US-08-450-578-22	Sequence 22, Appl	616	22	36.1	11	4	PCT-US96-06270-125	Sequence 125, App
544	22	36.1	10	2	US-08-127-688-13	Sequence 13, Appl	617	22	36.1	11	4	PCT-US96-06270-130	Sequence 130, App
545	22	36.1	10	2	US-08-922-048-138	Sequence 138, App	618	22	36.1	11	4	PCT-US96-06270-131	Sequence 131, App
546	22	36.1	10	2	US-08-922-048-139	Sequence 139, App	619	22	36.1	11	4	PCT-US96-06270-132	Sequence 132, App
547	22	36.1	10	2	US-08-922-048-140	Sequence 140, App	620	22	36.1	11	4	PCT-US96-06270-133	Sequence 133, App
548	22	36.1	10	2	US-08-922-048-141	Sequence 141, App	621	22	36.1	11	4	PCT-US96-06270-133	Sequence 133, App
549	22	36.1	10	2	US-08-922-048-146	Sequence 146, App	622	22	36.1	11	5	5190919-30	Patent No. 5190919
550	22	36.1	10	2	US-08-922-048-147	Sequence 147, App	623	22	36.1	12	1	US-08-197-205-4	Sequence 4, Appl
551	22	36.1	10	2	US-08-922-048-148	Sequence 148, App	624	22	36.1	12	1	US-08-197-205-8	Sequence 8, Appl
552	22	36.1	10	2	US-08-922-048-149	Sequence 149, App	625	22	36.1	12	1	US-08-190-788A-212	Sequence 212, App
553	22	36.1	10	2	US-08-922-048-149	Sequence 149, App	626	22	36.1	12	1	US-08-439-817-207	Sequence 207, App
554	22	36.1	10	2	US-08-726-306A-127	Sequence 127, App	627	22	36.1	12	1	US-08-383-474B-215	Sequence 215, App
555	22	36.1	10	2	US-08-986-234-4	Sequence 4, Appl	628	22	36.1	12	1	US-08-465-391A-212	Sequence 212, App
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557	22	36.1	10	2	US-09-014-880-22	Sequence 22, Appl	630	22	36.1	12	2	US-08-406-330-52	Sequence 52, Appl
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559	22	36.1	10	4	PCT-US93-08436-3	Sequence 3, Appl	632	22	36.1	12	2	US-08-464-538B-212	Sequence 212, App
560	22	36.1	10	4	PCT-US93-08436-4	Sequence 4, Appl	633	22	36.1	12	2	US-08-556-597-45	Sequence 45, Appl
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563	22	36.1	10	4	PCT-US93-08436-7	Sequence 7, Appl	636	22	36.1	13	1	US-08-197-205-3	Sequence 3, Appl
564	22	36.1	10	4	PCT-US93-08436-8	Sequence 8, Appl	637	22	36.1	13	4	PCT-US94-10257A-18	Sequence 18, Appl
565	22	36.1	10	4	PCT-US93-08436-11	Sequence 11, Appl	638	22	36.1	14	1	US-08-232-453A-43	Sequence 43, Appl
566	22	36.1	10	4	PCT-US93-08436-12	Sequence 12, Appl	639	22	36.1	14	1	US-08-433-318A-106	Sequence 106, App
567	22	36.1	10	4	PCT-US93-08436-13	Sequence 13, Appl	640	22	36.1	14	1	US-08-433-318A-107	Sequence 107, App
568	22	36.1	10	4	PCT-US93-08436-14	Sequence 14, Appl	641	22	36.1	14	1	US-08-433-318A-108	Sequence 108, App
569	22	36.1	10	4	PCT-US93-08436-17	Sequence 17, Appl	642	22	36.1	14	1	US-08-433-318A-109	Sequence 109, App
570	22	36.1	10	4	PCT-US93-08436-18	Sequence 18, Appl	643	22	36.1	14	1	US-08-433-318A-114	Sequence 114, App
571	22	36.1	10	4	PCT-US93-08436-19	Sequence 19, Appl	644	22	36.1	14	1	US-08-433-318A-115	Sequence 115, App
572	22	36.1	10	4	PCT-US96-06270-138	Sequence 138, App	645	22	36.1	14	1	US-08-433-318A-116	Sequence 116, App
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581	22	36.1	11	1	US-08-433-318A-122	Sequence 122, App	654	22	36.1	14	1	US-08-433-318A-179	Sequence 179, App
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583	22	36.1	11	1	US-08-433-318A-124	Sequence 124, App	656	22	36.1	14	1	US-08-173-510B-71	Sequence 71, Appl
584	22	36.1	11	1	US-08-433-318A-125	Sequence 125, App	657	22	36.1	14	1	US-08-458-218-69	Sequence 69, Appl
585	22	36.1	11	1	US-08-433-318A-130	Sequence 130, App	658	22	36.1	14	2	US-08-922-048-106	Sequence 106, App
586	22	36.1	11	1	US-08-433-318A-131	Sequence 131, App	659	22	36.1	14	2	US-08-922-048-107	Sequence 107, App
587	22	36.1	11	1	US-08-433-318A-132	Sequence 132, App	660	22	36.1	14	2	US-08-922-048-108	Sequence 108, App
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589	22	36.1	11	1	US-08-484-009-1	Sequence 1, Appl	662	22	36.1	14	2	US-08-922-048-114	Sequence 114, App
590	22	36.1	11	2	US-08-366-953A-25	Sequence 25, Appl	663	22	36.1	14	2	US-08-922-048-115	Sequence 115, App
591	22	36.1	11	2	US-08-456-112B-28	Sequence 28, Appl	664	22	36.1	14	2	US-08-922-048-116	Sequence 116, App
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593	22	36.1	11	2	US-08-922-048-122	Sequence 122, App	666	22	36.1	14	2	US-08-922-048-169	Sequence 169, App
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598	22	36.1	11	2	US-08-922-048-131	Sequence 131, App	671	22	36.1	14	2	US-08-922-048-178	Sequence 178, App
599	22	36.1	11	2	US-08-922-048-132	Sequence 132, App	672	22	36.1	14	2	US-08-922-048-179	Sequence 179, App
600	22	36.1	11	2	US-08-922-048-133	Sequence 133, App	673	22	36.1	14	2	US-08-922-048-180	Sequence 180, App
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604	22	36.1	11	2	US-08-665-202-18	Sequence 18, Appl	677	22	36.1	14	4	PCT-US96-06270-108	Sequence 108, App
605	22	36.1	11	2	US-08-665-202-19	Sequence 19, Appl	678	22	36.1	14	4	PCT-US96-06270-109	Sequence 109, App
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607	22	36.1	11	2	US-08-665-202-21	Sequence 21, Appl	680	22	36.1	14	4	PCT-US96-06270-115	Sequence 115, App
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609	22	36.1	11	2	US-08-665-202-23	Sequence 23, Appl	682	22	36.1	14	4	PCT-US96-06270-117	Sequence 117, App
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611	22	36.1	11	2	US-08-665-202-99	Sequence 99, Appl	684	22	36.1	14	4	PCT-US96-06270-170	Sequence 170, App
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613	22	36.1	11	4	PCT-US96-06270-122	Sequence 122, App	686	22	36.1	14	4	PCT-US96-06270-172	Sequence 172, App
												PCT-US96-06270-177	Sequence 177, App

687	22	36.1	14	4	PCT-US96-06270-178	Sequence 178, App	760	22	36.1	18	1	US-08-390-156A-80	Sequence 80, Appl
688	22	36.1	14	4	PCT-US96-06270-179	Sequence 179, App	761	22	36.1	18	1	US-08-439-817-81	Sequence 81, Appl
689	22	36.1	14	4	PCT-US96-06270-180	Sequence 180, App	762	22	36.1	18	1	US-08-485-508-101	Sequence 101, App
690	22	36.1	15	1	US-08-433-318A-90	Sequence 90, Appl	763	22	36.1	18	2	US-08-816-105A-11	Sequence 11, Appl
691	22	36.1	15	1	US-08-433-318A-91	Sequence 91, Appl	764	22	36.1	19	1	US-08-308-116A-1	Sequence 1, Appl
692	22	36.1	15	1	US-08-433-318A-92	Sequence 92, Appl	765	22	36.1	19	1	US-08-162-102C-2	Sequence 2, Appl
693	22	36.1	15	1	US-08-433-318A-93	Sequence 93, Appl	766	22	36.1	19	2	US-08-637-759B-68	Sequence 68, Appl
694	22	36.1	15	1	US-08-433-318A-98	Sequence 98, Appl	767	22	36.1	19	4	PCT-US93-08786-2	Sequence 2, Appl
695	22	36.1	15	1	US-08-433-318A-99	Sequence 99, Appl	768	22	36.1	20	1	US-08-218-025A-32	Sequence 32, Appl
696	22	36.1	15	1	US-08-433-318A-100	Sequence 100, App	769	22	36.1	20	1	US-07-678-974D-36	Sequence 26, Appl
697	22	36.1	15	1	US-08-433-318A-101	Sequence 101, App	770	22	36.1	20	1	US-08-241-05A-85	Sequence 86, Appl
698	22	36.1	15	1	US-08-433-318A-133	Sequence 153, App	771	22	36.1	20	1	US-08-390-156A-73	Sequence 73, Appl
699	22	36.1	15	1	US-08-433-318A-154	Sequence 154, App	772	22	36.1	20	1	US-08-439-817-66	Sequence 66, Appl
700	22	36.1	15	1	US-08-433-318A-155	Sequence 155, App	773	22	36.1	20	1	US-08-485-508-86	Sequence 86, Appl
701	22	36.1	15	1	US-08-433-318A-156	Sequence 156, App	774	22	36.1	20	2	US-08-934-915-69	Sequence 69, Appl
702	22	36.1	15	1	US-08-433-318A-161	Sequence 161, App	775	22	36.1	20	2	US-08-945-168-31	Sequence 31, Appl
703	22	36.1	15	1	US-08-433-318A-162	Sequence 162, App	776	22	36.1	20	4	PCT-US92-07218-1	Sequence 1, Appl
704	22	36.1	15	1	US-08-433-318A-163	Sequence 163, App	777	22	36.1	20	7	US-08-253-854-81	Sequence 81, Appl
705	22	36.1	15	1	US-08-433-318A-164	Sequence 164, App	778	22	36.1	6	1	US-08-014-979-81	Sequence 81, Appl
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707	22	36.1	15	2	US-08-922-048-90	Sequence 90, Appl	780	22	34.4	6	2	US-08-488-659A-17	Sequence 17, Appl
708	22	36.1	15	2	US-08-922-048-91	Sequence 91, Appl	781	22	34.4	7	2	US-08-408-095-3	Sequence 3, Appl
709	22	36.1	15	2	US-08-922-048-92	Sequence 92, Appl	782	22	34.4	8	2	US-08-350-260A-464	Sequence 464, App
710	22	36.1	15	2	US-08-922-048-93	Sequence 93, Appl	783	22	34.4	9	1	US-08-660-626-3	Sequence 3, Appl
711	22	36.1	15	2	US-08-922-048-98	Sequence 98, App	784	22	34.4	10	1	US-08-294-386C-11	Sequence 11, Appl
712	22	36.1	15	2	US-08-922-048-99	Sequence 99, App	785	22	34.4	10	1	US-08-306-116A-36	Sequence 36, Appl
713	22	36.1	15	2	US-08-922-048-100	Sequence 100, App	786	22	34.4	10	2	US-08-406-330-9	Sequence 9, Appl
714	22	36.1	15	2	US-08-922-048-101	Sequence 101, App	787	22	34.4	10	2	US-08-406-330-10	Sequence 10, Appl
715	22	36.1	15	2	US-08-922-048-153	Sequence 153, App	788	22	34.4	10	2	US-08-737-316A-5	Sequence 5, Appl
716	22	36.1	15	2	US-08-922-048-154	Sequence 154, App	789	22	34.4	10	2	US-08-556-597-9	Sequence 9, Appl
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718	22	36.1	15	2	US-08-922-048-156	Sequence 156, App	791	22	34.4	10	2	US-08-556-597-125	Sequence 125, App
719	22	36.1	15	2	US-08-922-048-161	Sequence 161, App	792	22	34.4	10	4	PCT-US95-10224-11	Sequence 11, Appl
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722	22	36.1	15	2	US-08-922-048-164	Sequence 164, App	795	22	34.4	11	2	US-08-637-759B-308	Sequence 308, App
723	22	36.1	15	2	US-08-876-874-3	Sequence 3, Appl	796	22	34.4	11	2	US-08-190-788A-110	Sequence 110, App
724	22	36.1	15	4	PCT-US96-06270-90	Sequence 90, Appl	797	22	34.4	12	1	US-08-190-788A-110	Sequence 110, App
725	22	36.1	15	4	PCT-US96-06270-91	Sequence 91, Appl	798	22	34.4	12	1	US-08-190-788A-210	Sequence 210, App
726	22	36.1	15	4	PCT-US96-06270-92	Sequence 92, Appl	799	22	34.4	12	1	US-08-383-474B-115	Sequence 115, App
727	22	36.1	15	4	PCT-US96-06270-93	Sequence 93, Appl	800	22	34.4	12	1	US-08-383-474B-213	Sequence 213, App
728	22	36.1	15	4	PCT-US96-06270-98	Sequence 98, App	801	22	34.4	12	1	US-08-737-757-17	Sequence 17, Appl
729	22	36.1	15	4	PCT-US96-06270-99	Sequence 99, App	802	22	34.4	12	1	US-08-787-547-75	Sequence 75, Appl
730	22	36.1	15	4	PCT-US96-06270-100	Sequence 100, App	803	22	34.4	12	1	US-08-465-391A-110	Sequence 110, App
731	22	36.1	15	4	PCT-US96-06270-101	Sequence 101, App	804	22	34.4	12	1	US-08-465-391A-210	Sequence 210, App
732	22	36.1	15	4	PCT-US96-06270-153	Sequence 153, App	805	22	34.4	12	2	US-08-464-538B-110	Sequence 110, App
733	22	36.1	15	4	PCT-US96-06270-154	Sequence 154, App	806	22	34.4	12	2	US-08-464-538B-210	Sequence 210, App
734	22	36.1	15	4	PCT-US96-06270-155	Sequence 155, App	807	22	34.4	12	2	US-08-463-076E-264	Sequence 264, App
735	22	36.1	15	4	PCT-US96-06270-156	Sequence 156, App	808	22	34.4	12	4	PCT-US95-03742-8	Sequence 8, Appl
736	22	36.1	15	4	PCT-US96-06270-161	Sequence 161, App	809	22	34.4	13	1	US-08-168-809-20	Sequence 20, Appl
737	22	36.1	15	4	PCT-US96-06270-162	Sequence 162, App	810	22	34.4	13	2	US-08-480-190-5	Sequence 5, Appl
738	22	36.1	15	4	PCT-US96-06270-163	Sequence 163, App	811	22	34.4	13	2	US-08-480-190-209	Sequence 209, App
739	22	36.1	15	4	PCT-US96-06270-164	Sequence 164, App	812	22	34.4	13	2	US-08-480-190-210	Sequence 210, App
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752	22	36.1	17	2	US-08-497-599-4	Sequence 4, App	825	22	34.4	14	2	US-08-488-379-3	Sequence 3, Appl
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757	22	36.1	17	4	PCT-US94-05591-15	Sequence 15, App	830	22	34.4	14	2	US-08-564-225-10	Sequence 10, Appl
758	22	36.1	17	4	PCT-US94-05684-17	Sequence 17, App	831	22	34.4	14	3	US-08-481-985B-55	Sequence 55, Appl
759	22	36.1	18	1	US-08-241-054-101	Sequence 101, App	832	22	34.4	14	4	PCT-US93-07545-3	Sequence 3, Appl

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ALIGNMENTS

RESULT 1
US-08-406-330-38
; Sequence 38, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406.330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-38

Query Match 100.0%; Score 61; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 243, App
Sequence 2, Appl
Sequence 25, Appl
Sequence 26, Appl
Sequence 1, Appl
Patent No. 5217869
Sequence 34, Appl
Sequence 22, Appl
Sequence 12, Appl
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Sequence 76, Appl
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Sequence 10, Appl
Sequence 9, Appl
Sequence 31, Appl
Sequence 3, Appl

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Db 1 WNWRYREYV 9

RESULT 2
US-08-556-597-38
; Sequence 38, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556.597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406.330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-38

Query Match 100.0%; Score 61; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.9e+04;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 WNWRYREYV 9
Db 1 WNWRYREYV 9

RESULT 3
US-08-406-330-1
; Sequence 1, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle

STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-1

Query Match 100.0%; Score 61; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNNRYREYV 9
Db 2 WNNRYREYV 10

RESULT 4
US-08-556-597-1
Sequence 1, Application US/08556597
Patent No. 5877155
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESS: Nixon, Hargrave, Devans & Doyle LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101

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TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-1

Query Match 100.0%; Score 61; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNNRYREYV 9
Db 2 WNNRYREYV 10

RESULT 5
US-08-406-330-2
Sequence 2, Application US/08406330
Patent No. 5817748
GENERAL INFORMATION:
APPLICANT: Miller, Jonathan L.
APPLICANT: Lyle, Vicki A.
TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESS: Nixon, Hargrave, Devans & Doyle
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
COUNTRY: USA
ZIP: 14603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-2

Query Match 73.8%; Score 45; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 0.072;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNNRYREYV 9
Db 2 WNNRNKKYV 10

RESULT 6
US-08-556-597-2
; Sequence 2, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-2

Query Match 73.8%; Score 45; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 0.072; 1; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 2

QY 1 WNWRYREYV 9
Db 2 WNWRRKRYV 10

RESULT 7
US-08-406-330-4
; Sequence 4, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,330
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-406-330-4

Query Match 62.3%; Score 38; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.91;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
Db 4 WRYSEYV 10

RESULT 8
US-08-556-597-4
; Sequence 4, Application US/08556597
; Patent No. 5877155
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IB/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/556,597
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/406,330
; FILING DATE: 17-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Timian, Susan J.
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 20884/101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 263-1636
; TELEFAX: (716) 263-1600
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:

;
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-556-597-4

Query Match 62.3%; Score 38; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 0.91;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
 | | | | |
DB 4 WRYFEYV 10

RESULT 9
US-08-406-330-3
; Sequence 3, Application US/08406330
; Patent No. 5817748
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN ID/IX
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,330
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-3

Query Match 59.0%; Score 36; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
 | | | | |
DB 4 WRYFEYV 10

RESULT 10
US-08-556-597-3
; Sequence 3, Application US/08556597
; Patent No. 5877155

;
; GENERAL INFORMATION:
; APPLICANT: Miller, Jonathan L.
; APPLICANT: Lyle, Vicki A.
; TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
; HUMAN PLATELET GLYCOPROTEIN ID/IX
; NUMBER OF SEQUENCES: 173
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
; STREET: Clinton Square, P.O. Box 1051
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,597
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,330
FILING DATE: 17-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 20884/101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1636
TELEFAX: (716) 263-1600

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-556-597-3

Query Match 59.0%; Score 36; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 1.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYREYV 9
 | | | | |
DB 4 WRYFEYV 10

RESULT 11
US-08-592-646A-19
; Sequence 19, Application US/08592646A
; Patent No. 5851535
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
; HUMAN PLATELET GLYCOPROTEIN ID/IX
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-19

Query Match 57.4%; Score 35; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYR 6
|:|:|:
Db 10 WWRHR 15

RESULT 12
US-08-592-646A-20
Sequence 20, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MINOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-20

Query Match 57.4%; Score 35; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYR 6
|:|:|:
Db 9 WWRHR 14

RESULT 13
US-08-592-646A-21
Sequence 21, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MINOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-21

Query Match 57.4%; Score 35; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYR 6
|:|:|:
Db 8 WWRHR 13

RESULT 14
US-08-592-646A-22
Sequence 22, Application US/08592646A
Patent No. 5851535
GENERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MINOTOPIC POLYPEPTIDES OF TOXOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA


```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,646A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36923
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-592-646A-22

Query Match 57.4%; Score 35; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYR 6
Db 7 WHWRHR 12

RESULT 15
US-08-592-646A-23
; Sequence 23, Application US/08592646A
; Patent No. 5851535
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA
; TITLE OF INVENTION: GONDII AND APPLICATIONS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/592,646A
; FILING DATE: 26-JAN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36923
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
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```
;
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-592-646A-23
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Query Match 57.4%; Score 35; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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QY 1 WNWRYR 6
Db 6 WHWRHR 11
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Search completed: May 2, 2000, 00:22:39
Job time: 81 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:20:48 ; Search time 13.58 Seconds
(without alignments)

31.261 Million cell updates/sec

Title: US-09-258-947-38

Perfect score: 61

Sequence: 1 WNWRYREV 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 142080 seqs, 47169319 residues

Total number of hits satisfying chosen parameters: 3999

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Listing first 1000 summaries

Database :

PIR_62: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	24	39.3	17	2	S03533
2	24	39.3	18	2	PT0286
3	23	37.7	11	2	B41946
4	23	37.7	12	2	A40763
5	23	37.7	15	2	E49037
6	23	37.7	17	2	A29834
7	22.5	36.9	19	2	PC1251
8	22	36.1	11	2	B49164
9	22	36.1	12	2	PH1605
10	22	36.1	14	2	S58426
11	22	36.1	15	2	PH1366
12	22	36.1	16	2	B44820
13	22	36.1	20	2	PH1380
14	22	36.1	20	2	A56894
15	21	34.4	12	2	PH0746
16	21	34.4	15	2	PA0099
17	21	34.4	20	2	S33787
18	21	34.4	20	2	B61333
19	20	32.8	12	1	U06M2
20	20	32.8	12	2	S42765
21	20	32.8	12	2	JS0423
22	20	32.8	12	2	JS0424
23	20	32.8	13	2	PQ0445
24	20	32.8	15	2	S02381
25	20	32.8	15	2	C48401
26	20	32.8	17	2	A46592
27	20	32.8	19	2	A38382
28	20	32.8	20	2	B38382
29	19	31.1	7	2	S09552
30	19	31.1	9	2	PT0272

31	19	31.1	10	2	PT0245	Ig heavy chain CRD
32	19	31.1	10	2	S38849	Ig heavy chain V r
33	19	31.1	12	2	S25039	Ig heavy chain V r
34	19	31.1	12	2	PH0771	T-cell receptor be
35	19	31.1	13	2	PT0293	Ig heavy chain CRD
36	19	31.1	13	2	S32551	glutathione transf
37	19	31.1	14	1	OMVHXX	mastoparan X - hor
38	19	31.1	15	2	PQ0232	cystatin Cr-4a - m
39	19	31.1	17	2	S24570	Ig heavy chain J r
40	19	31.1	17	2	E40442	integrase homolog
41	19	31.1	20	2	I64036	hypothetical prote
42	18	29.5	10	1	RHPGG	gonadoliberin - pi
43	18	29.5	10	1	RHSHG	gonadoliberin - sh
44	18	29.5	10	1	RHAQ1	gonadoliberin I -
45	18	29.5	10	2	A21114	gonadoliberin - ch
46	18	29.5	12	2	C49215	urease (EC 3.5.1.5
47	18	29.5	14	2	A44515	trp EG leader pept
48	18	29.5	15	2	S29174	D-galactose-bindin
49	18	29.5	16	2	D49037	TCR delta chain V-
50	18	29.5	17	2	I67526	CD33 antigen homol
51	18	29.5	18	2	B49215	urease (EC 3.5.1.5
52	18	29.5	18	2	T03799	leader peptide trp
53	18	29.5	18	2	C56046	urinary tract ston
54	18	29.5	18	2	S56211	progesterone recep
55	18	29.5	18	2	PH1621	Ig H chain V-D-J r
56	18	29.5	19	2	PT0244	Ig heavy chain CDR
57	18	29.5	20	2	D49215	acyl coenzyme A--6
58	18	29.5	20	2	S09090	gut pentapeptide -
59	17	27.9	5	2	JH0253	Ig heavy chain CRD
60	17	27.9	5	2	PT0281	Ig heavy chain CRD
61	17	27.9	6	2	B31263	dihydrofolate redu
62	17	27.9	6	2	I37027	proctamine PI - gor
63	17	27.9	6	2	PT0532	T-cell receptor be
64	17	27.9	8	2	S08995	hypertrehalosemic
65	17	27.9	8	2	S08996	hypertrehalosemic
66	17	27.9	8	2	A49823	adipokinetic hormo
67	17	27.9	8	2	B49823	adipokinetic hormo
68	17	27.9	8	2	A4960	neuropeptide led-C
69	17	27.9	8	2	B44960	neuropeptide led-C
70	17	27.9	8	2	A43976	hypertrehalosemic
71	17	27.9	8	2	B43976	hypertrehalosemic
72	17	27.9	8	2	A39308	glycine reductase
73	17	27.9	8	2	A05169	neuropeptide M-I -
74	17	27.9	8	2	A41117	acetylcholinestera
75	17	27.9	9	2	PT0299	Ig heavy chain CRD
76	17	27.9	9	2	PT0562	T-cell receptor be
77	17	27.9	10	1	XAVI6B	angiotensin-conver
78	17	27.9	10	2	JC1416	hypertrehalosemic
79	17	27.9	10	2	S05138	hypertrehalosemic
80	17	27.9	10	2	A40753	aldenhyde ferredoxi
81	17	27.9	10	2	A27617	triose-phosphate i
82	17	27.9	10	2	B37196	bradykinin-potenti
83	17	27.9	10	2	PT0289	Ig heavy chain CRD
84	17	27.9	11	2	S32575	ribosomal protein
85	17	27.9	11	2	A34662	Achattina cardlo-ex
86	17	27.9	11	2	PH1343	Ig heavy chain DJ
87	17	27.9	12	2	PH1324	Ig heavy chain DJ
88	17	27.9	12	2	PH1308	Ig heavy chain DJ
89	17	27.9	12	2	I54259	L-lactate dehydrog
90	17	27.9	13	2	S04360	lacB protein - Sta
91	17	27.9	13	2	B28810	glutathione transf
92	17	27.9	13	2	PC4391	cysteine proteinas
93	17	27.9	14	2	B44854	L-2,4-diaminobuty
94	17	27.9	14	2	I54284	C1-inhibitor - hum
95	17	27.9	14	2	PH1757	T cell receptor al
96	17	27.9	14	2	S37572	T cell receptor V-
97	17	27.9	14	2	PH1586	Ig H chain V-D-J r
98	17	27.9	14	2	S29878	Na+/K+-exchanging
99	17	27.9	15	2	A61266	glucuronosyltransf
100	17	27.9	15	2	B60763	endo-1,3-beta-gluc
101	17	27.9	15	2	PQ0192	stylar glycoprotei
102	17	27.9	15	2	S29485	GTP-binding protei
103	17	27.9	15	2	PH1365	Ig heavy chain DJ

104	17	27.9	15	2	A35417	28K serine protein	177	16	26.2	17	2	B49404	T-cell receptor be
105	17	27.9	15	4	I38335	hypothetical TEL/M	178	16	26.2	17	2	A27636	cytotoxin B - C10s
106	17	27.9	16	2	S03532	Ig heavy chain J r	179	16	26.2	17	2	J02310	hypothetical 2.1K
107	17	27.9	16	2	PS0383	Ig heavy chain J r	180	16	26.2	17	2	J02320	hypothetical 2.1K
108	17	27.9	16	2	S13898	alkaline phosphata	181	16	26.2	17	2	A61557	major merozoite su
109	17	27.9	16	2	S55307	glutathione transf	182	16	26.2	17	2	A38824	tachyplexin I - ho
110	17	27.9	17	2	I49048	T-cell receptor be	183	16	26.2	17	2	JX0125	tachyplexin III -
111	17	27.9	17	2	I54262	pyruvate dehydroge	184	16	26.2	17	2	A30068	tachyplexin II - h
112	17	27.9	18	2	PH1323	Ig heavy chain DJ	185	16	26.2	17	2	JU0123	tachyplexin II - h
113	17	27.9	18	2	A60118	22K protein - Lyme	186	16	26.2	17	2	S57514	T cell receptor be
114	17	27.9	18	2	A00256	interleukin-7 rece	187	16	26.2	17	2	S57519	T cell receptor be
115	17	27.9	18	2	I68647	retinoblastoma sus	188	16	26.2	17	2	S75556	T cell receptor be
116	17	27.9	18	2	S39009	oviductin - golden	189	16	26.2	17	2	C49255	CD33 antigen homol
117	17	27.9	19	2	I49422	L-lactate dehydrog	190	16	26.2	17	2	I67524	very-high-density
118	17	27.9	19	2	A60894	gamma crystallin I	191	16	26.2	17	2	PD0005	NTU1 protein - cur
119	17	27.9	19	2	I40063	shikimate 5-dehydr	192	16	26.2	18	2	S46418	gluten - wheat
120	17	27.9	19	2	A44854	L-2,4-diaminobuty	193	16	26.2	18	2	S20322	polyphemusin I - A
121	17	27.9	19	2	S32675	nitrogen fixation	194	16	26.2	18	2	JU0124	polyphemusin II -
122	17	27.9	19	2	S19613	globin - polychaet	195	16	26.2	18	2	JU0125	FSHR - human (frag
123	17	27.9	19	2	S60110	hypothetical prote	196	16	26.2	18	2	I52623	kidney stone prote
124	17	27.9	19	2	S57558	T cell receptor V-	197	16	26.2	19	2	C56049	gamma crystallin I
125	17	27.9	19	2	PH1624	Ig H chain V-D-J r	198	16	26.2	19	2	B60894	tachyplexin I prec
126	17	27.9	19	2	PH1609	Ig H chain V-D-J r	199	16	26.2	19	2	JX0124	T-cell receptor be
127	17	27.9	20	1	DIET	dental fluid tra	200	16	26.2	19	2	I49039	TCR delta chain V-
128	17	27.9	20	2	PH0110	style glycoprotein	201	16	26.2	19	2	I49037	pepsin (EC 3.4.23.
129	17	27.9	20	2	S46205	comosain (EC 3.4.2	202	16	26.2	20	2	PN0133	macrophage chemota
130	17	27.9	20	2	S46204	ananain (EC 3.4.22	203	16	26.2	20	2	S39049	cytotoxin-binding
131	17	27.9	20	2	C49164	chromogranin-B - r	204	16	26.2	20	2	A42934	heat shock protein
132	17	27.9	20	2	D60894	gamma crystallin V	205	16	26.2	20	2	A40451	dormancy-related p
133	17	27.9	20	2	A44773	pollen allergen I	206	15	24.6	5	2	A44692	fulicin - giant Af
134	17	27.9	20	2	S65605	dimeric protein (B	207	15	24.6	7	2	I56695	protein L2 - human
135	17	27.9	20	2	S38763	S-adenosyl-L-methi	208	15	24.6	8	2	PT0311	Ig heavy chain CRD
136	17	27.9	20	2	S15861	estrogen receptor	209	15	24.6	9	2	A37027	gonadoliberin II -
137	17	27.9	20	2	S03508	T-cell receptor al	210	15	24.6	10	1	RUAQ2	gonadoliberin II -
138	17	27.9	20	2	S56756	link protein - rat	211	15	24.6	10	1	A61126	clotting protein -
139	16.5	27.0	14	1	LFEGW	trp operon leader	212	15	24.6	10	2	S30348	gonadoliberin II -
140	16.5	27.0	14	1	LFEBWC	trp operon leader	213	15	24.6	10	2	B46030	T-cell receptor ga
141	16.5	27.0	14	1	LFEBWT	trp operon leader	214	15	24.6	10	2	F49033	Ig heavy chain CRD
142	16	26.2	7	2	A38081	amine oxidase (cop	215	15	24.6	11	2	PT0249	amine oxidase (cop
143	16	26.2	7	2	S33245	neuromodulatory pe	216	15	24.6	11	2	A32428	T-cell receptor ga
144	16	26.2	9	2	C36730	hutu protein - Kle	217	15	24.6	12	2	C38887	phospholipase A2 (
145	16	26.2	9	2	B57444	neuropeptide Grb-A	218	15	24.6	12	2	A39169	Ig heavy chain - m
146	16	26.2	9	2	C57444	neuropeptide Grb-A	219	15	24.6	12	2	S25056	glutathione transf
147	16	26.2	10	2	S33995	hypotrehalosemic h	220	15	24.6	13	2	A61514	Ig heavy chain CRD
148	16	26.2	10	2	E49033	T-cell receptor ga	221	15	24.6	13	2	PT0304	leukotriene B-4 12
149	16	26.2	10	2	PT0215	T-cell receptor be	222	15	24.6	14	2	A47421	avenin gamma-4 - O
150	16	26.2	11	2	S68649	spermadhesin AQN-3	223	15	24.6	15	2	S29207	orf3 3' to aadr -
151	16	26.2	11	2	PT0214	T-cell receptor be	224	15	24.6	15	2	C43334	27K protein A 3.4/
152	16	26.2	12	1	A53709	alpha-conotoxin Im	225	15	24.6	15	2	PS0185	allatostatin - tob
153	16	26.2	12	2	S18362	aspartate transami	226	15	24.6	15	2	A61612	T-cell-receptor be
154	16	26.2	12	2	A34858	proteinase E - bla	227	15	24.6	15	2	G49655	Ig H chain V-D-J r
155	16	26.2	13	2	S47359	T-cell antigen rec	228	15	24.6	15	2	PH1616	T antigen variant
156	16	26.2	13	2	S47361	T-cell antigen rec	229	15	24.6	15	2	PH1378	T antigen variant
157	16	26.2	13	2	S47365	T-cell antigen rec	230	15	24.6	15	2	PH1377	locustapyrokinin -
158	16	26.2	13	2	S47368	T-cell antigen rec	231	15	24.6	16	1	A49761	T-cell surface gly
159	16	26.2	13	2	S47372	T-cell antigen rec	232	15	24.6	16	2	B45895	aleurone protein -
160	16	26.2	13	2	S47383	T-cell antigen rec	233	15	24.6	17	2	S40530	acrosin (EC 3.4.21
161	16	26.2	13	2	S47384	T-cell antigen rec	234	15	24.6	18	2	S02175	L-ascorbate peroxi
162	16	26.2	13	2	S47374	T-cell antigen rec	235	15	24.6	18	2	PS0211	Acetolactate synth
163	16	26.2	13	2	S54344	glycerolaldehyde-3-p	236	15	24.6	18	3	PQ0736	amine oxidase (cop
164	16	26.2	13	2	PH1479	T-cell receptor be	237	15	24.6	19	2	A44239	hypothetical prote
165	16	26.2	14	2	PT0026	calotropin DI - mu	238	15	24.6	19	2	PC1324	hypothetical prote
166	16	26.2	14	2	PT0029	karatasin - karata	239	15	24.6	19	2	PG1322	14-3-3 protein hom
167	16	26.2	14	2	PH1322	Ig heavy chain DJ	240	15	24.6	19	2	E60977	T-cell receptor de
168	16	26.2	14	2	JH0328	probursin tetradece	241	15	24.6	19	2	I45654	T-cell receptor de
169	16	26.2	14	2	PH0755	T-cell receptor be	242	15	24.6	19	2	I45654	Ca2+-transporting
170	16	26.2	15	2	F28587	T-cell receptor be	243	15	24.6	19	2	A38386	recombinational prot
171	16	26.2	15	2	I53284	T-cell receptor be	244	15	24.6	20	2	S71601	ribosomal protein
172	16	26.2	15	2	PH1590	Ig H chain V-D-J r	245	15	24.6	20	2	S78760	hepocokinin VII -
173	16	26.2	15	2	PH0770	T-cell receptor be	246	14	23.0	7	1	NRP7	leucokinin VIII -
174	16	26.2	16	2	E37290	homeotic protein G	247	14	23.0	8	2	JS0318	endosperm protein,
175	16	26.2	16	2	S08133	virA protein - Agr	248	14	23.0	9	2	S70334	T-cell receptor be
176	16	26.2	17	2	H49048	T-cell receptor be	249	14	23.0	9	2	PT0634	

250	14	23.0	10	2	S71868	glutathione transf	323	13	21.3	11	1	GMROL	leucosulfakinin -
251	14	23.0	10	2	A60624	angiotensin I - Ja	324	13	21.3	11	2	S07207	Crinia-angiotensin
252	14	23.0	10	2	F41839	ribosomal protein	325	13	21.3	11	2	PH1375	r antigen variant
253	14	23.0	10	2	A49187	gonadotropin-relea	326	13	21.3	12	2	S69123	proton-translocati
254	14	23.0	10	2	A90917	angiotensin precu	327	13	21.3	12	2	S18722	matk protein - bee
255	14	23.0	10	2	PT0284	ig heavy chain CRD	328	13	21.3	12	2	S47394	T-cell antigen rec
256	14	23.0	10	2	A90345	angiotensin precu	329	13	21.3	12	2	H41946	T-cell receptor ga
257	14	23.0	11	2	I60434	68kDa neurofilamen	330	13	21.3	12	2	S34048	phospholipase A2 (
258	14	23.0	11	4	PC2124	aminotransferase c	331	13	21.3	13	1	UNOPR	neurotensin - brus
259	14	23.0	12	2	S26548	T-cell receptor be	332	13	21.3	13	2	PN0122	OIL protein - vacc
260	14	23.0	12	2	PH1611	Ig H chain V-D-J r	333	13	21.3	13	2	S14316	photosystem I 9K C
261	14	23.0	13	1	UNBO	neurotensin - bovi	334	13	21.3	13	2	S52356	hypothetical prote
262	14	23.0	13	2	A61067	neurotensin - comm	335	13	21.3	13	2	S23372	T-cell receptor al
263	14	23.0	13	2	S08575	botulinum neurotox	336	13	21.3	13	2	PH0138	T-cell receptor be
264	14	23.0	13	2	A24553	phloroglucinol red	337	13	21.3	13	2	B47415	mannose-1-phosphat
265	14	23.0	13	2	A28505	neurotensin-like p	338	13	21.3	13	2	B56864	dipeptidyl-peptida
266	14	23.0	13	2	A53608	neurotensin - guin	339	13	21.3	13	2	B25448	Ig kappa-1 chain,
267	14	23.0	14	1	OMWAPP	polistes mastopara	340	13	21.3	13	2	B26406	Ig kappa chain J r
268	14	23.0	14	2	S29632	xylan 1,4-beta-xy	341	13	21.3	13	2	A47630	Ig kappa chain J r
269	14	23.0	14	2	E33098	214K exoantigen (v	342	13	21.3	13	2	A01250	angiotensin precu
270	14	23.0	14	2	S03530	Ig heavy chain J r	343	13	21.3	14	2	C60414	somatostatin - sli
271	14	23.0	14	2	PH1623	Ig H chain V-D-J r	344	13	21.3	14	2	B60842	somatostatin I - C
272	14	23.0	14	2	F49037	Tcr delta chain V-	345	13	21.3	14	2	A60622	somatostatin - spo
273	14	23.0	15	2	S04586	NADH dehydrogenase	346	13	21.3	14	2	A60840	somatostatin I - E
274	14	23.0	15	2	S10388	Ig heavy chain J r	347	13	21.3	14	2	S00172	somatostatin I - s
275	14	23.0	15	2	S10386	Ig heavy chain J r	348	13	21.3	14	2	PI0077	proteochondroitin c
276	14	23.0	15	2	PH1329	Ig heavy chain DJ	349	13	21.3	14	2	I56388	Km(r) protein - Es
277	14	23.0	15	2	PH1582	Ig H chain V-D-J r	350	13	21.3	14	2	I56388	botulinum neurotox
278	14	23.0	16	2	S10807	protein kinase C i	351	13	21.3	14	2	S58862	homeotic protein E
279	14	23.0	16	2	S10809	protein kinase C i	352	13	21.3	14	2	S58866	botulinum neurotox
280	14	23.0	16	2	B60278	24K antigen - Myco	353	13	21.3	14	2	PC1215	ovostatin - duck (
281	14	23.0	16	2	PA00048	protein QAL00047 -	354	13	21.3	14	2	S00150	B144 protein A - m
282	14	23.0	16	2	PT0224	Ig heavy chain CDR	355	13	21.3	14	2	C48394	major fat-globule
283	14	23.0	17	2	PT0234	Ig heavy chain CRD	356	13	21.3	14	3	PC2373	IMP dehydrogenase
284	14	23.0	17	2	A34704	Ig heavy chain CRD	357	13	21.3	15	2	PQ0175	stylar glycoprotei
285	14	23.0	18	2	S04229	protein-tyrosine k	358	13	21.3	15	2	PQ0174	stylar glycoprotei
286	14	23.0	18	2	S29264	N4-(beta-N-acetyl	359	13	21.3	15	2	PQ0195	Sfil-glycoprotein
287	14	23.0	18	2	S21215	ovohemerythrin - d	360	13	21.3	15	2	A60834	angiotensin I prec
288	14	23.0	18	2	A43334	gamma2-gliadin p25	361	13	21.3	15	2	PH1319	Ig heavy chain DJ
289	14	23.0	18	2	A61577	orfi 5' of aadr -	362	13	21.3	15	2	PS0382	Ig heavy chain J r
290	14	23.0	18	2	PH1792	24K serine protein	363	13	21.3	15	2	PS0382	urease (EC 3.5.1.5
291	14	23.0	18	2	S29379	T cell receptor al	364	13	21.3	15	2	A35389	keratin 5 helix te
292	14	23.0	18	2	PH1629	sorbitol dehydroge	365	13	21.3	15	2	PA0018	T cell receptor al
293	14	23.0	19	2	I53673	Ig H chain V-D-J r	366	13	21.3	15	2	PS0212	T cell receptor V-
294	14	23.0	19	2	C39305	amyloid protein -	367	13	21.3	15	2	B41436	Ig heavy chain J r
295	14	23.0	19	2	PS0332	neurotoxin Tx3 - s	368	13	21.3	15	2	I58080	bone acidic glycop
296	14	23.0	20	2	S71869	phospholipase A2 (369	13	21.3	15	2	A29541	little gastrin - C
297	14	23.0	20	2	S37520	glutathione transf	370	13	21.3	15	2	PH1762	Ig heavy chain J7
298	14	23.0	20	2	S29100	glutathione transf	371	13	21.3	15	2	S57584	hypothetical prote
299	14	23.0	20	2	S30381	glutathione transf	372	13	21.3	15	2	A31902	caldesmon - turkey
300	14	23.0	20	2	S18669	glutathione transf	373	13	21.3	16	2	PH1622	Ig heavy chain DJ
301	14	23.0	20	2	A54519	tubulin alpha chai	374	13	21.3	16	2	D49021	T cell receptor be
302	14	23.0	20	2	PC1240	calcium-binding pr	375	13	21.3	16	2	S51610	Ig mu chain V-D-J r
303	14	23.0	20	2	T01691	hypothetical prote	376	13	21.3	16	2	A35552	aldehyde dehydroge
304	14	23.0	20	2	S74101	alkaline phosphata	377	13	21.3	16	2	PH1346	gastrin - sheep
305	14	23.0	20	2	I54189	galactose-1-phosph	378	13	21.3	16	2	S57517	gastrin - rhesus m
306	14	23.0	20	2	PH1326	Ig heavy chain DJ	379	13	21.3	16	2	E45066	chlorophyll a/b-b1
307	14	23.0	20	2	A54077	cytochrome b558 -	380	13	21.3	16	2	SI0808	adherence lectin l
308	14	23.0	20	2	C56894	intracrystalline c	381	13	21.3	16	2	PH1522	T-cell receptor be
309	14	23.0	20	2	B56894	intracrystalline c	382	13	21.3	16	2	PH1588	platelet-derived g
310	13.5	22.1	10	2	S38887	T-cell receptor ga	383	13	21.3	16	2	PH1604	retinol-binding pr
311	13.5	22.1	15	2	S21241	oligo-1,6-glucosid	384	13	21.3	16	2	C33932	1H-4-oxoquinoline
312	13.5	22.1	15	2	S21240	alpha-glucosidase	385	13	21.3	16	2	A48839	S locus-linked pro
313	13.5	22.1	15	2	S21202	glucan 1,4-alpha-g	386	13	21.3	16	2	I52226	
314	13	21.3	5	2	S37325	pap fibribrial regul	387	13	21.3	17	1	GMSH	
315	13	21.3	7	2	S33244	neuromodulatory pe	388	13	21.3	17	2	A60071	
316	13	21.3	7	2	S32246	neuromodulatory pe	389	13	21.3	17	2	S50901	
317	13	21.3	8	2	A35065	clonin - sea squir	390	13	21.3	17	2	B31435	
318	13	21.3	9	2	A61357	phyllocaerulein -	391	13	21.3	17	2	B49255	
319	13	21.3	10	1	RHLMS	gonadoliberin - se	392	13	21.3	18	2	PS0387	
320	13	21.3	10	2	A60410	beta-neoendorphin	393	13	21.3	18	2	A56871	
321	13	21.3	10	2	S65432	angiotensin I - ho	394	13	21.3	18	2	S21669	
322	13	21.3	10	2	A46030	gonadoliberin I -	395	13	21.3	18	2	T08159	

336	13	21.3	18	2	S27141	hypothetical prote	469	12	19.7	8	2	S15422	adipokinetic hormo
337	13	21.3	18	2	B44239	amine oxidase (cop	470	12	19.7	8	2	S11545	adipokinetic hormo
338	13	21.3	18	2	A35678	hypothetical prote	471	12	19.7	8	2	A58641	adipokinetic hormo
339	13	21.3	18	2	S09087	proteasome chain 6	472	12	19.7	8	2	S16324	hypothetical prote
400	13	21.3	18	4	I56393	lacZ/IS1 mutant fu	473	12	19.7	8	2	PT0030	inulinase (EC 3.2.
401	13	21.3	19	2	I45950	opiate peptide e-1	474	12	19.7	8	2	JS0315	leucokinin V - Mad
402	13	21.3	19	2	S60269	tubulin beta-3 cha	475	12	19.7	8	2	JS0316	leucokinin VI - Ma
403	13	21.3	19	2	C48363	2-hydroxyglutaryl-	476	12	19.7	8	2	JS0317	leucokinin VII - M
404	13	21.3	19	2	S63489	dissimilatory sulf	477	12	19.7	8	2	S21663	neuropeptide - flo
405	13	21.3	19	2	PH1315	Ig heavy chain DJ	478	12	19.7	8	2	I50621	c-myc protein - Ch
406	13	21.3	19	2	S75151	T cell receptor be	479	12	19.7	8	2	PT0724	T-cell receptor be
407	13	21.3	19	2	S03509	T-cell receptor al	480	12	19.7	8	2	A38887	T-cell receptor ga
408	13	21.3	20	2	A38875	creatine kinase (E	481	12	19.7	8	2	S69165	ferredoxin a2 - Ja
409	13	21.3	20	2	PC2347	base nonspecific a	482	12	19.7	9	1	AKLQIM	locustamyoinhibiti
410	13	21.3	20	2	A56900	chymotrypsin I (EC	483	12	19.7	9	2	A24244	adipokinetic hormo
411	13	21.3	20	2	C54052	phosphoribosyl-AMP	484	12	19.7	9	2	I55386	lysosome-associate
412	13	21.3	20	2	PT0248	Ig heavy chain CDR	485	12	19.7	9	2	D58503	translation elonga
413	13	21.3	20	2	A49048	T-cell receptor be	486	12	19.7	9	2	S66607	quinoline 2-oxidor
414	13	21.3	20	2	S86620	histone H4 - sea u	487	12	19.7	9	2	A43848	cell surface adhes
415	13	21.3	20	2	C60894	gamma crystallin I	488	12	19.7	9	2	S70332	endosperm protein,
416	13	21.3	20	2	B33761	actin - Acanthamo	489	12	19.7	9	2	S70345	amine oxidase (cop
417	13	21.3	20	2	A31049	calsequestrin, fas	490	12	19.7	9	2	A57444	neuropeptide Grb-A
418	13	21.3	20	2	A36045	thrombospondin hom	491	12	19.7	9	2	D57444	neuropeptide Grb-A
419	13	21.3	20	2	I85242	homeotic protein H	492	12	19.7	9	2	S77984	cytochrome-c oxida
420	13	21.3	20	2	A44921	hydroxypyruvate re	493	12	19.7	9	2	I52705	gene hGRP protein
421	13	21.3	20	2	S71017	hypothetical prote	494	12	19.7	9	2	S36850	Ig heavy chain V r
422	13	21.3	20	2	P02015	metalloendopeptida	495	12	19.7	9	2	PH0108	late Gl-69 protein
423	13	21.3	20	2	S16202	pyrroline-5-carbox	496	12	19.7	9	2	G41946	T-cell receptor ga
424	13	21.3	20	2	D37396	pollen allergen Fe	497	12	19.7	9	2	I58350	gene c-mpl protein
425	13	21.3	20	2	D35507	proteinase inhibit	498	12	19.7	10	2	S65388	cytochrome-c oxida
426	13	21.3	20	2	S35460	alliin lyase (EC 4	499	12	19.7	10	2	A60647	neuromedin C - bov
427	13	21.3	20	2	PC1152	equinatoxin 1D - s	500	12	19.7	10	2	JO0943	hypothetical 1.3K
428	13	21.3	20	2	PC2248	lambda 112 protein	501	12	19.7	10	2	PC4442	cytochrome c553 -
429	13	21.3	20	2	C28457	sialoprotein I, bo	502	12	19.7	10	2	D28027	protein p7 - curle
430	13	21.3	20	2	A38689	1-phosphatidylinos	503	12	19.7	10	2	PQ0753	beta-fructofuranos
431	13	21.3	20	2	A61506	alpha-1-antitrypsi	504	12	19.7	10	2	S39030	lysyl-bradykinin -
432	12.5	20.5	13	2	S61798	T-cell-specific tr	505	12	19.7	10	2	D46285	formaldehyde dehyd
433	12.5	20.5	13	2	A05313	apolipoprotein A-I	506	12	19.7	10	2	PQ0177	neuromedin C - lau
434	12	19.7	3	2	A22565	R-phycocerythrin A	507	12	19.7	10	2	PT0322	Ig heavy chain CRD
435	12	19.7	4	2	I61883	protamine P1 - ora	508	12	19.7	10	2	PH1344	Ig heavy chain DJ
436	12	19.7	4	2	B53284	T-cell receptor be	509	12	19.7	10	2	S23370	T-cell receptor al
437	12	19.7	4	2	PT0661	T-cell receptor be	510	12	19.7	10	2	A43405	6-phosphofructo-2-
438	12	19.7	4	2	I37013	protamine P1 - Cer	511	12	19.7	10	2	S39374	mannose receptor -
439	12	19.7	4	2	I84439	protamine P1 - sav	512	12	19.7	10	2	I48778	small nuclear ribo
440	12	19.7	5	1	H0ROHA	proctolin - Americ	513	12	19.7	10	2	C41946	T-cell receptor ga
441	12	19.7	5	2	I39964	ribosomal protein	514	12	19.7	10	2	PH0916	T-cell receptor be
442	12	19.7	5	2	I39966	ribosomal protein	515	12	19.7	10	2	PH0923	T-cell receptor be
443	12	19.7	5	2	I39965	ribosomal protein	516	12	19.7	10	2	T12325	cytochrome c oxida
444	12	19.7	5	2	F22565	R-phycocerythrin ga	517	12	19.7	10	2	T12329	cytochrome c oxida
445	12	19.7	5	2	A60411	proctolin - Atlant	518	12	19.7	10	2	T14215	cytochrome c oxida
446	12	19.7	5	2	PT0308	Ig heavy chain CRD	519	12	19.7	10	2	T14223	cytochrome c oxida
447	12	19.7	5	2	PT0729	T-cell receptor be	520	12	19.7	10	2	S53789	neuropeptide Pec-H
448	12	19.7	5	2	PT0580	T-cell receptor be	521	12	19.7	10	2	A56758	urechistachykinin
449	12	19.7	6	2	B44510	hypothetical prote	522	12	19.7	11	2	A58838	hemolysin - Porphy
450	12	19.7	6	2	A12163	dihydrofolate redu	523	12	19.7	11	2	S70338	napin small chain
451	12	19.7	6	2	A61068	locustakinin - mig	524	12	19.7	11	2	JQ2307	hypothetical 1.5K
452	12	19.7	6	2	PT0629	T-cell receptor be	525	12	19.7	11	2	S41747	chaperonin 10 homo
453	12	19.7	6	2	PT0519	T-cell receptor be	526	12	19.7	11	2	JQ2317	hypothetical 1.5K
454	12	19.7	6	2	PT0637	T-cell receptor be	527	12	19.7	11	2	A38590	transforming prote
455	12	19.7	6	2	PT0641	T-cell receptor be	528	12	19.7	11	2	S45698	gamma-MSH-like pro
456	12	19.7	6	2	PT0726	T-cell receptor be	529	12	19.7	11	2	B60409	kassinin-like pept
457	12	19.7	6	2	A14946	T-cell receptor ga	530	12	19.7	11	2	C60409	kassinin-like pept
458	12	19.7	7	2	S57274	triacylglycerol 11	531	12	19.7	11	2	D60409	kassinin-like pept
459	12	19.7	7	2	PN0629	alpha-dextrin endo	532	12	19.7	11	2	A61365	phyllokinin - Rohd
460	12	19.7	7	2	A61081	typtophyllin, basi	533	12	19.7	11	2	PT0273	Ig heavy chain CRD
461	12	19.7	7	2	PT0526	T-cell receptor be	534	12	19.7	11	2	PT0302	Ig heavy chain CRD
462	12	19.7	7	2	PT0628	T-cell receptor be	535	12	19.7	11	2	I41946	T-cell receptor ga
463	12	19.7	7	2	PT0642	T-cell receptor be	536	12	19.7	11	2	A49037	TcR gamma V-J regi
464	12	19.7	7	2	PT0722	T-cell receptor be	537	12	19.7	11	2	B49037	TcR gamma V-J regi
465	12	19.7	7	2	PT0688	T-cell receptor be	538	12	19.7	11	2	C49037	TcR gamma V-J regi
466	12	19.7	7	2	PT0728	T-cell receptor be	539	12	19.7	11	2	PD0441	translation elonga
467	12	19.7	7	2	I48293	transforming prote	540	12	19.7	11	2	S78422	ribosomal protein
468	12	19.7	8	2	S10596	adipokinetic hormo	541	12	19.7	11	2	PH0938	T-cell receptor be

542	12	19.7	11	2	A48973	glucoamylase A1 (E	615	12	19.7	15	2	A54397	ubiquitin-carrier
543	12	19.7	11	3	P00702	Unidentified 6.7/2	616	12	19.7	15	2	I65478	c-Ki-ras - hamster
544	12	19.7	12	2	S28557	T-cell receptor be	617	12	19.7	15	2	G35141	T-cell receptor de
545	12	19.7	12	2	S28553	T-cell receptor be	618	12	19.7	15	2	PL0109	complement factor
546	12	19.7	12	2	PH1675	Ig heavy chain V r	619	12	19.7	15	2	I37452	D-galactose-blind
547	12	19.7	12	2	S21168	disulfide bond-for	620	12	19.7	15	4	I38032	hypothetical MNL/T
548	12	19.7	12	2	JU0356	cycloleucurinin -	621	12	19.7	16	1	MTDFBS	melanotropin beta
549	12	19.7	12	2	S70344	amine oxidase (cop	622	12	19.7	16	2	E41425	cytochrome P450 1F
550	12	19.7	12	2	A33099	163K exoantigen -	623	12	19.7	16	2	I57530	gene c-fms protein
551	12	19.7	12	2	I77529	estrogen receptor	624	12	19.7	16	2	A60551	leukocyte elastase
552	12	19.7	12	2	PT0228	Ig heavy chain CDR	625	12	19.7	16	2	A44413	multicatalytic end
553	12	19.7	12	2	PT0274	Ig heavy chain CDR	626	12	19.7	16	2	A39109	hypothetical prote
554	12	19.7	12	2	A49110	interleukin-10 - h	627	12	19.7	16	2	S51057	ribosomal protein
555	12	19.7	12	2	A49033	T-cell receptor de	628	12	19.7	16	2	S05732	phosphatase I prot
556	12	19.7	12	2	B49033	T-cell receptor de	629	12	19.7	16	2	S22040	phosphatase I prot
557	12	19.7	12	2	PN0663	dystrophin-associa	630	12	19.7	16	2	A31963	cob protein - comm
558	12	19.7	12	2	PN0046	ATP synthase D cha	631	12	19.7	16	2	A47393	neuropeptide calla
559	12	19.7	12	2	PH1470	T-cell receptor be	632	12	19.7	16	2	S28213	glutathione transf
560	12	19.7	12	2	A42324	cytochrome P450c27	633	12	19.7	16	2	A48630	glutathione transf
561	12	19.7	12	2	S21163	NAD+ ADP-ribosyltr	634	12	19.7	16	2	PT0237	bothrojaracin - ja
562	12	19.7	12	2	PH0930	T-cell receptor be	635	12	19.7	16	2	PH1302	Ig heavy chain CDR
563	12	19.7	12	2	I57678	gene rPLP-A protei	636	12	19.7	16	2	PC3320	Ig heavy chain DJ
564	12	19.7	12	2	S23168	Z protein - guinea	637	12	19.7	16	2	I37452	multicatalytic end
565	12	19.7	13	1	MTCAD	melanotropin alpha	638	12	19.7	16	2	PH1778	protein kinase - h
566	12	19.7	13	2	A32734	melanotropin alpha	639	12	19.7	16	2	D24687	T-cell receptor al
567	12	19.7	13	2	PH1676	enkephalin precurs	640	12	19.7	16	2	D24687	T-cell receptor be
568	12	19.7	13	2	PH1676	Ig heavy chain V r	641	12	19.7	16	2	I79565	TCL3 oncogene (put
569	12	19.7	13	2	S39413	tubulin beta chain	642	12	19.7	16	2	A45133	casein kinase II (
570	12	19.7	13	2	I54984	aeg-46.5 protein -	643	12	19.7	16	2	G53284	T-cell receptor be
571	12	19.7	13	2	S60046	early nodulin 40 -	644	12	19.7	16	2	PH0748	T-cell receptor be
572	12	19.7	13	2	JQ2309	hypothetical 1.6K	645	12	19.7	17	2	S71864	glutathione transf
573	12	19.7	13	2	JQ2319	hypothetical 1.6K	646	12	19.7	17	2	S71864	glutathione transf
574	12	19.7	13	2	E60396	antigen 7H8/2 - Pl	647	12	19.7	17	2	A61117	somatostatin precu
575	12	19.7	13	2	S29488	GRP-binding protei	648	12	19.7	17	2	S26744	Ig heavy chain J r
576	12	19.7	13	2	A60379	factor X activator	649	12	19.7	17	2	I57941	beta 3-adrenergic
577	12	19.7	13	2	A33660	osteoclast functio	650	12	19.7	17	2	S20490	photosystem II chl
578	12	19.7	13	2	S57567	T cell receptor V-	651	12	19.7	17	2	A44560	terephthalate 1,2-
579	12	19.7	13	2	S47358	T-cell antigen rec	652	12	19.7	17	2	S16144	spOVA protein - Ba
580	12	19.7	13	2	S47362	T-cell antigen rec	653	12	19.7	17	2	B28027	protein P4 - curle
581	12	19.7	13	2	S47373	T-cell antigen rec	654	12	19.7	17	2	B44923	carboxypeptidase 3
582	12	19.7	13	2	S65612	T-cell antigen rec	655	12	19.7	17	2	S19614	globin - polychaet
583	12	19.7	13	2	PH1593	tubulin alpha-chain	656	12	19.7	17	2	FC1318	large granule L6 c
584	12	19.7	13	2	PH1593	Ig H chain V-D-J r	657	12	19.7	17	2	P40442	integrase homolog
585	12	19.7	13	2	PH1595	Ig H chain V-D-J r	658	12	19.7	17	2	PT0235	Ig heavy chain CDR
586	12	19.7	13	3	PC2371	T-cell receptor be	659	12	19.7	17	2	PH1357	Ig heavy chain DJ
587	12	19.7	14	1	NYP614	atp protein - Bac	660	12	19.7	17	2	PH1820	T cell receptor al
588	12	19.7	14	2	PH1327	hypothalamic tetra	661	12	19.7	17	2	I58129	type I keratin K16
589	12	19.7	14	2	PH1705	Ig heavy chain V r	662	12	19.7	17	2	S10786	enamelin, 26K - bo
590	12	19.7	14	2	PL0142	Ig heavy chain V r	663	12	19.7	17	2	PH0794	T-cell receptor al
591	12	19.7	14	2	PQ0152	carbon-monoxide de	664	12	19.7	17	2	PH0809	T-cell receptor al
592	12	19.7	14	2	A61306	18K iron-sulfur pr	665	12	19.7	17	2	A61019	17K basolateral pl
593	12	19.7	14	2	S14336	ribonuclease M (EC	666	12	19.7	17	2	B48943	phage antigenic de
594	12	19.7	14	2	PH1327	mastoparan B - hor	667	12	19.7	17	2	S69164	ferredoxin al - Ja
595	12	19.7	14	2	A59018	MUC1 enhancer bind	668	12	19.7	18	1	MTDFBC	melanotropin beta
596	12	19.7	14	2	S23369	T-cell receptor al	669	12	19.7	18	2	B24735	glutathione transf
597	12	19.7	14	2	PH1628	Ig H chain V-D-J r	670	12	19.7	18	2	D24780	protein-tyrosine k
598	12	19.7	14	2	S68095	calcium-binding pr	671	12	19.7	18	2	D49570	plasma membrane ca
599	12	19.7	15	1	NTKNAG	alpha-conotoxin GI	672	12	19.7	18	2	S43834	DNA topoisomerase
600	12	19.7	15	2	B26997	unspecific monooxy	673	12	19.7	18	2	A25941	Ig heavy chain J-H
601	12	19.7	15	2	S24159	leukocyte elastase	674	12	19.7	18	2	PH1368	Ig heavy chain DJ
602	12	19.7	15	2	I52734	gene c-Ki-ras prot	675	12	19.7	18	2	I73024	T cell receptor be
603	12	19.7	15	2	E49021	Ig heavy chain J8	676	12	19.7	18	2	I68642	retinoblastoma sus
604	12	19.7	15	2	PQ0017	terminal protein -	677	12	19.7	18	2	I40062	shikimate 5-dehydr
605	12	19.7	15	2	PH0216	agarase (EC 3.2.1.	678	12	19.7	18	2	S46241	NAD(P)H-flavin oxi
606	12	19.7	15	2	A60763	endo-1,3-beta-gluc	679	12	19.7	18	2	E47088	methanol:N,N'-dime
607	12	19.7	15	2	S36893	ribosomal protein	680	12	19.7	18	2	A31817	fasciclin I - Amer
608	12	19.7	15	2	A48372	benzoyl-CoA ligase	681	12	19.7	18	2	S54272	CTC 75 protein - h
609	12	19.7	15	2	A56970	GLIM1 - soybean (682	12	19.7	18	2	S65412	defensin HNP 1 hom
610	12	19.7	15	2	S08209	hypothetical prote	683	12	19.7	18	2	S65414	defensin HNP2 hom
611	12	19.7	15	2	PC4269	unidentified OR310	684	12	19.7	18	2	S65413	defensin HNP3 hom
612	12	19.7	15	2	S28981	tubulin alpha-4 ch	685	12	19.7	18	2	S43958	Ig mu chain V regi
613	12	19.7	15	2	PA0057	adenylate isopente	686	12	19.7	18	2	PH1815	T cell receptor al
614	12	19.7	15	2	PA0076	fructose-bisphosph	687	12	19.7	18	2	A24749	neuropeptide A - b

688	12	19.7	18	2	S48863	cyclin C - mouse (761	11	18.0	4	2	S68059	low molecularweig
689	12	19.7	18	2	S48862	murine cyclin H -	762	11	18.0	5	2	A60803	neuropeptide - sea
690	12	19.7	18	2	PH0768	T-cell receptor be	763	11	18.0	5	2	G37196	bradykinin-potentl
691	12	19.7	18	2	I35141	T-cell receptor de	764	11	18.0	5	2	A32516	cholecystokinin-5
692	12	19.7	18	2	C49254	TcR C gamma 1 chai	765	11	18.0	6	2	S66195	alcohol dehydrogen
693	12	19.7	19	1	EMSWAN	ancovenin - Strept	766	11	18.0	6	2	B34835	dnA protein - Pse
694	12	19.7	19	2	I37424	glutamate dehydrog	767	11	18.0	6	2	S11536	hydrogensulfite re
695	12	19.7	19	2	PN0467	nitrogenase (EC 1.	768	11	18.0	6	2	PD0028	pev-kinin 2 - pena
696	12	19.7	19	2	PC1323	ATP-dependent clp	769	11	18.0	6	2	I81229	antithrombin - hum
697	12	19.7	19	2	C32735	thyroglobulin - pi	770	11	18.0	6	2	I79564	gene TCRD protein
698	12	19.7	19	2	B32735	thyroglobulin - sh	771	11	18.0	6	2	B35640	cerebellar degener
699	12	19.7	19	2	G49048	T-cell receptor be	772	11	18.0	6	2	F41946	T-cell receptor ga
700	12	19.7	19	2	S43657	hsp90 protein homo	773	11	18.0	7	2	AS8512	venom heptapeptide
701	12	19.7	19	2	B61409	genome polyprotein	774	11	18.0	7	2	S17976	glucose isomerase
702	12	19.7	19	2	A48354	nonstructural prot	775	11	18.0	7	2	PD0029	pev-kinin 1 - pena
703	12	19.7	19	2	S63510	phosphonoacetaldeh	776	11	18.0	7	2	S33567	tubulin beta-3 cha
704	12	19.7	19	2	PC0062	beta-galactoside-b	777	11	18.0	7	2	S21230	dermorphin [Trp(4)
705	12	19.7	19	2	PC1309	small granule S2 c	778	11	18.0	7	2	E48394	glycoprotein compo
706	12	19.7	19	2	PH1360	Ig heavy chain DJ	779	11	18.0	7	2	PH1602	Ig H chain V-D-J r
707	12	19.7	19	2	PH1330	Ig heavy chain DJ	780	11	18.0	7	2	PT0586	T-cell receptor be
708	12	19.7	19	2	S57516	T cell receptor be	781	11	18.0	7	2	PT0586	T-cell receptor be
709	12	19.7	19	2	S03519	T-cell receptor ga	782	11	18.0	7	2	B48394	major fat-globule
710	12	19.7	19	2	S02269	UDPglucose-glycog	783	11	18.0	7	3	PQ0727	H2 class I protein
711	12	19.7	20	2	B61080	5-carboxymethyl-2	784	11	18.0	7	4	I53382	hypothetical pepti
712	12	19.7	20	2	E60894	crystallin - Pacif	785	11	18.0	7	4	AS8725	red pigment-concen
713	12	19.7	20	2	S09022	carboxylesterase (786	11	18.0	8	2	A61348	adipokinetic hormo
714	12	19.7	20	2	S09025	carboxylesterase (787	11	18.0	8	2	A28004	adipokinetic hormo
715	12	19.7	20	2	S09023	carboxylesterase (788	11	18.0	8	2	A33995	adipokinetic hormo
716	12	19.7	20	2	A37111	ribulose-bisphosph	789	11	18.0	8	2	S55310	adipokinetic hormo
717	12	19.7	20	2	D49164	chromogranin-B - r	790	11	18.0	8	2	AS8620	adipokinetic hormo
718	12	19.7	20	2	F49048	T-cell receptor be	791	11	18.0	8	2	PQ0012	cholecystokinin -
719	12	19.7	20	2	A61264	MHC class I histoc	792	11	18.0	8	2	A43001	cholecystokinin -
720	12	19.7	20	2	I59073	MHC class II histo	793	11	18.0	8	2	S19288	acylase - Kluyvera
721	12	19.7	20	2	I79432	MHC class II histo	794	11	18.0	8	2	C61512	variant surface gl
722	12	19.7	20	2	B60505	hemoglobin beta ch	795	11	18.0	8	2	D61512	variant surface gl
723	12	19.7	20	2	C61570	gamma-crystallin (796	11	18.0	8	2	D47393	neuropeptide calla
724	12	19.7	20	2	A61570	gamma-crystallin (797	11	18.0	8	2	A31570	angiotensin-conver
725	12	19.7	20	2	B61570	gamma-crystallin (798	11	18.0	8	2	T13818	cytochrome oxidase
726	12	19.7	20	2	S03335	photosystem II pho	799	11	18.0	9	1	QDRB	delta sleep-induci
727	12	19.7	20	2	S04988	gag core shell pro	800	11	18.0	9	2	A61620	locustamytropin I
728	12	19.7	20	2	PQ0544	Capsid protein VP5	801	11	18.0	9	2	A44787	calliFMRamide 10
729	12	19.7	20	2	B53592	H+-transporting AT	802	11	18.0	9	2	A60522	spem-activating p
730	12	19.7	20	2	A54538	39k major outer me	803	11	18.0	9	2	S07205	litorin 2-Glu - Au
731	12	19.7	20	2	S18582	hypothetical prote	804	11	18.0	9	2	S07204	litorin I - Austr
732	12	19.7	20	2	PQ0046	citrate (si)-synth	805	11	18.0	9	2	S07241	litorin - Rohde's
733	12	19.7	20	2	S29635	Jacalin beta chain	806	11	18.0	9	2	JS0302	xenopsin-related p
734	12	19.7	20	2	S03987	agglutinin beta-2	807	11	18.0	9	2	PT0231	Ig heavy chain CRD
735	12	19.7	20	2	A57106	bull allergen Gly	808	11	18.0	9	2	PT0238	Ig heavy chain CRD
736	12	19.7	20	2	S50741	probable trypsin 1	809	11	18.0	9	2	PT0270	Ig heavy chain CRD
737	12	19.7	20	2	PC2084	serine proteinase	810	11	18.0	9	2	PT0288	Ig heavy chain CRD
738	12	19.7	20	2	A34817	collagenolytic pro	811	11	18.0	9	2	PT0315	Ig heavy chain CRD
739	12	19.7	20	2	A20569	C-reactive protein	812	11	18.0	9	2	PT0324	Ig heavy chain CRD
740	12	19.7	20	2	S43627	cytochrome-c oxida	813	11	18.0	9	2	I46016	Ig heavy chain CRD
741	12	19.7	20	2	S23981	outer layer protei	814	11	18.0	9	2	I46023	cytokeratin 4 - bo
742	12	19.7	20	2	S58382	hypothetical prote	815	11	18.0	9	2	A60320	growth hormone rec
743	12	19.7	20	2	PH1338	Ig heavy chain DJ	816	11	18.0	9	2	S78426	xenopsin-related p
744	12	19.7	20	2	I67551	monocyte chemotact	817	11	18.0	9	3	PW0002	52.5K protein - Pa
745	12	19.7	20	2	S60350	kallikrein, pankre	818	11	18.0	10	1	XASNPC	light-harvesting c
746	12	19.7	20	2	PN0459	basic eosinophil p	819	11	18.0	10	2	JC1367	angiotensin-conver
747	12	19.7	20	2	S78759	ribosomal protein	820	11	18.0	10	2	A60421	thyloliberin poten
748	12	19.7	20	2	PQ0071	T-cell receptor be	821	11	18.0	10	2	S08997	hypertrehalosemic
749	12	19.7	20	2	S66222	defensin AMP2 - Da	822	11	18.0	10	2	S08998	hypertrehalosemic
750	12	19.7	20	3	PQ0710	Primase (EC 2.7.7.	823	11	18.0	10	2	A26381	hypertrehalosemic
751	11.5	18.9	9	2	S56004	glucan 1,3-beta-gl	824	11	18.0	10	2	A31571	hypertrehalosemic/
752	11.5	18.9	11	1	LFTWE	probable trpEG lea	825	11	18.0	10	2	A61337	caerulein - frog (
753	11.5	18.9	11	2	C53652	rhlR protein - Pse	826	11	18.0	10	2	S59625	beta-galactosidase
754	11.5	18.9	14	2	S33801	chaperone, TCPI-re	827	11	18.0	10	2	C35191	hypothetical prote
755	11.5	18.9	14	2	S33802	chaperone, TCPI-re	828	11	18.0	10	2	A44871	monodehydroascorba
756	11.5	18.9	17	2	A40442	integrase homolog	829	11	18.0	10	2	S66248	processing enzyme,
757	11.5	18.9	20	2	S12268	Oa-2 antigen - mou	830	11	18.0	10	2	S63696	DNA polymerase - y
758	11.5	18.9	20	2	A56899	serum heterodimer,	831	11	18.0	10	2	S77990	cytochrome-c oxida
759	11	18.0	3	2	F37196	bradykinin-potentl	832	11	18.0	10	2	A13687	caerulein-like pep
760	11	18.0	4	2	A36266	RPCH-related neuro	833	11	18.0	10	2	H37196	bradykinin-potentl

834	11	18.0	10	2	A35556	hypothetical prote	907	11	18.0	14	2	A35105	hypothetical prote
835	11	18.0	10	2	PT0310	Ig heavy chain CRD	908	11	18.0	14	2	S45655	cathepsin L (EC 3.
836	11	18.0	10	2	F33932	Ig mu chain J regi	909	11	18.0	14	2	PT0223	Ig heavy chain CDR
837	11	18.0	10	2	E41946	T-cell receptor ga	910	11	18.0	14	2	PT0232	Ig heavy chain CRD
838	11	18.0	10	2	T13976	cytochrome c oxida	911	11	18.0	14	2	PT0252	Ig heavy chain CRD
839	11	18.0	10	2	T12303	cytochrome c oxida	912	11	18.0	14	2	PH1348	Ig heavy chain DJ
840	11	18.0	10	2	T12303	cytochrome c oxida	913	11	18.0	14	2	PH1356	Ig heavy chain DJ
841	11	18.0	10	2	T14019	cytochrome c oxida	914	11	18.0	14	2	PH1332	Ig heavy chain DJ
842	11	18.0	10	2	T14054	cytochrome c oxida	915	11	18.0	14	2	PH1758	T cell receptor al
843	11	18.0	10	2	T12308	cytochrome c oxida	916	11	18.0	14	2	PH1759	T cell receptor al
844	11	18.0	10	2	T12312	cytochrome c oxida	917	11	18.0	14	2	PH1766	T cell receptor al
845	11	18.0	10	2	T12316	cytochrome c oxida	918	11	18.0	14	2	PH1767	T cell receptor al
846	11	18.0	10	2	T14212	cytochrome c oxida	919	11	18.0	14	2	PH1768	T cell receptor al
847	11	18.0	10	2	T12321	cytochrome c oxida	920	11	18.0	14	2	PH1769	T cell receptor al
848	11	18.0	10	2	T14219	cytochrome c oxida	921	11	18.0	14	2	PH1625	Ig H chain V-D-J r
849	11	18.0	11	2	S66196	alcohol dehydrogen	922	11	18.0	14	2	PH1626	Ig H chain V-D-J r
850	11	18.0	11	2	S68392	H+-transporting AT	923	11	18.0	14	2	PH1627	Ig H chain V-D-J r
851	11	18.0	11	2	S35490	type II site-speci	924	11	18.0	14	2	PH1594	Ig H chain V-D-J r
852	11	18.0	11	2	H54346	pyruvate synthase	925	11	18.0	14	2	PH0792	T-cell receptor al
853	11	18.0	11	2	S05002	corazonin - Americ	926	11	18.0	14	2	PH0801	T-cell receptor al
854	11	18.0	11	2	A60656	perisulfakinin - A	927	11	18.0	14	2	PH0747	T-cell receptor be
855	11	18.0	11	2	S23306	substance P - Atla	928	11	18.0	14	2	S50197	binding protein SK
856	11	18.0	11	2	PT0250	Ig heavy chain CRD	929	11	18.0	14	2	A56632	neurofascin-II -
857	11	18.0	11	2	A33571	follistatin - bovi	930	11	18.0	14	2	S39331	S-allele-associated
858	11	18.0	11	2	PH1376	T antigen variant	931	11	18.0	15	2	A26997	unspecific monooxy
859	11	18.0	11	2	D41946	T-cell receptor ga	932	11	18.0	15	2	A47146	topoisomerase I -
860	11	18.0	11	2	S21704	asparagine--trNA l	933	11	18.0	15	2	S26791	Ig heavy chain V r
861	11	18.0	11	2	T12264	cytochrome-c oxida	934	11	18.0	15	2	B56661	S-locus specific g
862	11	18.0	11	2	T12253	cytochrome-c oxida	935	11	18.0	15	2	JN0730	hypothetical 1.7K
863	11	18.0	11	2	T12244	cytochrome-c oxida	936	11	18.0	15	2	S39012	protease - Therm
864	11	18.0	11	2	T12248	cytochrome-c oxida	937	11	18.0	15	2	S21411	modulation protein
865	11	18.0	11	3	PQ0731	Unidentified 5.7/3	938	11	18.0	15	2	S33781	acetoacetate synth
866	11	18.0	12	2	I64829	gene HEXA protein	939	11	18.0	15	2	T09463	ribosomal protein
867	11	18.0	12	2	S09082	proteasome chain 1	940	11	18.0	15	2	S32450	pol polyprotein -
868	11	18.0	12	2	I41235	glutamine--trNA l	941	11	18.0	15	2	PA0036	Sz-glycoprotein -
869	11	18.0	12	2	A26093	microbial collagen	942	11	18.0	15	2	PQ0194	self-incompatibili
870	11	18.0	12	2	G64003	hypothetical prote	943	11	18.0	15	2	PQ0750	15K protein 5106 -
871	11	18.0	12	2	S36899	ribosomal protein	944	11	18.0	15	2	PS0251	gamma 2 gliadin -
872	11	18.0	12	2	PQ0776	NADH dehydrogenase	945	11	18.0	15	2	B56891	protein OF200006 -
873	11	18.0	12	2	S10624	lipovitelin - Afr	946	11	18.0	15	2	PA0053	cytochrome-c oxida
874	11	18.0	12	2	A49637	MHC class II histo	947	11	18.0	15	2	S43634	cytochrome-c oxida
875	11	18.0	12	2	S43957	Ig mu chain V regi	948	11	18.0	15	2	S77988	Fc gamma receptor
876	11	18.0	12	2	S43170	kinesin light chai	949	11	18.0	15	2	A47628	Ig heavy chain DJ
877	11	18.0	12	2	PH1454	T-cell receptor al	950	11	18.0	15	2	PH1342	Ig heavy chain DJ
878	11	18.0	12	2	PH0802	T-cell receptor al	951	11	18.0	15	2	PH1320	Ig mu chain V regi
879	11	18.0	12	2	PH0790	T-cell receptor be	952	11	18.0	15	2	S43956	T cell receptor al
880	11	18.0	12	2	PH0936	T-cell receptor be	953	11	18.0	15	2	PH1788	T-cell receptor be
881	11	18.0	12	2	I58273	thyroglobulin - ra	954	11	18.0	15	2	PH0136	casin kinase II (
882	11	18.0	13	1	XAV19B	angiotensin-conver	955	11	18.0	15	2	B45133	chromogranin A - b
883	11	18.0	13	2	A37196	bradykinin-potenti	956	11	18.0	15	2	S38976	T-cell receptor be
884	11	18.0	13	2	A39044	epsilon-conotoxin	957	11	18.0	15	2	PQ0073	7 alpha-hydroxy-4-
885	11	18.0	13	2	B26093	microbial collagen	958	11	18.0	15	2	A45103	Ig H chain V-D-J r
886	11	18.0	13	2	A60409	bombesin-like pept	959	11	18.0	15	2	PH1613	Ig H chain V-D-J r
887	11	18.0	13	2	A05174	tryptophyllin-13	960	11	18.0	15	2	PH1612	Ig H chain V-D-J r
888	11	18.0	13	2	A54326	glandular kallikre	961	11	18.0	15	2	PT0096	pyruvate dehydrog
889	11	18.0	13	2	S03063	Ig lambda chain J	962	11	18.0	15	2	PH0782	T-cell receptor al
890	11	18.0	13	2	S24117	dystrophin - rabbi	963	11	18.0	15	2	I67525	CD33 antigen homol
891	11	18.0	13	2	PH1636	Ig H chain V-D-J r	964	11	18.0	15	2	S08301	epidermal growth f
892	11	18.0	13	2	PH1620	Ig H chain V-D-J r	965	11	18.0	15	2	PX0031	mixed lymphocyte r
893	11	18.0	13	2	G37266	Ig heavy chain C r	966	11	18.0	15	2	S21293	RIP protein - rat
894	11	18.0	13	2	D37267	Ig heavy chain C r	967	11	18.0	15	2	B26501	lipoprotein lipase
895	11	18.0	13	2	PH0788	T-cell receptor al	968	11	18.0	16	2	S03405	hydrogenase (EC 1.
896	11	18.0	13	2	PH0787	T-cell receptor al	969	11	18.0	16	2	C45143	protein-tyrosine-p
897	11	18.0	13	2	I51905	collecting duct wa	970	11	18.0	16	2	A36300	T-cell receptor ga
898	11	18.0	13	2	S66558	serine proteinase	971	11	18.0	16	2	S26746	Ig heavy chain J r
899	11	18.0	13	3	PC2369	Unidentified 85K p	972	11	18.0	16	2	S11290	matrix protein M1
900	11	18.0	14	1	BSTD	bombesin - fire-be	973	11	18.0	16	2	C37290	homeotic protein G
901	11	18.0	14	1	BSTDY	bombesin - yellow	974	11	18.0	16	2	S05703	homeotic protein c
902	11	18.0	14	2	S05709	homeotic protein c	975	11	18.0	16	2	A36889	leu operon leader
903	11	18.0	14	2	PA0158	disaggregatase - M	976	11	18.0	16	2	S02455	DNA-invertase - ph
904	11	18.0	14	2	PA0109	porin por 1B - Ara	977	11	18.0	16	2	S66613	protein p12e - Fri
905	11	18.0	14	2	PA0045	porin por1 - Arabi	978	11	18.0	16	2	S22677	heat shock protein
906	11	18.0	14	2	PA0015	seed storage prote	979	11	18.0	16	2	PC1299	subtilisin (EC 3.4

980	11	18.0	16	2	crystal protein, 2
981	11	18.0	16	2	hypodermin B - ear
982	11	18.0	16	2	Ig heavy chain CDR
983	11	18.0	16	2	Ig heavy chain CDR
984	11	18.0	16	2	T-cell receptor be
985	11	18.0	16	2	fibrinopeptide A -
986	11	18.0	16	2	redoxin
987	11	18.0	16	2	Ig H chain V-D-J r
988	11	18.0	16	2	Ig H chain V-D-J r
989	11	18.0	16	2	transforming prote
990	11	18.0	16	2	beta-crystallin A1
991	11	18.0	16	2	transcription fact
992	11	18.0	16	2	NADH dehydrogenase
993	11	18.0	17	2	alcohol dehydrogen
994	11	18.0	17	2	trypsin (EC 3.4.21
995	11	18.0	17	2	trypsin (EC 3.4.21
996	11	18.0	17	2	Ig heavy chain J5
997	11	18.0	17	2	Ig H chain V-D-J r
998	11	18.0	17	2	Ig heavy chain J r
999	11	18.0	17	2	caldesmon (fragmen
1000	11	18.0	17	2	SP-A2 - human (fira

ALIGNMENTS

RESULT 1
S03533
Ig heavy chain J region (JH-6) - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 09-Sep-1997
C:Accession: S03533
R:Schwager, J.; Grosberger, D.; du Pasquier, L.
EMBO J. 7, 2409-2415, 1988
A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus laevis
A:Reference number: S01158; MUID:89052653
A:Accession: S03533
A:Molecule type: DNA
A:Residues: 1-17 <SCH>
A:Cross-references: EMBL:X14918; NID:g64805; PID:e16058; PID:q1334659

Query Match 39.3%; Score 24; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. NO. 2.7e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy	1	WNWRYR	6
		::	
Db	2	YSWDYR	7

RESULT 2
PT0286
Ig heavy chain CDR3 region (clone 4-100B) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0286
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337
A:Accession: PT0286
A:Molecule type: DNA
A:Residues: 1-18 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

```
Query Match          39.3%; Score 24; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. NO. 2.9e+02;
Matches 3: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 2 NWRV 5

```

Db          6  WNY 9
|||
RESULT      3
B41946
T-cell receptor gamma chain (lt.57) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: B41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma
A:Reference number: A41946; MUID:92049316
A:Accession: B41946
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-11 <WHE>
C:Keywords: T-cell receptor

```

Query Match	37.7%	Score 23;	DB 2;	Length 11;
Best Local Similarity	100.0%;	Pred. No. 2.5e+02;		
Matches 3;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			

QY	3 WRY	5
Db	5 WRY	7

```

RESULT      4
A40763      sucrose-6-phosphate hydrolase [EC 3.2.-.-] - Lactococcus lactis subsp. lactis (fragme
C:Species: Lactococcus lactis subsp. lactis
C:Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 12-Sep-1997
C:Accession: A40763
R:Thompson, J.; Nguyen, N.Y.; Sackett, D.L.; Donkersloot, J.A.
J. Biol. Chem. 266, 14573-14579, 1991
A:Title: Transposon-encoded sucrose metabolism in Lactococcus lactis. Purification of
A:Reference number: A40763; MUID:91317821
A:Accession: A40763
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <THO>
C:Keywords: glycosidase; hydrolase

```

Query Match	37.7%	Score 23;	DB 2;	Length 12;
Best Local Similarity	80.0%	Pred. No. 2.8e+02;		
Matches	4;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY	4 RYREY 8
Dp	8 RYRTY 12

```

RESULT      5
E49037
Tcr delta chain V-D-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 29-Jan-1999
C:Accession: E49037
R:Esquerria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.
Eur. J. Immunol. 22, 491-498, 1992
A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of th
A:Reference number: E49037; MUID:92164730
A:Accession: E49037
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <EQO>
A:Cross-references: GB:S90653; NID:g246296; PID:g246297
A:Experimental source: dendritic epidermal T-cell lines
A:Note: sequence extracted from NCBI backbone (NCBIN:90653, NCBIIP:90665)

```

Query Match 37.7%; Score 23; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 3.5e+02;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYR 6
 | | |
 DB 4 WEYR 7

RESULT 6

A29834

trp leader peptide - Corynebacterium glutamicum

C:Species: Corynebacterium glutamicum

C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Sep-1999

C:Accession: A29834; A24723; A29458; S13087; A48967

R:Matsui, K.; Miwa, K.; Sano, K.

J. Bacteriol. 169, 5330-5332, 1987

A:Title: Two single-base-pair substitutions causing desensitization to tryptophan feedback.

A:Reference number: A29834; MUID:88032866

A:Contents: B. lactofermentum

A:Accession: A29834

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-17 <WAT>

A:Cross-references: GB:M17892; NID:gl44101; PIDN:AAB59110.1; PID:gl129101

R:Matsui, K.; Sano, K.; Ohtsubo, E.

Nucleic Acids Res. 14, 10113-10114, 1986

A:Title: Complete nucleotide and deduced amino acid sequences of the Brevibacterium lact

A:Reference number: A93606; MUID:87117512

A:Contents: B. lactofermentum

A:Accession: A24723

A:Molecule type: DNA

A:Residues: 1-17 <MA2>

A:Cross-references: GB:X04960; NID:g39591; PIDN:CAA28622.1; PID:g580785

R:Sano, K.; Matsui, K.

Gene 53, 191-200, 1987

A:Title: Structure and function of the trp operon control regions of Brevibacterium lact

A:Reference number: A91575; MUID:87277409

A:Contents: B. lactofermentum

A:Accession: A29458

A:Molecule type: DNA

A:Residues: 1-17 <SAN>

R:Heery, D.M.; Dunican, L.K.

Nucleic Acids Res. 18, 7138, 1990

A:Title: Nucleotide sequence of the Corynebacterium glutamicum trpE gene.

A:Reference number: S13087; MUID:91088299

A:Accession: S13087

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-17 <HEE>

A:Cross-references: EMBL:X55994; NID:g40521; PIDN:CAA39466.1; PID:g580992

R:Heery, D.M.; Dunican, L.K.

Appl. Environ. Microbiol. 59, 791-799, 1993

A:Title: Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Cory

A:Reference number: A48967; MUID:93243735

A:Accession: A48967

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 <HER>

A:Cross-references: GB:S59299; NID:g299877; PIDN:AAB26395.1; PID:g299878

A:Experimental source: ATCC 21850

A:Note: sequence extracted from NCBI backbone (NCBIN:130455, NCBIP:130456)

C:Genetics:

A:Gene: trpL

A:Start codon: GTG

C:Superfamily: unassigned leader peptides

Query Match

Best Local Similarity 37.7%; Score 23; DB 2; Length 17;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNWR 4
 | | |
 DB 12 WNR 15

RESULT 7

PC1251

testin II - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Feb-1997

C:Accession: PC1251

R:Cheng, C.Y.; Morris, I.; Bardin, C.W.

Biochem. Biophys. Res. Commun. 191, 224-231, 1993

A:Title: Testins are structurally related to the mouse cysteine proteinase precursor

A:Reference number: PC1250; MUID:93191698

A:Accession: PC1251

A:Molecule type: protein

A:Residues: 1-19 <CHE>

C:Superfamily: papain

Query Match

Best Local Similarity 36.9%; Score 22.5; DB 2; Length 19;

Matches 4; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 WN-WR 4
 | | |
 DB 13 WNEWR 17

RESULT 8

B49164

chromogranin-B - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997

C:Accession: B49164

R:Nielsen, E.; Welinder, B.S.; Madsen, O.D.

Endocrinology 129, 3147-3156, 1991

A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides

A:Reference number: A49164; MUID:92063871

A:Accession: B49164

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <NIE>

A:Note: sequence extracted from NCBI backbone (NCBIP:66370)

C:Superfamily: chromogranin B precursor

Query Match

Best Local Similarity 36.1%; Score 22; DB 2; Length 11;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWRY 5
 | | |
 DB 7 NWGY 10

RESULT 9

PH1605

Ig H chain V-D-J region (wild-type clone 328) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1605

R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less m

A:Reference number: PH1580; MUID:93301609

A:Accession: PH1605

A:Molecule type: DNA

A:Residues: 1-12 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C;Keywords: immunoglobulin

Query Match 36.1%; Score 22; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RYRE 7

||||

Db 4 RYRE 7

RESULT 10

S58426

spermadhesin AWN homolog - horse (fragment)

C;Species: Equus caballus (domestic horse)

C;Date: 12-Feb-1998 #sequence_revision 15-May-1998 #text_change 07-May-1999

C;Accession: S58426

R;Calvete, J.J.; Mann, K.; Schaefer, W.; Sanz, L.; Reinert, M.; Nessau, S.; Raida, M.;

Biochem. J. 310, 615-622, 1995

A;Title: Amino acid sequence of HSP-1, a major protein of stallion seminal plasma: effed

A;Reference number: S58424; MUID:95382782

A;Accession: S58426

A;Molecule type: protein

A;Residues: 1-14 <CAL>

A;Experimental source: seminal plasma

Query Match 36.1%; Score 22; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNRYSR 6

||||

Db 2 WNRYSR 7

RESULT 11

PHI366

Ig heavy chain DJ region (clone C111-106) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PHI366

R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A;Reference number: PHI302; MUID:93094761

A;Accession: PHI366

A;Molecule type: DNA

A;Residues: 1-15 <WAS>

C;Keywords: heterotrimer; immunoglobulin

Query Match 36.1%; Score 22; DB 2; Length 15;
Best Local Similarity 37.5%; Pred. No. 5.1e+02;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 WNRYSR 8

||||

Db 3 WSGYGYDY 10

RESULT 12

B44820

7K protein - Escherichia coli

C;Species: Escherichia coli

C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 24-Feb-1995

C;Accession: B44820

R;Lopez, J.; Delgado, D.; Andres, I.; Ortiz, J.M.; Rodriguez, J.C.

J. Gen. Microbiol. 137, 1093-1099, 1991

A;Title: Isolation and evolutionary analysis of a RepFVIB replicon of the plasmid pSU212

A;Reference number: A44820; MUID:91324851

A;Contents: IncFVI plasmid pSU212

A;Accession: B44820

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-16 <LOP>

A;Note: sequence extracted from NCBI backbone (NCBIN:45962, NCBIP:45966)

Query Match 36.1%; Score 22; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 5.5e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WRYR 6

||||

Db 2 WMYR 5

RESULT 13

PHI380

alpha-amylase (EC 3.2.1.1) (Halm sensitive) - Bacillus sp. (fragment)

C;Species: Bacillus sp.

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 07-May-1999

C;Accession: PHI380

R;Kawaguchi, T.; Nagae, H.; Murao, S.; Arai, M.

Biosci. Biotechnol. Biochem. 56, 1792-1796, 1992

A;Title: Purification and some properties of a Halm-sensitive alpha-amylase from newl

A;Reference number: PHI380; MUID:93113087

A;Accession: PHI380

A;Molecule type: protein

A;Residues: 1-20 <RAW>

A;Experimental source: strain NO.195

C;Comment: This enzyme has an optimum pH of 7.0.

C;Function:

A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds

A;Pathway: glycogen/starch degradation

C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 36.1%; Score 22; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 6.9e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNW 3

||||

Db 15 WTW 17

RESULT 14

A56894

Intracrystalline chromoprotein 1 - Terebratella sanguinea (fragment)

C;Species: Terebratella sanguinea

C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C;Accession: A56894

R;Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.

Comp. Biochem. Physiol. B Comp. Biochem. 102, 93-95, 1992

A;Title: An intracrystalline chromoprotein from red brachiopod shells: implications f

A;Reference number: A56894; MUID:92405551

A;Contents: Leach, red brachiopod shells

A;Accession: A56894

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-20 <CUS>

A;Note: sequence extracted from NCBI backbone (NCBIP:114882)

C;Keywords: chromoprotein

Query Match 36.1%; Score 22; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 6.9e+02;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 WRYREY 8

||||

Db 2 WEYLPY 7

RESULT 15
PH0746
T-cell receptor beta chain (B28) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 10-Sep-1997
C:Accession: PH0746
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846
A:Accession: PH0746
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Cross-references: EMBL:X60837; NID:g50098; PID:g50099
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 34.4%; Score 21; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RYREY 8
|| :|
Db 6 RYEQY 10

Search completed: May 2, 2000, 00:22:19
Job time: 91 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:22:03 ; Search time 7.62 Seconds
(without alignments)
35.273 Million cell updates/sec

Title: US-09-258-947-38
Perfect score: 61
Sequence: 1 WNRVREYV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 82229 seqs, 29864866 residues

Total number of hits satisfying chosen parameters: 1030

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	37.7	17	1	LPW_BRELA
2	22	36.1	19	1	CAT3_FASHE
3	21	34.4	20	1	ELAS_GADMO
4	20	32.8	12	1	UR2A_CATCO
5	20	32.8	12	1	UR2B_CATCO
6	20	32.8	12	1	UR2B_CYPCA
7	20	32.8	12	1	UR2_GOLMI
8	20	32.8	12	1	UR2_POLSP
9	20	32.8	12	1	UR2_SCYCA
10	20	32.8	13	1	UR2_RANRI
11	19	31.1	14	1	MAST_PARID
12	19	31.1	14	1	MAST_VESXA
13	19	31.1	15	1	UC08_MAZE
14	19	31.1	17	1	TPIS_PINPS
15	18	29.5	10	1	GON1_ALLMI
16	18	29.5	10	1	GON3_ONCKE
17	18	29.5	14	1	LPW_RHIME
18	18	29.5	15	1	LEC3_AXIPO
19	18	29.5	16	1	CAT9_FASHE
20	18	29.5	17	1	LPW_AZOBR
21	17.5	28.7	20	1	CAT4_FASHE
22	17	27.9	8	1	HTF1_PERAM
23	17	27.9	8	1	HTF2_PERAM
24	17	27.9	8	1	HTF_TENNO
25	17	27.9	10	1	BPP2_BOTIN
26	17	27.9	10	1	BPP2_BOTJA
27	17	27.9	10	1	HTF1_ROMMI
28	17	27.9	10	1	HTF2_CARMO
29	17	27.9	10	1	TPIS_NICPL
30	17	27.9	11	1	CEPI_ACHFU
31	17	27.9	11	1	RR2_CONAM
32	17	27.9	11	1	GLN2_PINPS
33	17	27.9	15	1	RBS_PHPYA
34	17	27.9	15	1	UC19_MAZE

35	17	27.9	16	1	VPR_HVLS3
36	17	27.9	19	1	AL22_HORSE
37	17	27.9	19	1	DCAM_ACACA
38	17	27.9	20	1	AMP_FUSNU
39	17	27.9	20	1	DFTS_RAT
40	17	27.9	20	1	HGL1_FASHE
41	16.5	27.0	14	1	LPW_CITFR
42	16.5	27.0	14	1	LPW_ECOLI
43	16.5	27.0	14	1	LPW_SALTY
44	16	26.2	7	1	WMA1_ACHFU
45	16	26.2	9	1	HUTU_KLEAE
46	16	26.2	10	1	HTF_TABAT
47	16	26.2	10	1	UXA6_CHLTR
48	16	26.2	12	1	CXAI_CONIM
49	16	26.2	13	1	IRBP_MOUSE
50	16	26.2	14	1	CALA_CALGI
51	16	26.2	14	1	KARA_BROPL
52	16	26.2	15	1	UC16_MAZE
53	16	26.2	15	1	UC20_MAZE
54	16	26.2	17	1	NEF_HVLU3
55	16	26.2	17	1	RANR_RANRU
56	16	26.2	17	1	TAC1_TAGGI
57	16	26.2	17	1	TAC3_TAGGI
58	16	26.2	18	1	GALS_SALTY
59	16	26.2	18	1	PPM1_LIMPO
60	16	26.2	18	1	PPM2_LIMPO
61	16	26.2	20	1	SODM_MYCHA
62	16	26.2	20	1	CS21_STRTR
63	16	26.2	20	1	EFTU_MYCSY
64	16	26.2	20	1	FIBR_PACLE
65	16	26.2	20	1	OXLA_AGRRH
66	15	24.6	10	1	GON2_CHICK
67	15	24.6	13	1	YPNP_PHOLU
68	15	24.6	15	1	ALLS_MANSE
69	15	24.6	15	1	YAA3_RHOPA
70	15	24.6	16	1	LPK1_LOCMI
71	15	24.6	19	1	ETFA_CLOPA
72	14	23.0	7	1	HY7_PIG
73	14	23.0	8	1	LCK8_LEUMA
74	14	23.0	10	1	ANG1_BOTJA
75	14	23.0	10	1	ANGT_BOVIN
76	14	23.0	10	1	ANGT_CHICK
77	14	23.0	10	1	GON3_PETMA
78	14	23.0	10	1	RL16_ACHLA
79	14	23.0	13	1	NEUT_CAVPO
80	14	23.0	13	1	NEUT_CHICK
81	14	23.0	13	1	NEUT_RANTE
82	14	23.0	14	1	MAST_POLJA
83	14	23.0	15	1	MILT_ONCKE
84	14	23.0	18	1	HEMH_THETS
85	14	23.0	18	1	YAA5_RHOPA
86	14	23.0	19	1	PA25_HUMAN
87	14	23.0	19	1	TX3_PHONI
88	14	23.0	20	1	CRTC_SPIOL
89	14	23.0	20	1	FIBB_SHEEP
90	14	23.0	20	1	RIPX_CUCPE
91	14	23.0	20	1	UCRQ_EQUAR
92	13.5	22.1	5	1	MALT_BACTQ
93	13	21.3	5	1	UF01_MOUSE
94	13	21.3	7	1	FAR2_ASCSU
95	13	21.3	7	1	WMA2_ACHFU
96	13	21.3	7	1	WMA3_ACHFU
97	13	21.3	8	1	ANG2_BOTJA
98	13	21.3	10	1	GON1_PETMA
99	13	21.3	10	1	GONL_SQUAC
100	13	21.3	11	1	ANGT_CRIGE
101	13	21.3	11	1	LSK1_LEUMA
102	13	21.3	13	1	NEUT_TRIVU
103	13	21.3	13	1	UVRD_SALTY
104	13	21.3	14	1	ANGT_HORSE
105	13	21.3	14	1	SMS1_MYOSC
106	13	21.3	14	1	SMS_ALLMI
107	13	21.3	15	1	ECDA_LYMDI

P19555	human immun
P81217	equus cabal
P34039	acanthamoeb
P81207	fusobacteri
P07448	tattus norv
P80527	fasciola he
P03056	citrobacter
P03053	escherichia
P03054	salmonella
P35919	achatina fu
P12381	klebsiella
P14596	tabanus atr
P38007	chlamydia t
P50993	conus imper
P49194	mus musculu
P20728	calotropis
P22442	bromelia pl
P80622	zea mays (m
P80626	zea mays (m
P12480	human immun
P08952	rana rugosa
P23684	tachypleus
P18252	tachypleus
P41030	salmonella
P14215	limulus pol
P14216	limulus pol
P80582	mycobacteri
P81621	streptococc
P1407	mycoplasma
P81070	pacifastacu
P81382	agkistrodon
P37043	gallus gall
P41122	photorhabdu
P42559	manduca sex
Q02006	rhodopseudo
P20404	locusta mig
P81342	clostridium
P01153	sus scrofa
P19990	leucophaea
Q10581	bothrops ja
P01017	bos taurus
P01018	gallus gall
P30948	petromyzon
P29221	acholeplasm
P32560	cavia porce
P13724	gallus gall
P41536	rana tempor
P01517	polistes ja
P81037	oncorhynchu
P80155	theromyzon
Q02005	rhodopseudo
P24605	homo sapien
P31010	phoneutria
P30805	spinacia ol
P14470	ovis aries
P80750	cucurbita p
P81247	equisetum a
P80072	bacillus th
P38639	mus musculu
P31890	ascaris suu
P35920	achatina fu
Q10582	bothrops ja
P04378	petromyzon
P27429	squalus aca
P09037	crinia geor
P04428	leucophaea
P31745	trichosurus
Q05311	salmonella
P01016	equus cabal
P20750	myoxocephal
P31885	alligator m
P80938	lymantria d

108	13	21.3	15	1	FKB7_P1NPS	P81104	pinus pinaea
109	13	21.3	15	1	PC20_BRANA	P81096	brassica napae
110	13	21.3	15	1	UC14_MAIZE	P80620	zea mays (maize)
111	13	21.3	15	1	URE1_MORMO	P17337	morganelia
112	13	21.3	16	1	FIBA_MUSVI	P14458	mustela vison
113	13	21.3	16	1	RL6_VIBPR	Q56715	vibrio proteolyticus
114	13	21.3	16	1	VPR_HVIC4	Q05953	human immunoglobulin G
115	13	21.3	17	1	EFQ_THRQA	Q01697	thermus aquaticus
116	13	21.3	17	1	GAST_MACMU	P33714	macaca mulatta
117	13	21.3	20	1	CAOS_RAT	P19633	rattus norvegicus
118	13	21.3	20	1	COGA_CHIOP	P34156	chionoecetes opilio
119	13	21.3	20	1	SUCB_CANFA	P99507	canis familiaris
120	13	21.3	20	1	VR90_BORPE	P81549	bordetella pertussis
121	12.5	20.5	20	1	APAI_ERYPA	P18647	erythrocebus propitius
122	12	19.7	5	1	FARP_ARTTR	P41853	artiopesthi
123	12	19.7	5	1	PRCT_PSRAM	P01373	periplaneta americana
124	12	19.7	6	1	LCK1_LOOMI	P41491	locusta migratoria
125	12	19.7	8	1	AKH_LIUBAU	P23418	libellula aegyptia
126	12	19.7	8	1	AKH_MEML	P25423	melolontha
127	12	19.7	8	1	LCK1_LEUMA	P21140	leucophaea
128	12	19.7	8	1	LCK2_LEUMA	P21141	leucophaea
129	12	19.7	8	1	LCK3_LEUMA	P21142	leucophaea
130	12	19.7	8	1	LCK4_LEUMA	P21143	leucophaea
131	12	19.7	8	1	LCK5_LEUMA	P19987	leucophaea
132	12	19.7	8	1	LCK6_LEUMA	P19988	leucophaea
133	12	19.7	8	1	LCK7_LEUMA	P19989	leucophaea
134	12	19.7	9	1	COXE_THUOB	P80975	thunnus obesus
135	12	19.7	9	1	LMIP_LOOMI	P31799	locusta migratoria
136	12	19.7	9	1	NEF_HV1Z8	P12481	human immunoglobulin G
137	12	19.7	9	1	UHA2_HUMAN	P40929	homo sapiens
138	12	19.7	10	1	AKHX_LOOMI	P81626	locusta migratoria
139	12	19.7	10	1	COXO_RAT	P80432	rattus norvegicus
140	12	19.7	10	1	GON1_CHEPR	P80677	chelysoma
141	12	19.7	10	1	GON2_CHEPR	P80678	chelysoma
142	12	19.7	10	1	GRP_RANR1	P23260	rana ridibundus
143	12	19.7	10	1	NO40_TOBAC	P55962	nicotiana glauca
144	12	19.7	10	1	RLA2_MOUSE	P99027	mus musculus
145	12	19.7	10	1	TKU1_UREUN	P40751	urechis unicolor
146	12	19.7	11	1	CH60_DROME	P35380	drosophila
147	12	19.7	11	1	MLG_THETS	P41989	theromyzon
148	12	19.7	11	1	TKN1_PSEGU	P42986	pseudophryn
149	12	19.7	11	1	TKN2_PSEGU	P42987	pseudophryn
150	12	19.7	11	1	TKN3_PSEGU	P42988	pseudophryn
151	12	19.7	12	1	GRAR_RANRU	P40754	rana rugosa
152	12	19.7	12	1	NO40_LOTJA	O22426	lotus japonicus
153	12	19.7	12	1	NO40_SSRSO	O24369	sesbania rostrata
154	12	19.7	13	1	MLA_ANOCA	P41589	anolis carolinensis
155	12	19.7	13	1	MLA_CAMDR	P01198	camelus dromedarius
156	12	19.7	13	1	NO40_PEA	P55959	pisum sativum
157	12	19.7	13	1	NO40_VICSA	P55961	vicia sativa
158	12	19.7	13	1	DCMW_PSECF	P19914	pseudomonas
159	12	19.7	14	1	EFTU_CANFA	P54835	canis familiaris
160	12	19.7	14	1	HY14_PIG	P01155	sus scrofa
161	12	19.7	14	1	MARI_ALTSP	P29399	alteromonas
162	12	19.7	14	1	MAST_VESBA	P21654	vespa basalis
163	12	19.7	14	1	NEJ2_FASHE	P80526	fasciola hepatica
164	12	19.7	14	1	PPBL_PSEAE	P35482	pseudomonas
165	12	19.7	15	1	CXAI_CONGE	P01519	conus geographus
166	12	19.7	15	1	HS11_P1NPS	P81083	pinus pinaster
167	12	19.7	15	1	LCK_DROME	P81829	drosophila
168	12	19.7	15	1	MK1_PALPR	P80408	palomena
169	12	19.7	15	1	MK2A_PALPR	P80409	palomena
170	12	19.7	15	1	TERM_BPW2	P19897	bacterioph
171	12	19.7	15	1	UC13_MAIZE	P80619	zea mays (maize)
172	12	19.7	16	1	ALLI_CALVO	P18839	calliphora
173	12	19.7	16	1	HTPG_ACICA	P81876	acinetobact
174	12	19.7	16	1	MK2B_PALPR	P80410	palomena
175	12	19.7	16	1	MK3_PALPR	P80411	palomena
176	12	19.7	16	1	MLB_SQUAC	P01207	squalus ac
177	12	19.7	16	1	PSAJ_SFIOL	P17230	spinnacia ol
178	12	19.7	17	1	LCK_RAT	Q01621	rattus norv
179	12	19.7	17	1	SP51_BACLI	P27642	bacillus li
180	12	19.7	18	1	AL13_CARMA	P81816	carcinus ma

18	1	CYCH_MOUSE	Q61458	mus musculus
18	1	MLB_HORSE	P01202	equus caballus
18	1	MLB_SCYCA	P01206	scyllorhinus
18	1	NODD_RHILO	Q52838	rhizobium 1
18	1	NPA_BOVIN	P15506	bos taurus
18	1	TOPI_KLEAE	P46155	klebsiella
18	1	UC21_MAIZE	P06503	streptomyces
19	1	DURC_STRGP	P06507	zea mays (m)
19	1	FIBB_VULVU	P14482	vulpes vulp
19	1	H3_NARPS	P00553	naricissus p
19	1	HMD_METWO	P32441	methanobact
19	1	LANC_STRSQ	P38655	streptomyces
19	1	OXLA_OPHHA	P81383	ophiophagus
19	1	UC31_MAIZE	P08637	zea mays (m)
20	1	CISY_STRHY	P20903	streptomyces
20	1	COGI_PARCM	P20731	paralithodea
20	1	COXE_ONCMY	P80329	oncorhynchus
20	1	CPXX_RRHOR	P31718	rhodococcus
20	1	DRP4_BOVIN	P19094	mustelus ca
20	1	DDP4_BOVIN	P81425	bos taurus
20	1	KORA_METTM	P08904	methanobact
20	1	LECI_ARTIN	P18671	artocarpus
20	1	LEC2_MACPO	P18676	maclura pom
20	1	LEC3_MACPO	P18677	maclura pom
20	1	OMPI_ACTAC	P20242	actinobacill
20	1	PSBH_SYNVU	P19052	synecococc
20	1	UN03_PFNPS	P81574	pinus pinas
10	1	LABA_JATMU	P13270	jatropha mu
11	1	LPW_THETH	P05624	thermus equ
11	1	BPP7_BOTIN	P30425	bothrops in
7	1	FARI_ASCSU	P31889	ascaris suu
7	1	FAR5_HIRME	P42564	hirudo medi
8	1	ACI_THUAL	P18691	thunnus alb
8	1	AKHG_GRYBI	P14086	gryllus bim
8	1	AKH_TABAT	P14595	tabanus atr
8	1	ALL4_CALVO	P41840	calliphora
8	1	CKKN_MACPU	P30369	macropus eu
8	1	PLP_BRANA	P81707	brassica na
8	1	RPCH_PANBO	P08939	pandanus bo
9	1	DI_NEPNO	P24816	nephrops no
9	1	DSIF_RABIT	P01158	oryctolagus
9	1	FARA_CALVO	P41865	calliphora
9	1	LITO_LITAU	P08945	litoria eur
9	1	LITR_PHYRO	P08946	phyllomedus
9	1	LMT3_LOCMI	P41489	locusta mig
9	1	PGLR_DRAAB	P81179	diaprepes a
10	1	APE_CAPGI	P80474	capnocytoph
10	1	BPP8_BOTIN	P30426	bothrops in
10	1	BPP_VIPAS	P31351	vipera aspi
10	1	CAER_LITXA	P56264	litoria xan
10	1	COXO_THUOB	P08982	thunnus obe
10	1	HTF_HEUZE	P16353	helleothis z
10	1	HTF_NAUCI	P10939	nauphoeta c
10	1	MP2_MICOC	P81533	microplitis
10	1	TOPI_SALTY	P40686	salmonella
10	1	UHA3_HUMAN	P40930	homo sapien
11	1	CORZ_PERAM	P11496	periplaneta
11	1	LSKP_PERAM	P36885	periplaneta
11	1	RANC_RANPI	P08951	rana pipien
11	1	T2PI_PROVU	P31031	proteus vul
11	1	TKNA_GADMO	P28498	gadus morhu
11	1	UF05_MOUSE	P38643	mus musculu
12	1	NO40_SOYBN	P55960	glycine max
12	1	UP01_CABEL	P59594	caenorhabdi
13	1	BOML_PESGU	P42991	pseudophryn
13	1	BPP1_BOTJA	P01020	bothrops ja
13	1	CXET_CONTE	P81755	conus texti
13	1	MPL1_MICOC	P81532	microplitis
13	1	TP13_PHYRO	P04096	phyllomedus
13	1	UN12_CLOPB	P81353	clostridium
14	1	ALYT_ALYOP	P08944	alytes obst
14	1	CAT2_FASHE	P80342	fasciola he
14	1	NSK2_SARBU	P41493	sarcophaga

254	11	18.0	14	1	RECJ_SALTY	P28355 salmonella	327	10	16.4	20	1	ITRA_ALBUJU	P24925 albizzia ju
255	11	18.0	15	1	COXJ_THUOB	P80979 thunnus obe	328	10	16.4	20	1	MCRG_METTE	P22950 methanosarc
256	11	18.0	15	1	RM12_YEAST	P36522 saccharomyc	329	10	16.4	20	1	NEUA_RAT	P29488 rattus norv
257	11	18.0	15	1	UC01_MAIZE	P80607 zea mays (m	330	10	16.4	20	1	OAR_PHOPY	P14803 photinus py
258	11	18.0	15	1	UC23_MAIZE	P80629 zea mays (m	331	10	16.4	20	1	PSAF_PEA	P20119 pisum sativ
259	11	18.0	16	1	FIBA_EQUAS	P14449 equus asinu	332	10	16.4	20	1	RLC1_HALMA	P12740 haloarcula
260	11	18.0	16	1	FIBA_FELCA	P14450 felis silve	333	10	16.4	20	1	YPRB_SERMA	P22581 serrata ma
261	11	18.0	16	1	FIBA_MELE	P14456 meles meles	334	9	14.8	4	1	FARP_HIRME	P42563 hirudo medi
262	11	18.0	17	1	GSHX_PINPS	P81087 pinus pinas	335	9	14.8	6	1	FARP_MONEX	P41366 moniezia ex
263	11	18.0	19	1	ALL7_OLEEU	P81430 olea europae	336	9	14.8	6	1	OVN_LEPDE	P42985 leptinotars
264	11	18.0	19	1	LANA_ACTLG	P56650 actinoplane	337	9	14.8	7	1	FAR1_PROCL	P38499 procambarus
265	11	18.0	19	1	PSBN_SYNUV	P12313 synechococc	338	9	14.8	7	1	FAR2_PROCL	P38499 procambarus
266	11	18.0	20	1	AIBG_EQUAS	P39090 equus asinu	339	9	14.8	7	1	FAR3_PANRE	P41874 panagrellus
267	11	18.0	20	1	CAT1_FASHE	Q09093 fasciola he	340	9	14.8	8	1	AL17_CARMA	P81820 carcinus ma
268	11	18.0	20	1	COGL_CHIOP	P34153 chionocete	341	9	14.8	8	1	B44K_PORGI	P81886 porphyromon
269	11	18.0	20	1	COXA_THUOB	P80972 thunnus obe	342	9	14.8	8	1	FAR3_HOMAM	P41486 homarus ame
270	11	18.0	20	1	COXN_THUOB	P80980 thunnus obe	343	9	14.8	8	1	FAR4_HOMAM	P41487 homarus ame
271	11	18.0	20	1	COXN_THUOB	P80980 thunnus obe	344	9	14.8	9	1	AL11_CARMA	P81337 clostridium
272	11	18.0	20	1	CP35_PAPSP	P80556 papio sp. (345	9	14.8	9	1	BUK_CLOPA	P81337 clostridium
273	11	18.0	20	1	LEC3_ARTIN	P18673 artocarpus	346	9	14.8	9	1	FARP_CALSI	P38495 callinectes
274	11	18.0	20	1	THIO_CANFA	P99505 canis famil	347	9	14.8	9	1	LPCA_STAAR	P36884 staphylococ
275	11	18.0	20	1	TRYL_STREX	P80420 streptomyc	348	9	14.8	9	1	NEUX_RAT	P04277 homo sapien
276	10	16.4	7	1	MSCL_SALTY	P39446 salmonella	349	9	14.8	9	1	FARP_MYTED	P42560 mytilus edu
277	10	16.4	7	1	UH11_RAT	P56576 rattus norv	350	9	14.8	10	1	LSK2_LEUMA	P09039 leucophaea
278	10	16.4	9	1	ISOT_CYPCA	P42893 cyprinus ca	351	9	14.8	10	1	TKNB_RANCA	P22889 rana catesb
279	10	16.4	9	1	NSK1_SARBU	P41492 sarcophaga	352	9	14.8	10	1	UH05_RAT	P56573 rattus norv
280	10	16.4	9	1	OXYA_SCYCA	P42996 scyllorhinu	353	9	14.8	10	1	UP11_CAEEL	P12797 megascolia
281	10	16.4	9	1	OXYA_SQAC	P42999 squaalus aca	354	9	14.8	10	1	CS15_BACSU	P81095 bacillus su
282	10	16.4	9	1	OXYT_BUFRE	P42995 bufo regula	355	9	14.8	11	1	BRK_MEGFL	P12797 megascolia
283	10	16.4	9	1	OXYT_CYPCA	P23879 cyprinus ca	356	9	14.8	11	1	NUHM_CANFA	P49820 canis famil
284	10	16.4	9	1	OXYT_RABIT	P32878 oryctolagus	357	9	14.8	11	1	TKNA_RANCA	P22888 rana catesb
285	10	16.4	9	1	OXYT_RAJCL	P42994 raja clavav	358	9	14.8	11	1	TKNA_RANCA	P22888 rana catesb
286	10	16.4	9	1	OXYV_SQAC	P43000 squaalus aca	359	9	14.8	11	1	TKNA_RANRI	P29207 rana ridibu
287	10	16.4	10	1	CU30_LOCOMI	P11735 locusta mig	360	9	14.8	11	1	TKND_RANCA	P22691 rana catesb
288	10	16.4	10	1	GS09_BACSU	P80243 bacillus su	361	9	14.8	11	1	UN05_CLOPA	P81350 clostridium
289	10	16.4	10	1	PNEU_RAT	P21996 rattus norv	362	9	14.8	12	1	LOSK_LOCOMI	P47733 locusta mig
290	10	16.4	10	1	UPA9_HUMAN	P30095 homo sapien	363	9	14.8	12	1	NUDM_CANFA	P54713 canis famil
291	10	16.4	11	1	MHBL_KLEPN	P80580 klebsiella	364	9	14.8	12	1	TKN1_KASMA	P08613 kassina mac
292	10	16.4	12	1	PSP3_PHYPA	P80662 physcomitre	365	9	14.8	12	1	TKN2_KASMA	P08614 kassina mac
293	10	16.4	12	1	UKA2_HUMAN	P31144 homo sapien	366	9	14.8	12	1	TKN_KASSE	P08611 kassina sen
294	10	16.4	13	1	CRTC_BOVIN	P28489 bos tauris	367	9	14.8	13	1	BRK_PARID	P42717 parapolylbia
295	10	16.4	13	1	PRC_SALTY	P43669 salmonella	368	9	14.8	13	1	CRBL_VESCR	P01518 vespa crabr
296	10	16.4	13	1	PSBP_PINPS	P81668 pinus pinas	369	9	14.8	13	1	CXAL_CONST	P15471 conus stria
297	10	16.4	14	1	LECB_PSOSC	P22584 psophocarpu	370	9	14.8	13	1	FIBB_RABIT	P14478 oryctolagus
298	10	16.4	14	1	LPF2_ECOLI	P06585 escherichia	371	9	14.8	13	1	NPI_LYNST	P80178 lymnaea sta
299	10	16.4	14	1	MY14_PHEVI	P46980 pheretima v	372	9	14.8	13	1	NP4_LYNST	P80181 lymnaea sta
300	10	16.4	14	1	UHA2_CANFA	P99506 canis famil	373	9	14.8	13	1	PSAJ_PEA	P17329 pisum sativ
301	10	16.4	14	1	YMTF_XANCP	Q03397 xanthomonas	374	9	14.8	13	1	SODM_CANFA	P54712 canis famil
302	10	16.4	15	1	ACEA_AGICA	P28467 acinetobact	375	9	14.8	13	1	UN02_PINPS	P81667 pinus pinas
303	10	16.4	15	1	KLOM_LUMTE	P11918 lumbricus t	376	9	14.8	14	1	CXAL_CONMA	P01521 conus magus
304	10	16.4	15	1	LECL_PSOSC	P22582 psophocarpu	377	9	14.8	14	1	DHSL_ANACY	P17874 anabaena cy
305	10	16.4	15	1	MAOX_CHICK	Q92060 gallus gall	378	9	14.8	14	1	ECDC_LYMDI	P80940 lymantria d
306	10	16.4	15	1	OBPA_MAMBR	P81285 mamestra br	379	9	14.8	14	1	FIBA_HORSE	P14452 equus cebal
307	10	16.4	15	1	THL_CLOPA	P81347 clostridium	380	9	14.8	14	1	H4_EUPCR	P80739 euplotes cr
308	10	16.4	15	1	UC27_MAIZE	P80633 zea mays (m	381	9	14.8	14	1	LPER_BACLI	Q04303 bacillus li
309	10	16.4	15	1	UE15_HORVU	P80635 zea mays (m	382	9	14.8	14	1	TKNM_RANMA	P40951 rana marger
310	10	16.4	15	1	UE15_HORVU	P34938 hordeum vul	383	9	14.8	14	1	ULAA_HUMAN	P30039 homo sapien
311	10	16.4	16	1	CXAL_CONEP	P56638 conus episc	384	9	14.8	15	1	ATP2_PINPS	P81663 pinus pinas
312	10	16.4	16	1	MPX_SOLITU	P80501 solanum tub	385	9	14.8	15	1	COXI_THUOB	P80978 thunnus obe
313	10	16.4	16	1	PA2_NAJSP	Q10756 najia sputat	386	9	14.8	15	1	DCNM_PSECA	P19820 pseudomonas
314	10	16.4	16	1	UPAB_HUMAN	P31935 homo sapien	387	9	14.8	15	1	DCNM_PSECH	P19817 pseudomonas
315	10	16.4	17	1	APID_BOMPA	P81464 bombus pasc	388	9	14.8	15	1	FIBA_SYNCA	P14633 syncerus ca
316	10	16.4	17	1	ATPI_PAVLU	P28529 pavlova lut	389	9	14.8	15	1	LEC3_PSOSC	P22585 psophocarpu
317	10	16.4	18	1	CPAX_BOVIN	P22779 bos taurus	390	9	14.8	15	1	LEC3_PSOSC	P22585 psophocarpu
318	10	16.4	19	1	FIBB_LAMGL	P14473 lama glama	391	9	14.8	15	1	GPTS_PELAC	P80564 pelobacter
319	10	16.4	19	1	FIBB_PIG	P14477 sus scrofa	392	9	14.8	15	1	SALC_ONCMY	P81369 oncorhynch
320	10	16.4	19	1	FIBB_TAPTE	P14539 tapirus ter.	393	9	14.8	15	1	SODM_STRGR	P80733 streptomyc
321	10	16.4	19	1	H170_RAT	P21794 rattus norv	394	9	14.8	15	1	UN01_PINPS	P81106 pinus pinas
322	10	16.4	19	1	ITHA_PERAM	P19986 periplaneta	395	9	14.8	16	1	ARCD_PSEPU	P41147 pseudomonas
323	10	16.4	19	1	RL35_LISMO	O53085 listeria mo	396	9	14.8	16	1	CXAA_CONAL	P56639 conus aulic
324	10	16.4	20	1	AROD_AMEME	P46380 amycolotops	397	9	14.8	16	1	CXAB_CONPE	P50984 conus penna
325	10	16.4	20	1	FIBB_FELCA	P14469 felis silve	398	9	14.8	16	1	CXAB_CONPE	P50985 conus penna
326	10	16.4	20	1	GR78_PHAVU	P80089 phaseolus v	399	9	14.8	16	1	FIBA_HYLLA	P14453 hyllobates l

400	9	14.8	16	1	FIBA_ODOHE	P14459 odocollus	473	8	13.1	12	1	CALM_TETHH	Q05055 tetrahymena
401	9	14.8	16	1	FIBA_TAPTE	P14536 tapirus ter	474	8	13.1	12	1	FARI_CALVO	P41869 calliphora
402	9	14.8	16	1	TL17_SPIOL	P81178 spinacia ol	475	8	13.1	12	1	HCYB_MEGCR	Q10584 megathura c
403	9	14.8	17	1	FIBA_PIG	P14460 sus scrofa	476	8	13.1	12	1	PA21_MICFM	P25072 micrurus f
404	9	14.8	18	1	FIBA_CAMDR	P14444 camelus dro	477	8	13.1	12	1	PA2B_VIPBO	P31859 vipera беру
405	9	14.8	18	1	FIBA_LAMGL	P14454 lama glama	478	8	13.1	12	1	UCRH_MOUSE	P99028 mus musculu
406	9	14.8	18	1	FIBA_ANAPL	P12802 anas platyr	479	8	13.1	12	1	UN39_CLOPA	P81359 clostridium
407	9	14.8	18	1	PHPT_PSESE	P25271 pseudotelia	480	8	13.1	13	1	BP37_LEUMA	P81754 leucophaea
408	9	14.8	18	1	RL23_HALCU	P05975 halobacteri	481	8	13.1	13	1	FARB_ASCSU	P43173 ascaris suu
409	9	14.8	19	1	AMY_DERPT	P49274 dermatophag	482	8	13.1	13	1	FIBA_CAVPO	P14445 cavia porce
410	9	14.8	19	1	FIBA_BUBAR	P14243 bubalus arn	483	8	13.1	13	1	RPOC_MVCGA	P47716 mycoplasma
411	9	14.8	19	1	FIBA_BUBBU	P14442 bubalus bub	484	8	13.1	13	1	UHA3_CANFA	P56535 canis famil
412	9	14.8	19	1	FIBA_CERNI	P14447 cervus nipp	485	8	13.1	14	1	HCYA_MEGCR	Q10583 megathura c
413	9	14.8	19	1	FIBA_MUNMU	P14457 muntiacus m	486	8	13.1	14	1	SCR3_LEIQU	P45661 leirurus qui
414	9	14.8	19	1	FIBA_RANTA	P14462 rangifer ta	487	8	13.1	14	1	UN37_CLOPA	P81358 clostridium
415	9	14.8	19	1	FIBA_SHEEP	P14451 ovnis aries	488	8	13.1	15	1	ACT_PINPS	P81085 pinus pinas
416	9	14.8	19	1	FIBB_HORSE	P14471 equus cabal	489	8	13.1	15	1	CBPB_PROAT	P19628 protoperus
417	9	14.8	19	1	G6PI_LACLA	P81181 lactococcus	490	8	13.1	15	1	COG1_RAT	P81563 rattus noiv
418	9	14.8	19	1	RS19_SPICI	O31159 spiroplasma	491	8	13.1	15	1	EFIA_MICCR	P81266 microplitis
419	9	14.8	20	1	ACPB_BOVIN	P80227 bos taurus	492	8	13.1	15	1	ESTJ_MANSE	P19885 manduca sex
420	9	14.8	20	1	FIBB_ELEMA	P14538 elephas max	493	8	13.1	15	1	FGF1_CANFA	P18651 canis famil
421	9	14.8	20	1	GTS2_ASCSU	P48429 ascaris suu	494	8	13.1	15	1	GR78_HORSE	P16392 equus cabal
422	9	14.8	20	1	RL7_NEIME	P80716 neisseria m	495	8	13.1	15	1	LMA2_LOCMI	P38497 locusta mig
423	9	14.8	20	1	SODM_HORVU	P28524 hordeum vul	496	8	13.1	15	1	SODM_ENTAE	P22799 enterobacte
424	8	13.1	4	1	FAR3_HIRME	P42562 hirudo medi	497	8	13.1	15	1	UC25_WAIZE	P80631 zea mays (m
425	8	13.1	4	1	FLRF_HIRME	P42561 hirudo medi	498	8	13.1	16	1	BAII_EUBSP	P32371 eubacterium
426	8	13.1	7	1	FMRF_MACNI	P01162 macrocallis	499	8	13.1	16	1	CFAB_BOVIN	P81187 bos taurus
427	8	13.1	7	1	FARI_HEITI	P41871 helisoma tr	500	8	13.1	16	1	CI4B_BACSU	P81094 bacillus su
428	8	13.1	7	1	FARA_PANRE	P41875 panagrellus	501	8	13.1	16	1	CXA3_CONAL	P56641 conus aulic
429	8	13.1	7	1	FARB_CALVO	P41866 calliphora	502	8	13.1	16	1	DBH3_RHILE	P80605 rhizobium l
430	8	13.1	7	1	GFRP_MOUSE	P99025 mus musculu	503	8	13.1	16	1	FIBA_CERSI	P14335 ceratotheri
431	8	13.1	7	1	MNP1_LEPDE	P42984 leptinotars	504	8	13.1	16	1	FIBA_WANLE	P14455 mandrillus
432	8	13.1	8	1	AL16_CARMA	P81819 carcinus ma	505	8	13.1	16	1	FOR2_MYRGU	P81437 thermocia gu
433	8	13.1	8	1	FAR1_PANRE	P41872 panagrellus	506	8	13.1	16	1	KPYK_THEAC	P20044 thermoplasm
434	8	13.1	8	1	FAR7_ASCSU	P43171 ascaris suu	507	8	13.1	16	1	KTRC_AREMA	P11917 arenicola m
435	8	13.1	8	1	FAR8_CALVO	P41863 calliphora	508	8	13.1	16	1	LPHI_ECOLI	P30358 escherichia
436	8	13.1	8	1	NPB_BOVIN	P15507 bos taurus	509	8	13.1	16	1	PGTL_PELAC	P80363 peibacter
437	8	13.1	9	1	FARI_CALVO	P41856 calliphora	510	8	13.1	16	1	RIPK_TRIKI	P16093 trichosanthe
438	8	13.1	9	1	FAR2_CALVO	P41857 calliphora	511	8	13.1	16	1	YMOR_PSEPU	Q02210 pseudomonas
439	8	13.1	9	1	FAR2_PANRE	P41873 panagrellus	512	8	13.1	17	1	ARGD_SALTY	P40732 salmonella
440	8	13.1	9	1	FAR3_CALVO	P41858 calliphora	513	8	13.1	17	1	ITHB_HIRME	P28502 hirudo medi
441	8	13.1	9	1	FAR4_CALVO	P41859 calliphora	514	8	13.1	17	1	NUAM_TRIRU	Q36834 trichophyto
442	8	13.1	9	1	FAR5_ASCSU	P43170 ascaris suu	515	8	13.1	17	1	PC24_BRANA	P81097 brassica na
443	8	13.1	9	1	FAR5_CALVO	P41860 calliphora	516	8	13.1	17	1	PROP_SALTY	P40862 salmonella
444	8	13.1	9	1	FAR6_CALVO	P41861 calliphora	517	8	13.1	17	1	PSBL_SYNVU	P12241 synechococc
445	8	13.1	9	1	FAR7_CALVO	P41862 calliphora	518	8	13.1	18	1	AROF_STRRM	P80575 streptomyce
446	8	13.1	9	1	FAR9_ASCSU	P43172 ascaris suu	519	8	13.1	18	1	FMS1_ECOLI	P20860 escherichia
447	8	13.1	9	1	FARD_CALVO	P41868 calliphora	520	8	13.1	18	1	HEX_ADECU	P35985 canine aden
448	8	13.1	9	1	FIBB_PAPAN	P19344 papio anubi	521	8	13.1	18	1	HSTB_ECOLI	P01360 escherichia
449	8	13.1	9	1	FLA2_TREHY	P80159 treponema h	522	8	13.1	18	1	LUXB_XRYAS	P18300 kryptophana
450	8	13.1	9	1	NEUU_CAVPO	P34966 cavia porce	523	8	13.1	18	1	RL24_PROVU	P20032 proteus vul
451	8	13.1	9	1	OXYT_OCTVU	P80027 octopus vul	524	8	13.1	18	1	RL24_SALTY	P37438 salmonella
452	8	13.1	9	1	ULAK_MOUSE	P99031 mus musculu	525	8	13.1	18	1	RL24_SERMA	P49624 serratia ma
453	8	13.1	9	1	UPA7_HUMAN	P30033 homo sapien	526	8	13.1	19	1	CXA2_CONST	P28879 conus stria
454	8	13.1	10	1	FARC_CALVO	P41867 calliphora	527	8	13.1	19	1	LCRP_PETMA	Q10996 petromyzon
455	8	13.1	10	1	FARP_LOCMI	P38553 locusta mig	528	8	13.1	19	1	LPGE_ECOLI	P33236 escherichia
456	8	13.1	10	1	FARP_MANSE	P81523 manduca sex	529	8	13.1	19	1	LPRM_STAUA	P03063 staphylococ
457	8	13.1	10	1	LCMS_LEUMA	P21144 leucophaea	530	8	13.1	19	1	NS2_MYCTU	P81136 mycobacteri
458	8	13.1	10	1	NEMS_DROME	P41494 drosophila	531	8	13.1	19	1	NUO6_SOLTU	P80729 solanum tub
459	8	13.1	10	1	PSBF_CAPAN	Q03367 capsicum an	532	8	13.1	19	1	PHLC_STAIN	P80324 staphylococ
460	8	13.1	10	1	RCA_PINPS	P81084 pinus pinas	533	8	13.1	20	1	ALAT_PIG	P13191 sus scrofa
461	8	13.1	10	1	SP34_DICMU	P81545 dictyosteli	534	8	13.1	20	1	COG2_CHIOP	P34154 chionocete
462	8	13.1	10	1	TKNB_ONCMY	P28500 oncorhynch	535	8	13.1	20	1	COG3_CHIOP	P34155 chionocete
463	8	13.1	10	1	TKN_PHYBI	P08610 phyllomedus	536	8	13.1	20	1	COGA_PARCM	P20732 paralichode
464	8	13.1	11	1	COXA_CANFA	P99501 canis famil	537	8	13.1	20	1	COGB_PARCM	P20733 paralichode
465	8	13.1	11	1	ESI_RAT	P56571 rattus norv	538	8	13.1	20	1	COGC_PARCM	P20734 paralichode
466	8	13.1	11	1	FAR9_CALVO	P41864 calliphora	539	8	13.1	20	1	LECB_TRIHO	P36331 iris hollan
467	8	13.1	11	1	NIFS_BRAJA	P70303 bradyrhizob	540	8	13.1	20	1	LPF3_HUMAN	P56643 homo sapien
468	8	13.1	11	1	POQC_PSEFL	P55173 pseudomonas	541	8	13.1	20	1	MDH_MIGGL	P19979 microtetras
469	8	13.1	11	1	TKN4_PSEGU	P42989 pseudophryn	542	8	13.1	20	1	OK11_TRIOK	P20005 trimeresuru
470	8	13.1	11	1	TKN5_PSEGU	P42990 pseudophryn	543	8	13.1	20	1	PGK_CLOPA	P81346 clostridium
471	8	13.1	11	1	TKNA_CHICK	P19850 gallus gall	544	8	13.1	20	1	PORC_METTM	P80302 methanobact
472	8	13.1	11	1	UXB2_YEAST	P99013 saccharomyc	545	8	13.1	20	1	PSAK_PSA	P17226 pisum sativ

546	8	13.1	20	1	PSAL_SYNNU	P25937	synecococc	619	7	11.5	13	1	ORCK_ORCLI	P37086	orconectes
547	8	13.1	20	1	PYRR_PYRAP	P37362	pyrrhocoris	620	7	11.5	13	1	UHAI_HUMAN	P40928	homo sapien
548	8	13.1	20	1	TRY8_ECOLI	P33789	escherichia	621	7	11.5	13	1	UN41_CLOPA	P81360	clostridium
549	8	13.1	20	1	VI01_VACCV	P16714	vaccinia vi	622	7	11.5	14	1	COCO_LINPO	P35586	limulus pol
550	5	11.5	5	1	AL14_CARMA	P81817	carcinus ma	623	7	11.5	14	1	MY14_EISFO	P46979	eisenia foe
551	7	11.5	5	1	BIOB_SALTY	P12678	salmonella	624	7	11.5	14	1	PH1_PRUSE	P29263	prunus sero
552	7	11.5	5	1	TPIS_CANFA	P54714	canis famil	625	7	11.5	14	1	SODN_STRGO	P80735	streptomyce
553	7	11.5	6	1	ACPH_RABIT	P25154	oryctolagus	626	7	11.5	14	1	SODN_STRGR	P80732	streptomyce
554	7	11.5	6	1	CIP1_MYTED	P13736	mytilus edu	627	7	11.5	14	1	SODN_STRSQ	P80734	streptomyce
555	7	11.5	6	1	CIP2_MYTED	P13737	mytilus edu	628	7	11.5	14	1	TAT_HV1W2	P12509	human immun
556	7	11.5	7	1	ALL2_CARMA	P81805	carcinus ma	629	7	11.5	14	1	TAT_HV128	P12511	human immun
557	7	11.5	7	1	ALL3_CARMA	P81806	carcinus ma	630	7	11.5	14	1	UN04_CLOPA	P81349	clostridium
558	7	11.5	7	1	ALL4_CARMA	P81807	carcinus ma	631	7	11.5	14	1	UN46_CLOPA	P81362	clostridium
559	7	11.5	7	1	ALL5_CARMA	P81808	carcinus ma	632	7	11.5	14	1	ALB2_TRASC	P81189	trachemys s
560	7	11.5	7	1	CCF1_ENTFA	P20104	enterococcu	633	7	11.5	15	1	CXA2_CONAL	P56640	conus aulic
561	7	11.5	7	1	UF03_MOUSE	P38641	mus musculus	634	7	11.5	15	1	CYSK_CLOPA	P81340	clostridium
562	7	11.5	7	1	UN06_PINPS	P81675	pinus pinas	635	7	11.5	15	1	ESTB_SCHGA	P81011	schizaphis
563	7	11.5	8	1	AL12_CARMA	P81815	carcinus ma	636	7	11.5	15	1	FIBA_ANAPL	P12801	anas platyr
564	7	11.5	8	1	AL15_CARMA	P81818	carcinus ma	637	7	11.5	15	1	LPL_THETH	P21234	thermus aqr
565	7	11.5	8	1	AL18_CARMA	P81821	carcinus ma	638	7	11.5	15	1	MCRA_MEITE	P22948	methanosarc
566	7	11.5	8	1	ALL5_CALVO	P41841	calliphora	639	7	11.5	15	1	METK_MAIZE	P80616	zea mays (m
567	7	11.5	8	1	ALL7_CARMA	P81809	carcinus ma	640	7	11.5	15	1	PH3_PRUSE	P29265	prunus sero
568	7	11.5	8	1	ALL8_CARMA	P81811	carcinus ma	641	7	11.5	15	1	SCOT_RAT	P01159	rattus norv
569	7	11.5	8	1	ALL9_CARMA	P81812	carcinus ma	642	7	11.5	15	1	TAL1_TREBR	P34070	tremella br
570	7	11.5	8	1	COXG_RAT	P80430	rattus norv	643	7	11.5	15	1	UC28_MAIZE	P80634	zea mays (m
571	7	11.5	8	1	GLUR_HUMAN	P02729	homo sapien	644	7	11.5	16	1	ALRX_PSEPU	P17916	pseudomonas
572	7	11.5	8	1	UC26_MAIZE	P80632	zea mays (m	645	7	11.5	16	1	CXA2_CONMA	P36636	conus magus
573	7	11.5	8	1	UF06_MOUSE	P38644	mus musculus	646	7	11.5	16	1	FENR_STRGR	P24134	streptomyce
574	7	11.5	8	1	UH09_RAT	P56575	rattus norv	647	7	11.5	16	1	ODPB_SOLTU	P81419	solanum tub
575	7	11.5	8	1	UPAA_HUMAN	P30096	homo sapien	648	7	11.5	16	1	PH2_PRUSE	P29264	prunus sero
576	7	11.5	9	1	AL10_CARMA	P81813	carcinus ma	649	7	11.5	16	1	TRYP_FELCA	P81071	fella silve
577	7	11.5	9	1	FIBB_ERYPA	P19346	erythrocebu	650	7	11.5	16	1	FLAW_AZOC	P30002	azotobacter
578	7	11.5	9	1	OXYF_SCYCA	P42997	scyllorhinu	651	7	11.5	17	1	RM35_YEAST	P36530	saccharomyc
579	7	11.5	9	1	OXYT_EISFO	P42998	eisenia foe	652	7	11.5	17	1	SRY_URSAR	P36396	ursus arcto
580	7	11.5	9	1	TAL3_PICJA	P17441	pichia jadi	653	7	11.5	17	1	UN15_CLOPA	P81354	clostridium
581	7	11.5	9	1	TKC1_CALVO	P41517	calliphora	654	7	11.5	18	1	A2M_OCTVU	P30800	octopus vul
582	7	11.5	9	1	TKL1_LOCFI	P16223	locusta mig	655	7	11.5	18	1	AGI_EUPCH	P33888	euphorbia c
583	7	11.5	9	1	ULAD_HUMAN	P31929	homo sapien	656	7	11.5	18	1	AGI_EUPMA	P33889	euphorbia m
584	7	11.5	9	1	XYLA_STRSQ	P19149	streptomyce	657	7	11.5	18	1	AHD2_TETPY	P35430	tetrahymena
585	7	11.5	10	1	AL19_CARMA	P81822	carcinus ma	658	7	11.5	18	1	CXA1_CONER	P50982	conus ermin
586	7	11.5	10	1	AMPN_RELAM	P81731	helicoverpa	659	7	11.5	18	1	DRPH_UCAPU	P08871	uca pugilat
587	7	11.5	10	1	ESTA_SCHGA	P81012	schizaphis	660	7	11.5	18	1	MCRE_MEITE	P22949	methanosarc
588	7	11.5	10	1	PKCK_FASHE	P80525	fasciola he	661	7	11.5	18	1	PSAT_SPIOL	P17228	spinacia ol
589	7	11.5	10	1	O2OB_COMTE	P80465	comamonas t	662	7	11.5	18	1	RS4_PSEAE	OS2759	pseudomonas
590	7	11.5	10	1	SPI_HALRO	Q10997	halocynthia	663	7	11.5	18	1	SFAH_HELAN	P81098	helianthus
591	7	11.5	10	1	SYK_CAMUP	Q46464	campylobact	664	7	11.5	18	1	TKN2_SCYCA	P08609	scyllorhinu
592	7	11.5	10	1	TKL2_LOCFI	P16224	locusta mig	665	7	11.5	18	1	UC03_MAIZE	P80609	zea mays (m
593	7	11.5	10	1	TKL3_LOCFI	P30249	locusta mig	666	7	11.5	18	1	COXR_THUOB	P80984	thunnus obe
594	7	11.5	10	1	TKN1_SCYCA	P08608	scyllorhinu	667	7	11.5	19	1	DHAB_COMTE	P80704	comamonas t
595	7	11.5	10	1	TKNB_CHICK	P19851	gallus gall	668	7	11.5	19	1	DURA_STRGV	P36504	streptovort
596	7	11.5	10	1	TKNK_PIG	P01292	sus scrofa	669	7	11.5	19	1	DURB_STRGW	P36502	streptovort
597	7	11.5	10	1	TKS1_AEDAE	P42634	aedes aegyp	670	7	11.5	19	1	MDH_COMAC	P80539	comamonas a
598	7	11.5	10	1	TKS2_AEDAE	P42635	aedes aegyp	671	7	11.5	19	1	PPBH_PSEAE	P35483	pseudomonas
599	7	11.5	10	1	TMOF_AEDAE	P19425	aedes aegyp	672	7	11.5	19	1	PSBM_SYNVU	P12312	synecococc
600	7	11.5	10	1	URAT_HUMAN	P34990	homo sapien	673	7	11.5	19	1	RL10_CITFR	P43448	citrobacter
601	7	11.5	11	1	HS70_PINPS	P81672	pinus pinas	674	7	11.5	19	1	SCX6_TITBA	P36610	tityus bahi
602	7	11.5	11	1	TKC2_CALVO	P41518	calliphora	675	7	11.5	20	1	ANCR_AGRBI	P33588	agkistrodon
603	7	11.5	11	1	TKN1_UPERU	P08612	uperoleia r	676	7	11.5	20	1	CATA_ACIRA	P81422	acinetobact
604	7	11.5	11	1	TKN2_UPERU	P08616	uperoleia r	677	7	11.5	20	1	CHP_THICU	P80486	thiobacillu
605	7	11.5	11	1	TKNA_ONCMY	P28499	oncorhynch	678	7	11.5	20	1	FLAW_AZOV	P52964	azotobacter
606	7	11.5	11	1	TKN1_PHYFU	P08615	physalaemus	679	7	11.5	20	1	KORC_MEITM	P80906	methanobact
607	7	11.5	12	1	EFTU_PSEAE	P09591	pseudomonas	680	7	11.5	20	1	LPP2_HUMAN	P36642	homo sapien
608	7	11.5	12	1	OPS3_DROVI	P17645	drosophila	681	7	11.5	20	1	LPTR_BACST	P05658	bacillus st
609	7	11.5	12	1	PORD_METTM	P80903	methanobact	682	7	11.5	20	1	LPTR_BACSU	P23053	bacillus su
610	7	11.5	12	1	SOI5_BACSU	P80863	bacillus su	683	7	11.5	20	1	MDH_KIBAR	P19978	kibdelospor
611	7	11.5	12	1	TAL0_TREME	P01371	tremella'ne	684	7	11.5	20	1	MIL7_BOVIN	P35451	bos taurus
612	7	11.5	12	1	Y2PY_ECOLI	P17776	escherichia	685	7	11.5	20	1	MIF_PIG	P80928	sus scrofa
613	7	11.5	13	1	CXAA_CONST	P28878	conus stria	686	7	11.5	20	1	PSAF_MAIZE	P13193	zea mays (m
614	7	11.5	13	1	GER1_HORVU	P28525	hordeum vul	687	7	11.5	20	1	RL10_PROVU	P51411	proteus vul
615	7	11.5	13	1	GER2_HORVU	P28526	hordeum vul	688	7	11.5	20	1	RNKD_PIG	P80551	sus scrofa
616	7	11.5	13	1	NP2_LYMST	P80179	lymnaea sta	689	7	11.5	20	1	SAMP_PLEPL	P20677	pleuronecte
617	7	11.5	13	1	NP3_LYMST	P80180	lymnaea sta	690	7	11.5	20	1	SODF_PASPI	P81527	pasteurella
618	7	11.5	13	1	NP5_LYMST	P80182	lymnaea sta	691	7	11.5	20	1	STYA_STYCL	P81469	styeala ciav

692 7 11.5 20 1 STYB_STYCL 111
693 7 11.5 20 1 SYR_RAT 111
694 7 11.5 20 1 TENB_ACTTE 111
695 7 11.5 20 1 TPX_CLOPA 111
696 5 9.8 5 1 TRM3_ECOLI 9.8
697 6 9.8 6 1 THOP_SARBU 9.8
698 6 9.8 6 1 UN06_CLOPA 9.8
699 6 9.8 6 1 VP19_HSVIK 9.8
700 6 9.8 6 1 CHOX_ALCSP 9.8
701 6 9.8 7 1 CIA_ENTFA 9.8
702 6 9.8 7 1 IGAO_DACDE 9.8
703 6 9.8 8 1 ACT_CARMA 9.8
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708 6 9.8 8 1 UPAL_HUMAN 9.8
709 6 9.8 8 1 CANP_CARMA 9.8
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712 6 9.8 9 1 DCML_PSECF 9.8
713 6 9.8 9 1 DNF1_LOCM1 9.8
714 6 9.8 9 1 FIBB_MACFU 9.8
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725 6 9.8 10 1 RRPL_PHODV 9.8
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794 6 9.8 15 1 UBL1_MONDO 111
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806 6 9.8 16 1 HP29_SARPE 111
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838	19	1	UKAL_HUMAN	P31940	homo sapien	911	5	8.2	13	1	P60_CANFA	P49818	canis faml
839	20	1	BULB_NARPS	P80554	narcissus p	912	5	8.2	13	1	PSAE_PEA	P20118	pisum sativ
840	20	1	CUDP_VERCH	P80406	verticillu	913	5	8.2	13	1	YCIA_SALTY	P25344	salmonella
841	20	1	DCMS_PSECF	P19515	pseudomonas	914	5	8.2	14	1	ATP6_SPIOL	P80086	spinacia ol
842	20	1	DNAK_CLOPA	P81341	clostridium	915	5	8.2	14	1	FIBB_WANLE	P14474	mandrillus
843	20	1	DNAK_MYCAV	P80462	mycobacteri	916	5	8.2	14	1	KPPI_SELMI	P25933	selenastrum
844	20	1	DNAK_THIFE	P29133	thiobacillu	917	5	8.2	14	1	SAP2_ARBPU	P11760	arbacia pun
845	20	1	FLA2_SPIAU	P21985	spirochaeta	918	5	8.2	14	1	UC15_WAIZE	P80621	zea mays (m
846	20	1	FRE3_LITIN	P56249	litoria inf	919	5	8.2	14	1	UHAI_CANFA	P99503	canis faml
847	20	1	HELT_HELHO	P46893	heloderma h	920	5	8.2	14	1	YGDH_THEAC	Q05213	thermoplasm
848	20	1	LIC_FELCA	P37155	felis silve	921	5	8.2	14	1	AH2_PRUSE	P29260	prunus sero
849	20	1	PSBW_WHEAT	P55967	trititum ae	922	5	8.2	15	1	GUAN_DIDMA	P41032	salmonella
850	20	1	SUCD_PSEAE	Q51567	pseudomonas	923	5	8.2	15	1	CYST_SALTY	P55936	didelphis m
851	20	1	TENA_ACTTE	P30833	actinia ten	924	5	8.2	15	1	ITRB_ALBUJ	P24927	albizzia ju
852	20	1	YOAH_KLEAE	P56506	klebsiella	925	5	8.2	15	1	KPPI_SELMI	P25934	selenastrum
853	4	1	EOSI_HUMAN	P02731	homo sapien	926	5	8.2	15	1	LEU3_SULS7	P50455	sulfolobus
854	4	1	TUFT_HUMAN	P01858	homo sapien	927	5	8.2	15	1	PDGB_PIG	P20034	sus scrofa
855	5	1	UC22_MAIZE	P80628	zea mays (m	928	5	8.2	15	1	PGKH_PHYPA	P80659	physcomitri
856	5	1	CARP_MYTED	P10420	mytilus edu	929	5	8.2	15	1	PLAS_MICAE	P10625	microcystis
857	7	1	LANC_CARUI	P36960	carinabacter	930	5	8.2	15	1	PRP_MYCBO	P80149	mycobacteri
858	7	1	MYOM_APLCA	P15513	aplysia cal	931	5	8.2	15	1	UC06_WAIZE	P80612	zea mays (m
859	7	1	UF04_MOUSE	P38642	mus musculus	932	5	8.2	15	1	AH1_PRUSE	P11921	eleginus gr
860	8	1	LMT2_LOCOMI	P22396	locusta mig	933	5	8.2	16	1	ANP8_ELEGR	P19259	prunus sero
861	8	1	LPK_LEUMA	P13049	leucophaea	934	5	8.2	16	1	H5_COTJA	P18638	coturnix co
862	8	1	NS3_MYCTU	P81152	mycobacteri	935	5	8.2	16	1	PGK_VIBCH	P96154	vibrio chol
863	8	1	RSI_ERWCH	P37985	erwinia chr	936	5	8.2	16	1	RBL_CAPAN	P27063	capsicum an
864	9	1	SAP_STOVA	P24947	stomopneute	937	5	8.2	16	1	RBL_CUCSA	P27064	cucumis sat
865	9	1	TRF4_LEUMA	P81736	leucophaea	938	5	8.2	16	1	RBL_VIGSI	P27067	vigna sinen
866	9	1	UF02_MOUSE	P38640	mus musculus	939	5	8.2	16	1	UVSK_BPT6	Q06728	bacteriophage
867	9	1	ULAH_HUMAN	P31934	homo sapien	940	5	8.2	16	1	A4SK_MYCBO	P80069	mycobacteri
868	9	1	UN19_CLOPA	P81355	clostridium	941	5	8.2	17	1	ALYS_MYCPH	P81328	mycobacteri
869	9	1	UPA3_HUMAN	P30089	homo sapien	942	5	8.2	17	1	JHBP_PLAVG	P56675	platyprepia
870	9	1	YBFR_AZOVI	P25825	azotobacter	943	5	8.2	17	1	MDH_ACIDE	P80340	acidovorax
871	10	1	AH3_PRUSE	P29261	prunus sero	944	5	8.2	17	1	TRP2_LEUMA	P81733	leucophaea
872	10	1	COX4_THUOB	P80971	thunus obe	945	5	8.2	17	1	YALA_TRYBB	P17961	trypanosoma
873	10	1	COXA_ONCMY	P80328	oncorhynch	946	5	8.2	18	1	FIXA_RHILE	P14313	rhizobium l
874	10	1	COXQ_RABIT	P80336	oryctolagus	947	5	8.2	18	1	OBP_HYACE	P34172	hyalophora
875	10	1	ESL_LACCA	P81758	lactobacill	948	5	8.2	18	1	YMDB_CHLAU	Q45827	chloroflexu
876	10	1	FIBB_CERSI	P14537	ceratotheri	949	5	8.2	18	1	PHSL_DESBN	P81336	clostridium
877	10	1	GAJU_HUMAN	P01358	homo sapien	950	5	8.2	19	1	AD_CLOPA	P11920	eleginus gr
878	10	1	GLEM_HUMAN	P02728	homo sapien	951	5	8.2	19	1	ANP7_ELEGR	P99504	canis faml
879	10	1	LPK2_LOCOMI	P41488	locusta mig	952	5	8.2	19	1	ATPB_CANFA	Q09148	sarcophaga
880	10	1	MALE_KLEPN	Q05564	klebsiella	953	5	8.2	19	1	COOT_SARBU	P14440	antilocapra
881	10	1	ODP2_BOVIN	P11180	bos taurus	954	5	8.2	19	1	FIBA_ANTAM	P49328	cavia porce
882	10	1	PAF1_PARMA	P81863	pardachirus	955	5	8.2	19	1	FMOL_CAVPO	P13066	desulfovibr
883	10	1	PNEU_HUMAN	P22103	homo sapien	956	5	8.2	19	1	PHSL_DESBN	P42047	cucumis sat
884	10	1	PORB_METTM	P80901	methanobact	957	5	8.2	19	1	PSAE_CUCSA	P24365	streptococ
885	10	1	TKL4_LOCOMI	P30250	locusta mig	958	5	8.2	19	1	TRPB_KLEAE	P14552	klebsiella
886	10	1	TKU2_UREUN	P40752	urechis uni	959	5	8.2	20	1	ATP4_SPIOL	P80085	spinacia ol
887	10	1	TRP5_LEUMA	P81737	leucophaea	960	5	8.2	20	1	CD4_SHEEP	P05542	ovis aries
888	10	1	TRF6_LEUMA	P81738	leucophaea	961	5	8.2	20	1	COXB_THUOB	P80974	thunus obe
889	10	1	TRP7_LEUMA	P81739	leucophaea	962	5	8.2	20	1	COXQ_ONCMY	P80335	oncorhynch
890	10	1	TRP8_LEUMA	P81740	leucophaea	963	5	8.2	20	1	EMR6_MOUSE	P80983	thunus obe
891	10	1	TRP9_LEUMA	P81741	leucophaea	964	5	8.2	20	1	FRHA_METBA	P80489	methanosarc
892	10	1	UPA2_HUMAN	P30088	homo sapien	965	5	8.2	20	1	PYR2_PSEFL	P56586	pseudomonas
893	10	1	URAI_HUMAN	P32118	homo sapien	966	5	8.2	20	1	RECX_AZOVI	P37863	azotobacter
894	10	1	URE3_MORMO	P17339	morganelia	967	5	8.2	20	1	UC33_WAIZE	P80639	zea mays (m
895	10	1	UXAL_CHLTR	P38002	chlamydia t	968	5	8.2	20	1	GRWM_HUMAN	P01157	homo sapien
896	11	1	BPBP_AGKHA	P01021	agkistrodon	969	5	8.2	20	1	LUXE_VIBFI	P24272	vibrio fisc
897	11	1	BPP_AGKHP	P04562	agkistrodon	970	5	8.2	20	1	THYL_PIG	P01151	sus scrofa
898	11	1	Q2OA_COMTE	P80464	comamonas t	971	5	8.2	20	1	ACH1_ACHFU	P35904	achatinna fu
899	11	1	TKNA_SCYCA	P41333	scyllorhinu	972	5	8.2	20	1	RM01_FEAST	P36515	saccharomyc
900	12	1	LMT1_LOCOMI	P22395	locusta mig	973	4	6.6	3	1	CADI_ENTFA	P13268	enterococcu
901	12	1	XYLA_STRVN	P14405	streptomyce	974	4	6.6	4	1	CPD1_ENTFA	P13269	enterococcu
902	13	1	ACT7_SOYBN	P15987	glycine max	975	4	6.6	4	1	VGLG_HSV2B	P81780	herpes simp
903	13	1	AH4_PRUSE	P29262	prunus sero	976	4	6.6	4	1	MOSF_CLYJA	P19853	clypeaster
904	13	1	CPI_APLCA	Q10998	aplysia cal	977	4	6.6	4	1	SAMP_MUSCMY	P19095	musculus ca
905	13	1	CRTC_RANES	P31832	rana escul	978	4	6.6	4	1	COXH_ONCMY	P80331	oncorhynch
906	13	1	CXA2_CONGE	P01520	conus geogr	979	4	6.6	4	1	COXM_RAT	P80431	rattus norv
907	13	1	FIBB_HYLLA	P14472	hylobates l	980	4	6.6	9	1			
908	13	1	IDHA_CANFA	P54836	canis faml	981	4	6.6	9	1			
909	13	1	NUPM_HUMAN	P51970	homo sapien	982	4	6.6	10	1			
910	13	1	ODFA_CANFA	P49823	canis faml	983	4	6.6	10	1			

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984 4 6.6 10 1 NSL_MYCTU
985 4 6.6 10 1 SLAP_BACTG
986 4 6.6 10 1 UPAB_HUMAN
987 4 6.6 10 1 DXA2_CHLTR
988 4 6.6 10 1 XYNB_DICB4
989 4 6.6 11 1 MORN_HUMAN
990 4 6.6 12 1 UH03_RAT
991 4 6.6 13 1 CRBL_ICASP
992 4 6.6 13 1 CRBL_VESAN
993 4 6.6 13 1 CRBL_VESLE
994 4 6.6 13 1 CRBL_VESMA
995 4 6.6 13 1 CRBL_VESTR
996 4 6.6 13 1 CRBL_VESXA
997 4 6.6 13 1 EP65_HUMAN
998 4 6.6 13 1 HPA1_RANES
999 4 6.6 13 1 HPB9_RANES
1000 4 6.6 14 1 CRBL_VESOR

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ALIGNMENTS

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RESULT 1
LPW_BRELA STANDARD; PRT; 17 AA.
ID LPW_BRELA
AC P06356;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRP OPERON LEADER PEPTIDE.
GN TRPL.
OS Corynebacterium lactofermentum, and
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae.
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-B.LACTOFERMENTUM;
RX MEDLINE; 87117512.
RA MATSUI K., SANO K., OHTSUBO E.;
RT "Complete nucleotide and deduced amino acid sequences of the
RT Brevibacterium lactofermentum tryptophan operon.";
RL Nucleic Acids Res. 14:10113-10114(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-B.LACTOFERMENTUM;
RX MEDLINE; 88032866.
RA MATSUI K., MIWA K., SANO K.;
RT "Two single-base-pair substitutions causing desensitization to
RT tryptophan feedback inhibition of anthranilate synthase and enhanced
RT expression of tryptophan genes of Brevibacterium lactofermentum.";
RL J. Bacteriol. 169:5330-5332(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-B.LACTOFERMENTUM;
RX MEDLINE; 87277409.
RA SANO K., MATSUI K.;
RT "Structure and function of the trp operon control regions of
RT Brevibacterium lactofermentum, a glutamic-acid-producing bacterium.";
RL Gene 53:191-200(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-C.GLUTAMICUM; STRAIN-ATCC 13059 / AS019;
RX MEDLINE; 91088299.
RA HEERY D.M., DUNICAN L.K.;
RT "Nucleotide sequence of the Corynebacterium glutamicum trpE gene.";
RL Nucleic Acids Res. 18:7138-7138(1990).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
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DR EMBL; X04960; CAA28622.1; -.
DR EMBL; M17892; AAB59110.1; -.
DR EMBL; M16663; -; NOT_ANNOTATED_CDS.
DR EMBL; X55994; CAA39466.1; -.
DR PIR; A29458; A29458.
DR PIR; A29834; A29834.
DR PIR; A34723; A24723.
DR PIR; S13087; S13087.
KW Tryptophan biosynthesis; Leader peptide.
SQ SEQUENCE 17 AA; 2112 MW; 4C1F02F2 CRC32;

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Query Match 37.7%; Score 23; DB 1; Length 17;
 Best Local Similarity 75.0%; Pred. No. 2.7e+02;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNRW 4
 DB 12 WNRW 15

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RESULT 2
CAT3_FASHE STANDARD; PRT; 19 AA.
ID CAT3_FASHE
AC P80532;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PUTATIVE CATHEPSIN L3 (EC 3.4.22.15) (NEWLY EXCYSTED JUVENILE PROTEIN
DE 8) (FRAGMENT).
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomatidae; Echinostomata; Fascioloidae;
OC Fasciolidae; Fasciola.
RN [1]
RP SEQUENCE.
RX MEDLINE; 95366993.
RA TKALCEVIC J., ASHMAN K., MEEUSEN E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proteins.";
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -1- FUNCTION: THIOIOL PROTEASE.
CC -1- SUBUNIT: DIMER OF AN HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
CC BONDS (POTENTIAL).
CC -1- SUBCELLULAR LOCATION: LYSOSOMAL (POTENTIAL).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT THE NEWLY EXCYSTED JUVENILE
CC STAGE.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
CC PAPAII FAMILY OF THIOIOL PROTEASES.
DR HSP; P25774; 1BXF.
DR PROSITE; PS00139; THIOIOL_PROTEASE_CYS; PARTIAL.
DR PROSITE; PS00639; THIOIOL_PROTEASE_HIS; PARTIAL.
DR PROSITE; PS00640; THIOIOL_PROTEASE_ASN; PARTIAL.
DR PFAM; PF00112; Peptidase_C1; 1.
KW Hydrolase; Thiol protease; Lysosome.
SQ NON_TER 19
SQ SEQUENCE 19 AA; 2242 MW; 363E4116 CRC32;

```

Query Match 36.1%; Score 22; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 4.4e+02;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 WNRW 9
 DB 7 DWREYGV 14

RESULT 3
ELAS_GADMO STANDARD; PRT; 20 AA.
AC P32197;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE ELASTASE (EC 3.4.21.-) (FRAGMENT).
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Paracanthopterygii; Gadiformes;
OC Gadoidae; Gadidae; Gadus.
RN [1]
RP SEQUENCE.
RC TISSUE-INTESTINE;
RX MEDLINE: 93298789.
RA ASGRINSON B., BYARNASON J.B.;
RT "Properties of elastase from Atlantic cod, a cold-adapted
RT proteinase.";
RL Biochim. Biophys. Acta 1164:91-100(1993).
CC -!- FUNCTION: DIGESTS MOST RAPIDLY AT THE C-TERMINAL SIDE OF ALANINE
CC RESIDUES, BUT ALSO CLEAVES AT VALINE AND LEUCINE RESIDUES.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY. BELONGS TO THE ELASTASE SUBFAMILY.
DR PIR: S33787; S33787.
DR PROSITE: PS00134; TRYPSIN_HIS; PARTIAL.
DR PROSITE: PS00135; TRYPSIN_SER; PARTIAL.
KW Hydrolase; Serine protease.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2284 MW; BAE54476 CRC32;

Query Match 34.4%; Score 21; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 6.6e+02;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 WNWNR 4
|:|
DB 12 WPMQ 15

RESULT 4
ID UR2A_CATCO STANDARD; PRT; 12 AA.
AC P04558;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-AUG-1988 (Rel. 08, Last annotation update)
DE UROTENSIN IIA.
OS Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cobitoidea; Catostomidae; Catostomus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 84041959
RA MCMASTER D., LEDERIS K.;
RT "Isolation and amino acid sequence of two urotensin II peptides from
RT Catostomus commersoni urophyses.";
RL Peptides 4:367-373(1983).
CC -!- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR.
DR PIR: JS0423; JS0423.
DR PROSITE: PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1336 MW; 6920AC0A CRC32;

Query Match 32.8%; Score 20; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 WRY 5
|:|
DB 8 WKY 10

RESULT 5
ID UR2B_CATCO STANDARD; PRT; 12 AA.
AC P04559;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-AUG-1988 (Rel. 08, Last annotation update)
DE UROTENSIN IIB.
OS Catostomus commersoni (White sucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cobitoidea; Catostomidae; Catostomus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 84041959.
RA MCMASTER D., LEDERIS K.;
RT "Isolation and amino acid sequence of two urotensin II peptides from
RT Catostomus commersoni urophyses.";
RL Peptides 4:367-373(1983).
CC -!- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR.
DR PIR: JS0424; JS0424.
DR PROSITE: PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1437 MW; BFC88060 CRC32;

Query Match 32.8%; Score 20; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 WRY 5
|:|
DB 8 WKY 10

RESULT 6
ID UR2B_CYPCA STANDARD; PRT; 12 AA.
AC P04561;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE UROTENSIN II, BETA.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cypriniinae; Cyprinus.
RN [1]
RP SEQUENCE.
RX MEDLINE: 84041959
RA MCMASTER D., LEDERIS K.;
RL (In) Rich D.H., Gross E. (eds.);
RL Proceedings of the 7th american peptide symposium, pp.69-72,
RL Pierce Chemical Co., Rockford IL. (1981).
CC -!- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR.
DR PROSITE: PS00984; UROTENSIN_II; 1.
KW Hormone.
FT VARIANT 2 2 G -> S.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1407 MW; A1E73729 CRC32;

Query Match 32.8%; Score 20; DB 1; Length 12;

Best Local Similarity 66.7%; Pred. No. 5.7e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 2; Conservative 1;

QY 3 WRY 5
|:|
Db 8 WKY 10

RESULT 7
UR2_GILMI STANDARD; PRT; 12 AA.
AC P01147;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 01-AUG-1988 (Rel. 08, Last annotation update)
DE UROTENSIN II.
OS Gillichthys mirabilis (Long-jawed mudsucker).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
OC Perciformes; Gobioidae; Gobiidae; Gillichthys.
RN [1]
RP SEQUENCE.
RX MEDLINE: 81054904.
RA PEARSON D., SHIVELY J.E., CLARK B.R., GESCHWIND I.I., BARKLEY M.,
RA NISHIOKA R., BERN H.A.;
RT "Urotensin II: a somatostatin-like peptide in the caudal
RT neurosecretory system of fishes."
RL Proc. Natl. Acad. Sci. U.S.A. 77:5021-5024(1980).
CC -1- FUNCTION: UROTENSIN IS FOUND IN THE TELEOST CAUDAL NEUROSECRETORY
CC SYSTEM. IT HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR.
DR PIR; A01409; UOGM2.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1364 MW; 54AB8448 CRC32;

Query Match 32.8%; Score 20; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WRY 5
|:|
Db 8 WKY 10

RESULT 8
UR2_POLSP STANDARD; PRT; 12 AA.
AC P81022;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE UROTENSIN II.
OS Polyodon spathula (North American paddlefish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Chondrostei; Acipenseriformes; Polyodontidae; Polyodon.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-SPINAL CORD;
RX MEDLINE: 96051494.
RA WAUGH D., YOUSON J., MIMS S.D., SOWER S., CONLON J.M.;
RT "Urotensin II from the river lamprey (Lampetra fluviatilis), the sea
RT lamprey (Petromyzon marinus), and the paddlefish (Polyodon
RT spathula)."
RL Gen. Comp. Endocrinol. 99:323-332(1995).
CC -1- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11 BY SIMILARITY.

SQ SEQUENCE 12 AA; 1410 MW; EB25FC88 CRC32;

Query Match 32.8%; Score 20; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WRY 5
|:|
Db 8 WKY 10

RESULT 9
UR2_SCYCA STANDARD; PRT; 12 AA.
AC P35490;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE UROTENSIN II.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Carcharhiniformes; Scyllorhinidae; Scyllorhinus.
RN [1]
RP SEQUENCE.
RC TISSUE-SPINAL CORD;
RX MEDLINE: 92319231.
RA CONLON J.M., O'HARTE F., SMITH D.D., BALMENT R.J., HAZON N.;
RT "Purification and characterization of urotensin II and parvalbumin
RT from an elasmobranch fish, Scyllorhinus canicula (common dogfish)."
RL Neuroendocrinology 55:230-235(1992).
CC -1- FUNCTION: HAS A SUGGESTED ROLE IN OSMOREGULATION AND AS A
CC CORTICOTROPIN-RELEASING FACTOR. PROBABLY INVOLVED IN SMOOTH
CC MUSCLE STIMULATION.
DR PROSITE; PS00984; UROTENSIN_II; 1.
KW Hormone.
FT DISULFID 6 11
SQ SEQUENCE 12 AA; 1526 MW; FC1F1E9E CRC32;

Query Match 32.8%; Score 20; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.7e+02;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WRY 5
|:|
Db 8 WKY 10

RESULT 10
UR2_RANRI STANDARD; PRT; 13 AA.
AC P33715;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE UROTENSIN II.
OS Rana ridibunda (Laughing frog) (Marsh frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Raninae; Rana.
RN [1]
RP SEQUENCE.
RC TISSUE-BRAIN;
RX MEDLINE: 93075134.
RA CONLON J.M., O'HARTE F., SMITH D.D., TONON M.-C., VAUDRY H.;
RT "Isolation and primary structure of urotensin II from the brain of a
RT tetrapod, the frog Rana ridibunda."
RL Biochem. Biophys. Res. Commun. 188:578-583(1992).
CC -1- FUNCTION: INVOLVED IN SMOOTH MUSCLE STIMULATING AND ION
CC MOBILIZING ACTIVITIES. IT HAS A SUGGESTED ROLE AS A
CC CORTICOTROPIN-RELEASING FACTOR.
CC -1- TISSUE SPECIFICITY: CENTRAL NERVOUS SYSTEM.
DR PIR; PQ0445; PQ0445.

DR PROSITE; PS00984; UROTENSIN_II; 1.
 KW Hormone.
 FT DISULFID 7 12
 SQ SEQUENCE 13 AA; 1520 MW; AE847C9B CRC32;

Query Match 32.8%; Score 20; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 6.2e+02;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 WRY 5
 Db 9 WKY 11

RESULT 11

MAST_PARID
 ID MAST_PARID STANDARD; PRT; 14 AA.
 AC P42716;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE MASTOPARAN.
 OS Parapolybia indica.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Vespoidea; Vespidae; Polistinae; Parapolybia.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RA TOKI T., YASUHARA T., NAKAJIMA T.;
 RT "Isolation and sequential analysis of peptides on the venom sac of
 RT Parapolybia indica."
 RL Eisel Dobutsu 39:105-111(1988).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
 CC THAT COUPLE TO PHOSPHOLIPASE C.
 KW Mast cell degranulation; Venom; Amidation.
 FT MOD_RES 14 14
 SQ SEQUENCE 14 AA; 1619 MW; 60D0EC3 CRC32;

Query Match 31.1%; Score 19; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 9.5e+02;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWR 4
 Db 2 NWK 4

RESULT 12

MAST_VESXA
 ID MAST_VESXA STANDARD; PRT; 14 AA.
 AC P01515;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MASTOPARAN X (MP-X).
 OS Vespa xanthoptera (Japanese hornet).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Vespoidea; Vespidae; Vespinae; Vespa.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RA HIRAI Y., KIWADA M., YASUHARA T., YOSHIDA H., NAKAJIMA T.;
 RT "A new mast cell degranulating peptide homologous to mastoparan in
 RT the venom of Japanese hornet (Vespa xanthoptera).";
 RL Chem. Pharm. Bull. 27:1945-1946(1979).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE; 92304942.

RA WAKAMATSU K., OKADA A., MIYAZAWA T., OHYA M., HIGASHIJIMA T.;
 RT "Membrane-bound conformation of mastoparan-X, a G-protein-activating
 RT peptide.";
 RL Biochemistry 31:5654-5660(1992).
 RN [3]
 RP STRUCTURE BY NMR.
 RX MEDLINE; 98206894.
 RA KUSUNOKI H., WAKAMATSU K., SATO K., MIYAZAWA T., KOHNO T.;
 RT "G protein-bound conformation of mastoparan-X: heteronuclear
 RT multidimensional transferred nuclear overhauser effect analysis of
 RT peptide uniformly enriched with 13C and 15N.";
 RL Biochemistry 37:4782-4790(1998).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
 CC THAT COUPLE TO PHOSPHOLIPASE C.
 DR PIR; A01778; QMVHXX.
 DR PDB; 1A13; 16-FEB-99.
 KW Mast cell degranulation; Venom; Amidation; 3D-structure.
 FT MOD_RES 14 14
 SQ SEQUENCE 14 AA; 1557 MW; F77FF365 CRC32;

Query Match 31.1%; Score 19; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 9.5e+02;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWR 4
 Db 2 NWK 4

RESULT 13

UC08_MAIZE
 ID UC08_MAIZE STANDARD; PRT; 15 AA.
 AC P80614;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF ETIOLATED COLEOPTILE (SPOT 159)
 DE (FRAGMENT).
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
 OC Poaceae; Zea.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=COLEOPTILE;
 RA TOUZET P., RICCARDI F., MORIN C., DAMERVAL C., HUET J.-C.,
 RA PERNOLLET J.-C., ZIVY M., DE VIENNE D.;
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program.";
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.4, ITS MW IS: 38.8 KD.
 CC -1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY
 DR MAIZE-2DPAGE; P80614; COLEOPTILE.
 DR MAIZEDB; 123934; -;
 FT NON_TER 1 1
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1785 MW; AD659C49 CRC32;

Query Match 31.1%; Score 19; DB 1; Length 15;
 Best Local Similarity 42.9%; Pred. No. 1e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NWRYREY 8
 Db 2 DWRNAMY 8

RESULT 14
 TPIS_PINPS

ID TPIS_PINPS STANDARD; PRT; 17 AA.
AC P8166;
DT 13-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (EC 5.3.1.1) (TIM) (FRAGMENTS).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE=NEEDLE;
RX MEDLINE; 99274088.
RA COSTA P., PIONNEAU C., BAUM G., DUBOS C., BAHRMAN N., KREMER A.,
RA FRIGERIO J.-M., PLOMON C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE - DIHYDROXY-
CC ACETONE PHOSPHATE.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).
CC -1- INDUCTION: BY WATER-STRESS.
CC -1- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN
CC (SPOT N139) IS: 5.9, ITS MW IS: 24 KD.
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR PROSITE; PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt; Multigene family.
FT NON_TER 1 1
FT NON_CONS 9 10
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2053 MW; 154A9640 CRC32;

Query Match 31.1%; Score 19; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NWR 4
||:
Db 15 NWK 17

RESULT 15
GONL_ALLMI
ID GONL_ALLMI STANDARD; PRT; 10 AA.
AC P37041; P20407;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GONADOLIBERIN I (GONADOTROPIN-RELEASING HORMONE I) (GNRH-I) (LH-RH I)
DE (LULIBERIN I).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
OC Crocodylidae; Alligatorinae; Alligator.
RN [1]
RP SEQUENCE.
RC TISSUE=BRAIN;
RX MEDLINE; 91352338.
RA LOVEJOY D.A., FISCHER W.H., PARKER D.B., MCRORY J.E., PARK M.,
RA LANCE V., SWANSON P., RIVIER J.E., SHERWOOD N.M.;
RT "Primary structure of two forms of gonadotropin-releasing hormone
RT from brains of the American alligator (Alligator mississippiensis).";
RL Regul. Pept. 33:105-116(1991).
CC -1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS.
CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
DR PIR; A60066; RHAQ1.
DR PROSITE; PS00473; GNRH; 1.

DR PFAM; PF00446; GNRH; 1.
KW Hormone; Amidation; Hypothalamus.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1172 MW; 4DDA2516 CRC32;

Query Match 29.5%; Score 18; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 9.8e+02;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NWR 5
||:
Db 2 HWS 5

Search completed: May 2, 2000, 00:23:22
Job time: 79 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 2, 2000, 00:21:33 ; Search time 14.61 Seconds
(without alignments)
42.711 Million cell updates/sec

Title: US-09-258-947-38
Perfect score: 61
Sequence: 1 WNNRYREYV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 2017

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Listing first 1000 summaries

Database : SPTRMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	27	44.3	17	4	Q16228 homo sapien
2	25	41.0	20	11	Q81714 mus musculu
3	24.5	40.2	19	8	P92689 podospora a
4	24	39.3	19	13	P87484 gallus gall
5	23	37.7	10	10	Q99213 aegilops sq
6	23	37.7	17	2	Q45304 brevibacter
7	23	37.7	18	12	Q73605 human immun
8	23	37.7	18	12	Q73549 human immun
9	23	37.7	18	12	Q73573 human immun
10	23	37.7	18	12	Q73575 human immun
11	23	37.7	18	12	Q73577 human immun
12	23	37.7	18	12	Q73579 human immun
13	23	37.7	18	12	Q73583 human immun
14	23	37.7	18	12	Q73587 human immun
15	23	37.7	18	12	Q73593 human immun
16	23	37.7	18	12	Q73601 human immun
17	23	37.7	18	12	Q73603 human immun
18	23	37.7	18	12	Q73607 human immun
19	23	37.7	18	12	Q73609 human immun
20	23	37.7	18	12	Q73613 human immun

21	23	37.7	18	12	Q73615	human immun
22	23	37.7	18	12	Q73629	human immun
23	23	37.7	18	12	Q73631	human immun
24	23	37.7	18	12	Q73639	human immun
25	23	37.7	18	12	Q73643	human immun
26	23	37.7	18	12	Q73645	human immun
27	23	37.7	18	12	Q73647	human immun
28	23	37.7	18	12	Q73649	human immun
29	23	37.7	18	12	Q73651	human immun
30	23	37.7	18	12	Q73653	human immun
31	23	37.7	18	12	Q73655	human immun
32	23	37.7	19	8	Q92Y71	heterospilu
33	22	36.1	7	10	Q49223	glycine max
34	21	34.4	17	2	P81526	agrobacteri
35	20	32.8	10	2	Q54217	staphylococ
36	20	32.8	13	4	Q16406	homo sapien
37	20	32.8	15	12	Q66543	human herpe
38	20	32.8	18	2	Q92G65	chlamydia t
39	20	32.8	19	6	Q46472	felis silve
40	19	31.1	13	12	Q86129	vesicular s
41	19	31.1	15	10	Q42223	arabidopsis
42	19	31.1	18	12	Q84129	influenza a
43	18	29.5	8	13	P79940	xenopus lae
44	18	29.5	14	2	Q54081	saccharopol
45	18	29.5	17	4	Q15276	homo sapien
46	18	29.5	17	11	Q63995	mus musculu
47	18	29.5	18	2	Q30588	streptomyce
48	18	29.5	18	2	Q68570	streptomyce
49	18	29.5	19	8	Q92YW7	aphidius ro
50	18	29.5	19	8	Q92YW5	jarrow phor
51	18	29.5	20	2	Q47830	ectothiorho
52	17	28.7	12	7	Q7919	pseudotroph
53	17	27.9	8	2	Q85406	coxiella bu
54	17	27.9	9	12	Q69349	herpes simp
55	17	27.9	10	2	Q47561	escherichia
56	17	27.9	11	2	Q56413	escherichia
57	17	27.9	11	4	Q60842	homo sapien
58	17	27.9	12	2	Q50959	neisseria g
59	17	27.9	12	12	Q89243	woodchuck h
60	17	27.9	13	1	Q50831	methanococ
61	17	27.9	13	8	Q95925	porphyra pu
62	17	27.9	15	13	Q90594	gallus gall
63	17	27.9	16	2	Q44543	anabaena va
64	17	27.9	16	12	Q9YQ11	porcine tra
65	17	27.9	17	7	Q30218	homo sapien
66	17	27.9	17	8	Q92YX4	xorides pra
67	17	27.9	17	11	Q62436	mus musculu
68	17	27.9	17	11	P97758	mus musculu
69	17	27.9	17	12	Q89807	epiphyas po
70	17	27.9	18	8	Q78379	theileria a
71	17	27.9	18	8	Q92YW9	agathieila
72	17	27.9	18	8	Q92YV6	bethylidae
73	17	27.9	18	8	Q92Y83	xylocopa vi
74	17	27.9	18	11	P70649	mus musculu
75	17	27.9	19	2	Q44506	anabaena va
76	17	27.9	19	2	Q44608	buchnera ap
77	17	27.9	19	2	Q47079	escherichia
78	17	27.9	19	2	Q47554	escherichia
79	17	27.9	19	8	Q92YW8	ichneutes b
80	17	27.9	19	8	Q92YW3	gnaptodon
81	17	27.9	19	8	Q92YW1	histeromeru
82	17	27.9	19	8	Q92YV7	myrmecia fo
83	17	27.9	19	8	Q92Y86	discomogus ar
84	17	27.9	19	8	Q92Y73	microplitis
85	17	27.9	19	10	Q43370	allium cepa
86	17	27.9	19	11	Q62637	rattus norv
87	17	27.9	19	11	Q62545	mus spretus
88	17	27.9	19	12	Q86950	human herpe
89	17	27.9	20	2	Q50089	mycobacteri
90	17	27.9	20	8	Q92Y85	bombus terr
91	17	27.9	20	8	Q92Y74	mirax sp. c
92	17	27.9	20	8	Q92Y72	sathon sp.
93	17	27.9	20	10	Q82275	arabidopsis

94	17	27.9	20	11	035353	035353 rattus norv	167	14	23.0	19	8	099759	099759 cathartes m
95	17	27.9	20	12	04861	04861 unidentified	168	14	23.0	19	8	099760	099760 cephus col
96	17	27.9	20	12	056842	056842 vibrio chol	169	14	23.0	19	8	099761	099761 chordelles
97	16	26.2	8	11	062721	062721 rattus norv	170	14	23.0	19	8	099762	099762 colaptes au
98	16	26.2	8	12	084156	084156 orf virus.	171	14	23.0	19	8	099763	099763 coccyzus er
99	16	26.2	11	7	077910	077910 oreochromis	172	14	23.0	19	8	099764	099764 colius stri
100	16	26.2	16	12	083960	083960 influenza a	173	14	23.0	19	8	099765	099765 diomedea ni
101	16	26.2	16	12	083967	083967 influenza a	174	14	23.0	19	8	099766	099766 eudromia el
102	16	26.2	16	12	084055	084055 influenza a	175	14	23.0	19	8	099767	099767 fulica amer
103	16	26.2	17	6	007270	007270 mycobacteri	176	14	23.0	19	8	099768	099768 gavia immar
104	16	26.2	17	6	046667	046667 macropus ro	177	14	23.0	19	8	099769	099769 grus canade
105	16	26.2	17	6	09XSG1	09XSG1 bos taurus	178	14	23.0	19	8	099770	099770 gyps fulvus
106	16	26.2	17	12	072017	072017 human immun	179	14	23.0	19	8	099771	099771 meleagris g
107	16	26.2	18	12	069185	069185 human cytom	180	14	23.0	19	8	099772	099772 mycteria am
108	16	26.2	19	2	053311	053311 streptococc	181	14	23.0	19	8	099773	099773 nyctanassa
109	16	26.2	19	12	083965	083965 influenza a	182	14	23.0	19	8	099774	099774 ophiostoma
110	16	26.2	20	4	016129	016129 homo sapien	183	14	23.0	19	8	099775	099775 otus asio.
111	5	25.4	16	8	09XNP6	09XNP6 boophilus m	184	14	23.0	19	8	099776	099776 pandion hal
112	15	24.6	13	3	093824	093824 candida tro	185	14	23.0	19	8	099777	099777 phasianus c
113	15	24.6	14	2	054394	054394 streptomyce	186	14	23.0	19	8	099778	099778 phalacrocor
114	15	24.6	16	2	053399	053399 bacillus th	187	14	23.0	19	8	099779	099779 phoenicopte
115	15	24.6	16	11	092134	092134 mus musculu	188	14	23.0	19	8	099780	099780 podilymbus
116	15	24.6	16	12	000340	000340 vaccinia vi	189	14	23.0	19	8	099781	099781 sphyrapius
117	15	24.6	20	2	049448	049448 mycoplasma	190	14	23.0	19	8	099782	099782 gavia pacif
118	15	24.6	20	11	09WVP3	09WVP3 mus musculu	191	14	23.0	19	8	099783	099783 urocolius m
119	14	23.0	9	4	095574	095574 homo sapien	192	14	23.0	19	8	099784	099784 tauraco har
120	14	23.0	11	7	077880	077880 oreochromis	193	14	23.0	19	8	099785	099785 podiceps ni
121	14	23.0	11	7	077892	077892 oreochromis	194	14	23.0	19	8	099786	099786 cathartes a
122	14	23.0	11	7	077906	077906 oreochromis	195	14	23.0	19	8	099787	099787 tockus eryt
123	14	23.0	11	7	077907	077907 oreochromis	196	14	23.0	19	8	099788	099788 trogon curu
124	14	23.0	11	7	077918	077918 pseudotroph	197	14	23.0	19	8	099789	099789 zenaida mac
125	14	23.0	11	13	090735	090735 gallus gall	198	14	23.0	19	8	099790	099790 centistes s
126	14	23.0	12	8	09XNR6	09XNR6 pylaiaella l	199	14	23.0	19	12	080228	080228 human immun
127	14	23.0	12	11	097733	097733 rattus norv	200	14	23.0	19	12	079581	079581 human immun
128	14	23.0	13	2	050038	050038 mycobacteri	201	14	23.0	19	12	080316	080316 human immun
129	14	23.0	13	8	035793	035793 saccharomyc	202	14	23.0	20	5	Q25281	Q25281 leishmania
130	14	23.0	13	8	099783	099783 caprimulgus	203	14	23.0	20	7	077859	077859 oreochromis
131	14	23.0	13	12	064813	064813 autographa	204	14	23.0	20	8	Q33294	Q33294 zea mays (m
132	14	23.0	14	2	050268	050268 phytoplasma	205	14	23.0	20	12	036978	036978 human papil
133	14	23.0	14	2	052636	052636 escherichia	206	14	23.0	20	12	085636	085636 moloney mur
134	14	23.0	14	9	038469	038469 bacterioph	207	14	23.0	20	12	073917	073917 human immun
135	14	23.0	15	2	052304	052304 escherichia	208	14	23.0	20	12	073918	073918 human immun
136	14	23.0	15	8	035188	035188 nicotiana t	209	13.5	22.1	10	4	Q15342	Q15342 homo sapien
137	14	23.0	16	7	077922	077922 oreochromis	210	13.5	22.1	12	2	Q47048	Q47048 escherichia
138	14	23.0	16	8	034374	034374 daphnia pul	211	13	21.3	7	8	Q95945	Q95945 saccharomyc
139	14	23.0	17	4	000595	000595 homo sapien	212	13	21.3	8	2	068928	068928 salmoneila
140	14	23.0	18	8	092XW6	092XW6 aleiodes sp	213	13	21.3	8	12	083332	083332 murine hepa
141	14	23.0	18	12	073920	073920 human immun	214	13	21.3	9	2	068936	068936 serratia ma
142	14	23.0	18	12	073921	073921 human immun	215	13	21.3	9	4	078484	078484 homo sapien
143	14	23.0	19	2	047078	047078 escherichia	216	13	21.3	9	12	082622	082622 avian infec
144	14	23.0	19	6	097584	097584 macaca mula	217	13	21.3	9	12	088953	088953 vaccinia vi
145	14	23.0	19	8	099720	099720 elminia lon	218	13	21.3	10	8	079912	079912 chamaeleo f
146	14	23.0	19	8	099722	099722 lamprocorni	219	13	21.3	10	8	09XMB4	09XMB4 aegilops sq
147	14	23.0	19	8	099724	099724 dryocoryx c	220	13	21.3	10	11	063036	063036 rattus norv
148	14	23.0	19	8	099726	099726 geococcyx c	221	13	21.3	11	2	Q47606	Q47606 escherichia
149	14	23.0	19	8	099728	099728 buteo jamai	222	13	21.3	11	7	077876	077876 oreochromis
150	14	23.0	19	8	099730	099730 chaetura ci	223	13	21.3	11	7	077911	077911 oreochromis
151	14	23.0	19	8	099732	099732 corvus brac	224	13	21.3	11	7	078121	078121 oreochromis
152	14	23.0	19	8	099734	099734 dendrocygna	225	13	21.3	11	12	089269	089269 xestia c-ni
153	14	23.0	19	8	099738	099738 sayornis ph	226	13	21.3	11	12	083083	083083 leucania se
154	14	23.0	19	8	099740	099740 scolopax ml	227	13	21.3	11	12	086555	086555 tomato yell
155	14	23.0	19	8	099742	099742 sturnus vul	228	13	21.3	12	2	Q35579	Q35579 rhodobacter
156	14	23.0	19	8	099744	099744 certhia fam	229	13	21.3	13	12	083171	083171 cauliflower
157	14	23.0	19	8	099746	099746 crocodylus	230	13	21.3	14	2	045876	045876 clostridium
158	14	23.0	19	8	099750	099750 neophema el	231	13	21.3	14	2	045872	045872 clostridium
159	14	23.0	19	8	099751	099751 alcedo cris	232	13	21.3	14	2	Q44172	Q44172 synecococc
160	14	23.0	19	8	099752	099752 coracias sp	233	13	21.3	14	2	071199	071199 escherichia
161	14	23.0	19	8	099753	099753 acryllium v	234	13	21.3	14	2	Q52638	Q52638 escherichia
162	14	23.0	19	8	099754	099754 anseranas s	235	13	21.3	14	4	Q14342	Q14342 homo sapien
163	14	23.0	19	8	099755	099755 aptenodytes	236	13	21.3	14	5	Q10757	Q10757 theronyzon
164	14	23.0	19	8	099756	099756 bonasa umbe	237	13	21.3	14	11	Q92184	Q92184 mus musculu
165	14	23.0	19	8	099757	099757 burhinus oe	238	13	21.3	15	2	Q53580	Q53580 rhodobacter
166	14	23.0	19	8	099758	099758 cacaetua gof	239	13	21.3	15	10	P93515	P93515 arabidopsis

240	13	21.3	15	10	P93516	P93516 arabidopsis	313	12	19.7	11	7	077917	077917 oreochromis
241	13	21.3	15	11	O35411	O35411 mus musculus	314	12	19.7	11	7	077921	077921 pseudotroph
242	13	21.3	16	2	O45260	O45260 bradyrhizob	315	12	19.7	11	7	078118	078118 oreochromis
243	13	21.3	16	2	P70990	P70990 bacillus su	316	12	19.7	11	7	078120	078120 oreochromis
244	13	21.3	16	11	O70545	O70545 mus musculus	317	12	19.7	11	8	079921	079921 phrynocephala
245	13	21.3	16	11	O63039	O63039 rattus norv	318	12	19.7	11	11	O64068	O64068 mus musculus
246	13	21.3	16	12	O79456	O79456 human immun	319	12	19.7	11	12	O84073	O84073 influenza a
247	13	21.3	16	12	O79459	O79459 human immun	320	12	19.7	12	2	O56947	O56947 yersinia ps
248	13	21.3	17	2	P78199	P78199 escherichia	321	12	19.7	12	2	O56442	O56442 unidentified
249	13	21.3	17	4	O13376	O13376 homo sapien	322	12	19.7	12	4	O16405	O16405 homo sapien
250	13	21.3	18	2	O57323	O57323 yersinia ps	323	12	19.7	12	7	O77889	O77889 oreochromis
251	13	21.3	18	4	O47337	O47337 escherichia	324	12	19.7	12	7	O77890	O77890 oreochromis
252	13	21.3	18	4	O99625	O99625 h l-isoaspa	325	12	19.7	12	7	O77891	O77891 oreochromis
253	13	21.3	18	7	O77923	O77923 oreochromis	326	12	19.7	12	7	O77915	O77915 oreochromis
254	13	21.3	18	8	O92X00	O92X00 blacus sp.	327	12	19.7	12	7	O77920	O77920 pseudotroph
255	13	21.3	18	10	O96345	O96345 brassica na	328	12	19.7	12	8	P92680	P92680 trimeresuru
256	13	21.3	18	11	O62256	O62256 mus musculus	329	12	19.7	12	10	O41856	O41856 zea mays (m
257	13	21.3	18	11	O9WU06	O9WU06 mus musculus	330	12	19.7	12	11	O63929	O63929 rattus norv
258	13	21.3	18	12	O87589	O87589 chimpanzee	331	12	19.7	12	11	O64313	O64313 rattus norv
259	13	21.3	18	12	O87591	O87591 chimpanzee	332	12	19.7	12	12	O75729	O75729 human immun
260	13	21.3	18	12	O87593	O87593 chimpanzee	333	12	19.7	12	12	O86202	O86202 porcine tra
261	13	21.3	19	2	O57012	O57012 staphylococ	334	12	19.7	12	12	O41611	O41611 human immun
262	13	21.3	19	8	O92X03	O92X03 glycine soj	335	12	19.7	12	12	O72765	O72765 porcine tra
263	13	21.3	19	12	O85728	O85728 spleen necr	336	12	19.7	13	2	O52920	O52920 rhizobium m
264	13	21.3	19	12	O86832	O86832 human herpe	337	12	19.7	13	2	O86260	O86260 klebsiella
265	13	21.3	19	12	O83273	O83273 cucumber mo	338	12	19.7	13	2	O53300	O53300 escherichia
266	13	21.3	19	12	O9YQ55	O9YQ55 porcine cir	339	12	19.7	13	4	O16392	O16392 homo sapien
267	13	21.3	19	13	O91983	O91983 gallus gall	340	12	19.7	13	5	O24365	O24365 drosophila
268	13	21.3	20	2	P72423	P72423 saccharopol	341	12	19.7	13	8	O9XLI2	O9XLI2 bemisia tab
269	13	21.3	20	2	O34193	O34193 ehrlichia c	342	12	19.7	13	12	O65331	O65331 autographa
270	13	21.3	20	11	O55051	O55051 rattus norv	343	12	19.7	14	10	O92R83	O92R83 arabidopsis
271	13	21.3	20	11	O63667	O63667 rattus norv	344	12	19.7	14	10	O88400	O88400 simian t-ce
272	13	21.3	20	11	O64080	O64080 rattus norv	345	12	19.7	14	12	O89818	O89818 murine minu
273	12	20.5	18	2	O47246	O47246 escherichia	346	12	19.7	14	12	O86578	O86578 sigma virus
274	12	19.7	7	8	O98866	O98866 spinacia ol	347	12	19.7	15	2	O54325	O54325 staphylococ
275	12	19.7	8	2	O52062	O52062 bacillus me	348	12	19.7	15	2	O52640	O52640 pseudomonas
276	12	19.7	8	4	O15888	O15888 homo sapien	349	12	19.7	15	2	O93046	O93046 homo sapien
277	12	19.7	8	6	O02831	O02831 oryctolagus	350	12	19.7	15	4	O16158	O16158 homo sapien
278	12	19.7	8	11	P70243	P70243 mus musculus	351	12	19.7	15	5	O97430	O97430 drosophila
279	12	19.7	9	2	O47410	O47410 escherichia	352	12	19.7	15	8	O95773	O95773 conolophus
280	12	19.7	9	4	O16220	O16220 homo sapien	353	12	19.7	15	9	O93854	O93854 sus scrofa
281	12	19.7	9	9	O38366	O38366 bacterioph	354	12	19.7	15	9	O38574	O38574 bacterioph
282	12	19.7	9	12	O65711	O65711 berne virus	355	12	19.7	15	11	O64100	O64100 cricetidae
283	12	19.7	9	12	O85723	O85723 simian sarc	356	12	19.7	15	11	O88954	O88954 vaccinia vi
284	12	19.7	9	12	O90350	O90350 hepatitis g	357	12	19.7	15	12	O45530	O45530 bacillus su
285	12	19.7	10	8	P92733	P92733 rana limnoc	358	12	19.7	16	2	O45530	O45530 bacillus su
286	12	19.7	10	8	P92766	P92766 varanus gri	359	12	19.7	16	4	O15632	O15632 homo sapien
287	12	19.7	10	8	P92774	P92774 xantusia vi	360	12	19.7	16	4	O15632	O15632 homo sapien
288	12	19.7	10	8	O79888	O79888 basiliscus	361	12	19.7	16	6	P79137	P79137 cercopithe
289	12	19.7	10	8	O79897	O79897 hoplocercus	362	12	19.7	16	8	O34699	O34699 helianthus
290	12	19.7	10	8	O79915	O79915 leiolepis b	363	12	19.7	16	11	O92072	O92072 mus musculus
291	12	19.7	10	8	O79924	O79924 elgaria pan	364	12	19.7	16	12	O66737	O66737 equine infe
292	12	19.7	10	8	O92X72	O92X72 leiocephalu	365	12	19.7	16	12	O79453	O79453 human immun
293	12	19.7	10	8	O92Y56	O92Y56 stenocercus	366	12	19.7	16	12	O75710	O75710 human immun
294	12	19.7	10	12	O64971	O64971 alfalfa mos	367	12	19.7	16	12	O9WU66	O9WU66 sigma virus
295	12	19.7	10	12	O83978	O83978 influenza a	368	12	19.7	17	2	O45529	O45529 bacillus su
296	12	19.7	10	12	O82625	O82625 infection	369	12	19.7	17	2	O92E26	O92E26 buchneza ap
297	12	19.7	11	5	O25916	O25916 plasmodium	370	12	19.7	17	2	O06946	O06946 salmonella
298	12	19.7	11	7	O77886	O77886 oreochromis	371	12	19.7	17	2	O9X616	O9X616 bacillus th
299	12	19.7	11	7	O77894	O77894 oreochromis	372	12	19.7	17	3	O06800	O06800 saccharomyc
300	12	19.7	11	7	O77895	O77895 oreochromis	373	12	19.7	17	4	O95794	O95794 homo sapien
301	12	19.7	11	7	O77896	O77896 oreochromis	374	12	19.7	17	6	O29395	O29395 canis famli
302	12	19.7	11	7	O77898	O77898 oreochromis	375	12	19.7	17	6	O18774	O18774 oryctolagus
303	12	19.7	11	7	O77899	O77899 oreochromis	376	12	19.7	17	6	O62645	O62645 saquinus oe
304	12	19.7	11	7	O77900	O77900 oreochromis	377	12	19.7	17	8	O92XW0	O92XW0 betyobrac
305	12	19.7	11	7	O77901	O77901 oreochromis	378	12	19.7	17	8	O92X77	O92X77 triassolcus
306	12	19.7	11	7	O77902	O77902 oreochromis	379	12	19.7	17	8	O9XN01	O9XN01 boophilus m
307	12	19.7	11	7	O77903	O77903 oreochromis	380	12	19.7	17	11	O62548	O62548 mus musculus
308	12	19.7	11	7	O77904	O77904 oreochromis	381	12	19.7	17	11	O88868	O88868 mus musculus
309	12	19.7	11	7	O77905	O77905 oreochromis	382	12	19.7	17	12	O85004	O85004 porcine tes
310	12	19.7	11	7	O77908	O77908 oreochromis	383	12	19.7	17	12	O69074	O69074 human herpe
311	12	19.7	11	7	O77914	O77914 oreochromis	384	12	19.7	17	12	O73442	O73442 human immun
312	12	19.7	11	7	O77916	O77916 oreochromis	385	12	19.7	17	12	O85072	O85072 pepper seve

386	12	19.7	17	12	Q85463	Q85463 avian sarco	459	12	19.7	18	12	Q73595	Q73595 human immun
387	12	19.7	17	12	Q73531	Q73531 human immun	460	12	19.7	18	12	Q73597	Q73597 human immun
388	12	19.7	17	12	Q73533	Q73533 human immun	461	12	19.7	18	12	Q73599	Q73599 human immun
389	12	19.7	17	12	Q73535	Q73535 human immun	462	12	19.7	18	12	Q73611	Q73611 human immun
390	12	19.7	17	12	Q73537	Q73537 human immun	463	12	19.7	18	12	Q73617	Q73617 human immun
391	12	19.7	17	12	Q73539	Q73539 human immun	464	12	19.7	18	12	Q73619	Q73619 human immun
392	12	19.7	17	12	Q73541	Q73541 human immun	465	12	19.7	18	12	Q73621	Q73621 human immun
393	12	19.7	17	12	Q73543	Q73543 human immun	466	12	19.7	18	12	Q73623	Q73623 human immun
394	12	19.7	17	12	Q73545	Q73545 human immun	467	12	19.7	18	12	Q73625	Q73625 human immun
395	12	19.7	17	12	Q73547	Q73547 human immun	468	12	19.7	18	12	Q73627	Q73627 human immun
396	12	19.7	18	2	Q44607	Q44607 buchiera ap	469	12	19.7	18	12	Q73633	Q73633 human immun
397	12	19.7	18	2	Q52411	Q52411 thermophili	470	12	19.7	18	12	Q73635	Q73635 human immun
398	12	19.7	18	3	Q06711	Q06711 saccharomyc	471	12	19.7	18	12	Q73637	Q73637 human immun
399	12	19.7	18	4	Q12995	Q12995 homo sapien	472	12	19.7	18	12	Q73641	Q73641 human immun
400	12	19.7	18	7	Q29820	Q29820 homo sapien	473	12	19.7	19	2	Q43964	Q43964 azotobacter
401	12	19.7	18	7	Q29817	Q29817 homo sapien	474	12	19.7	19	4	Q16184	Q16184 homo sapien
402	12	19.7	18	7	Q29819	Q29819 homo sapien	475	12	19.7	19	6	Q19107	Q19107 bos taurus
403	12	19.7	18	7	Q30980	Q30980 pan troglod	476	12	19.7	19	8	Q36277	Q36277 zea mays (m
404	12	19.7	18	8	Q921X7	Q921X7 perga conde	477	12	19.7	19	8	Q99748	Q99748 sphendon p
405	12	19.7	18	8	Q921X8	Q921X8 encarsia fo	478	12	19.7	19	11	Q9WT25	Q9WT25 mus musculus
406	12	19.7	18	8	Q921X8	Q921X8 amitus sp.	479	12	19.7	19	12	Q86583	Q86583 murine hepa
407	12	19.7	18	9	Q37852	Q37852 bacterioph	480	12	19.7	19	12	Q90622	Q90622 simian herp
408	12	19.7	18	11	Q61840	Q61840 mus musculu	481	12	19.7	19	12	Q90625	Q90625 simian herp
409	12	19.7	18	11	Q63653	Q63653 rattus norv	482	12	19.7	19	12	Q90628	Q90628 simian herp
410	12	19.7	18	12	Q73461	Q73461 human immun	483	12	19.7	19	12	Q90630	Q90630 baboon herp
411	12	19.7	18	12	Q73487	Q73487 human immun	484	12	19.7	19	12	Q90633	Q90633 baboon herp
412	12	19.7	18	12	Q73463	Q73463 human immun	485	12	19.7	19	12	Q90635	Q90635 simian herp
413	12	19.7	18	12	Q73465	Q73465 human immun	486	12	19.7	19	12	Q90637	Q90637 human immun
414	12	19.7	18	12	Q73467	Q73467 human immun	487	12	19.7	19	12	Q9W9U1	Q9W9U1 simian herp
415	12	19.7	18	12	Q73469	Q73469 human immun	488	12	19.7	20	2	P70739	P70739 alcaligenes
416	12	19.7	18	12	Q73471	Q73471 human immun	489	12	19.7	20	2	O50180	O50180 pseudomonas
417	12	19.7	18	12	Q73473	Q73473 human immun	490	12	19.7	20	2	P97146	P97146 escherichia
418	12	19.7	18	12	Q73475	Q73475 human immun	491	12	19.7	20	2	Q53121	Q53121 rhodobacter
419	12	19.7	18	12	Q73477	Q73477 human immun	492	12	19.7	20	5	O46158	O46158 lumbricus r
420	12	19.7	18	12	Q73479	Q73479 human immun	493	12	19.7	20	6	Q28734	Q28734 oryctolagus
421	12	19.7	18	12	Q73481	Q73481 human immun	494	12	19.7	20	7	Q30135	Q30135 homo sapien
422	12	19.7	18	12	Q73483	Q73483 human immun	495	12	19.7	20	7	Q36127	Q36127 thyrophagus
423	12	19.7	18	12	Q73485	Q73485 human immun	496	12	19.7	20	8	Q36127	Q36127 thyrophagus
424	12	19.7	18	12	Q73489	Q73489 human immun	497	12	19.7	20	12	Q89700	Q89700 human immun
425	12	19.7	18	12	Q73491	Q73491 human immun	498	12	19.7	20	12	Q83416	Q83416 pseudorabie
426	12	19.7	18	12	Q73493	Q73493 human immun	499	12	19.7	20	12	Q83416	Q83416 simian herp
427	12	19.7	18	12	Q73495	Q73495 human immun	500	11.5	18.9	9	12	Q89491	Q89491 murine minu
428	12	19.7	18	12	Q73497	Q73497 human immun	501	11.5	18.9	12	4	O60773	O60773 homo sapien
429	12	19.7	18	12	Q73499	Q73499 human immun	502	11.5	18.9	13	2	Q53313	Q53313 corynebacte
430	12	19.7	18	12	Q73501	Q73501 human immun	503	11.5	18.9	13	8	O99736	O99736 lanius coll
431	12	19.7	18	12	Q73503	Q73503 human immun	504	11.5	18.9	19	11	O06028	O06028 mus musculu
432	12	19.7	18	12	Q73505	Q73505 human immun	505	11	18.0	7	12	Q9YVE3	Q9YVE3 human adeno
433	12	19.7	18	12	Q73507	Q73507 human immun	506	11	18.0	7	12	Q9YIR0	Q9YIR0 human adeno
434	12	19.7	18	12	Q73509	Q73509 human immun	507	11	18.0	7	12	O9YIQ9	O9YIQ9 human adeno
435	12	19.7	18	12	Q73511	Q73511 human immun	508	11	18.0	8	4	Q15890	Q15890 homo sapien
436	12	19.7	18	12	Q73513	Q73513 human immun	509	11	18.0	8	8	Q35792	Q35792 saccharomyc
437	12	19.7	18	12	Q73515	Q73515 human immun	510	11	18.0	8	11	O35835	O35835 rattus norv
438	12	19.7	18	12	Q73517	Q73517 human immun	511	11	18.0	9	4	O00610	O00610 homo sapien
439	12	19.7	18	12	Q73519	Q73519 human immun	512	11	18.0	9	4	O16386	O16386 homo sapien
440	12	19.7	18	12	Q73521	Q73521 human immun	513	11	18.0	9	4	O95953	O95953 homo sapien
441	12	19.7	18	12	Q73523	Q73523 human immun	514	11	18.0	9	6	Q28093	Q28093 bos taurus
442	12	19.7	18	12	Q73525	Q73525 human immun	515	11	18.0	9	6	Q28121	Q28121 bos taurus
443	12	19.7	18	12	Q73527	Q73527 human immun	516	11	18.0	9	12	O69100	O69100 herpes simp
444	12	19.7	18	12	Q73529	Q73529 human immun	517	11	18.0	10	2	Q52762	Q52762 rhizobium s
445	12	19.7	18	12	Q73531	Q73531 human immun	518	11	18.0	10	5	Q25355	Q25355 locusta mig
446	12	19.7	18	12	Q73533	Q73533 human immun	519	11	18.0	10	5	Q25356	Q25356 locusta mig
447	12	19.7	18	12	Q73535	Q73535 human immun	520	11	18.0	10	8	P92616	P92616 cnemidophor
448	12	19.7	18	12	Q73537	Q73537 human immun	521	11	18.0	10	8	P92632	P92632 eremias gra
449	12	19.7	18	12	Q73539	Q73539 human immun	522	11	18.0	10	8	P92707	P92707 platysaurus
450	12	19.7	18	12	Q73541	Q73541 human immun	523	11	18.0	10	8	P92758	P92758 teratoscinc
451	12	19.7	18	12	Q73543	Q73543 human immun	524	11	18.0	10	8	P92762	P92762 uromastix a
452	12	19.7	18	12	Q73545	Q73545 human immun	525	11	18.0	10	8	P92771	P92771 xenosaurus
453	12	19.7	18	12	Q73547	Q73547 human immun	526	11	18.0	10	8	P92648	P92648 lialis jica
454	12	19.7	18	12	Q73549	Q73549 human immun	527	11	18.0	10	8	P92654	P92654 mabuya aura
455	12	19.7	18	12	Q73551	Q73551 human immun	528	11	18.0	10	8	O79885	O79885 anolis pate
456	12	19.7	18	12	Q73553	Q73553 human immun	529	11	18.0	10	8	O79891	O79891 crotophytus
457	12	19.7	18	12	Q73555	Q73555 human immun	530	11	18.0	10	8	O79894	O79894 gambelia wl
458	12	19.7	18	12	Q73557	Q73557 human immun	531	11	18.0	10	8	O79900	O79900 liolaemus p

532	11	18.0	10	8	079903	079903 oplurus cuv	605	11	18.0	13	8	095808	095808 gracilarlop
533	11	18.0	10	8	079906	079906 phrynosoma	606	11	18.0	13	8	092460	092460 taxus bacca
534	11	18.0	10	8	079909	079909 saurumalus	607	11	18.0	13	8	099188	099188 rivulus cau
535	11	18.0	10	8	0921V3	0921V3 diposaurus	608	11	18.0	13	10	043174	043174 solanum tub
536	11	18.0	10	8	0921V0	0921V0 petrosaurus	609	11	18.0	13	11	063935	063935 rattus norv
537	11	18.0	10	8	0921U7	0921U7 sator angus	610	11	18.0	13	11	088176	088176 mus musculus
538	11	18.0	10	8	0921U4	0921U4 sceloporos	611	11	18.0	13	12	085645	085645 mouse mamma
539	11	18.0	10	8	0921U1	0921U1 uma scopari	612	11	18.0	14	2	056945	056945 yersinia ps
540	11	18.0	10	8	0921T8	0921T8 urosaurus g	613	11	18.0	14	2	054861	054861 streptococc
541	11	18.0	10	8	0921T5	0921T5 uta stansbu	614	11	18.0	14	4	013022	013022 homo sapien
542	11	18.0	10	8	0921S9	0921S9 phymaturus	615	11	18.0	14	4	099902	099902 homo sapien
543	11	18.0	10	11	070580	070580 mus musculus	616	11	18.0	14	5	018502	018502 schistosoma
544	11	18.0	10	12	090349	090349 hepatitis g	617	11	18.0	14	6	090961	090961 bos taurus
545	11	18.0	10	13	042355	042355 brachydantio	618	11	18.0	14	6	09XSL4	09XSL4 capra hircu
546	11	18.0	11	2	047602	047602 escherichia	619	11	18.0	14	11	063937	063937 mesocricetu
547	11	18.0	11	2	096319	096319 desulfovibr	620	11	18.0	14	12	010231	010231 human immun
548	11	18.0	11	2	047567	047567 escherichia	621	11	18.0	14	12	010234	010234 human immun
549	11	18.0	11	5	024227	024227 drosophila	622	11	18.0	14	12	010226	010226 human immun
550	11	18.0	11	7	077884	077884 oreochromis	623	11	18.0	14	12	010227	010227 human immun
551	11	18.0	11	7	077885	077885 oreochromis	624	11	18.0	14	12	010228	010228 human immun
552	11	18.0	11	7	077893	077893 oreochromis	625	11	18.0	14	12	010229	010229 human immun
553	11	18.0	11	7	077897	077897 oreochromis	626	11	18.0	14	12	010230	010230 human immun
554	11	18.0	11	7	077913	077913 oreochromis	627	11	18.0	14	12	010232	010232 human immun
555	11	18.0	11	8	079636	079636 laudakia hi	628	11	18.0	14	12	010233	010233 human immun
556	11	18.0	11	8	079639	079639 laudakia le	629	11	18.0	14	12	010235	010235 human immun
557	11	18.0	11	8	079642	079642 laudakia ml	630	11	18.0	15	2	005003	005003 rhizobium l
558	11	18.0	11	8	079918	079918 physignathu	631	11	18.0	15	2	092F32	092F32 salmonella
559	11	18.0	11	8	079985	079985 laudakia ca	632	11	18.0	15	4	016297	016297 homo sapien
560	11	18.0	11	8	079986	079986 laudakia er	633	11	18.0	15	8	095762	095762 ctenosaura
561	11	18.0	11	12	083410	083410 mouse mamma	634	11	18.0	15	8	078794	078794 pylaiaella l
562	11	18.0	11	12	084117	084117 influenza a	635	11	18.0	15	9	038427	038427 bacterioph
563	11	18.0	12	2	046747	046747 escherichia	636	11	18.0	15	12	086576	086576 subterranea
564	11	18.0	12	2	005328	005328 pseudomonas	637	11	18.0	15	12	086865	086865 lymphocytic
565	11	18.0	12	2	054226	054226 saccharopol	638	11	18.0	15	12	086867	086867 lymphocytic
566	11	18.0	12	4	013865	013865 homo sapien	639	11	18.0	15	12	086869	086869 lymphocytic
567	11	18.0	12	6	09XT42	09XT42 canis fami	640	11	18.0	16	2	051436	051436 pseudomonas
568	11	18.0	12	7	007884	007884 pan troglod	641	11	18.0	16	2	048417	048417 klebsiella
569	11	18.0	12	8	036623	036623 picea abies	642	11	18.0	16	3	094554	094554 schizosacch
570	11	18.0	12	8	036669	036669 pinus sylve	643	11	18.0	16	4	016183	016183 homo sapien
571	11	18.0	12	8	037790	037790 larix eurol	644	11	18.0	16	6	062810	062810 equus cabal
572	11	18.0	12	8	092454	092454 cycas revol	645	11	18.0	16	8	095765	095765 cyclura nub
573	11	18.0	12	8	092457	092457 ephedra sp.	646	11	18.0	16	8	092070	092070 euhadra her
574	11	18.0	12	8	003815	003815 abies alba	647	11	18.0	16	8	035214	035214 oenothara b
575	11	18.0	12	8	003816	003816 metasequoia	648	11	18.0	16	9	021922	021922 streptococc
576	11	18.0	12	10	092NT6	092NT6 oryza brach	649	11	18.0	16	12	086717	086717 human immun
577	11	18.0	12	11	063579	063579 rattus norv	650	11	18.0	17	2	034216	034216 pseudomonas
578	11	18.0	12	11	061331	061331 mus musculus	651	11	18.0	17	4	078490	078490 homo sapien
579	11	18.0	12	12	012088	012088 caprine art	652	11	18.0	17	4	075289	075289 homo sapien
580	11	18.0	12	12	012074	012074 caprine art	653	11	18.0	17	5	061238	061238 onchocerca
581	11	18.0	12	12	012076	012076 caprine art	654	11	18.0	17	7	019716	019716 homo sapien
582	11	18.0	12	12	012078	012078 caprine art	655	11	18.0	17	7	012862	012862 homo sapien
583	11	18.0	12	12	012080	012080 caprine art	656	11	18.0	17	8	007055	007055 crithidia f
584	11	18.0	12	12	012082	012082 caprine art	657	11	18.0	17	11	063233	063233 rattus norv
585	11	18.0	12	12	012084	012084 caprine art	658	11	18.0	17	11	088173	088173 rattus norv
586	11	18.0	12	12	012086	012086 caprine art	659	11	18.0	17	12	084098	084098 influenza a
587	11	18.0	12	12	012090	012090 caprine art	660	11	18.0	17	13	091352	091352 gallus gall
588	11	18.0	12	12	012092	012092 caprine art	661	11	18.0	18	2	006514	006514 escherichia
589	11	18.0	12	12	012094	012094 caprine art	662	11	18.0	18	2	009053	009053 methylomona
590	11	18.0	12	12	012106	012106 caprine art	663	11	18.0	18	2	050076	050076 mycobacteri
591	11	18.0	12	12	012108	012108 caprine art	664	11	18.0	18	2	053503	053503 lactobacill
592	11	18.0	12	12	012110	012110 caprine art	665	11	18.0	18	2	097166	097166 streptococc
593	11	18.0	12	12	012112	012112 caprine art	666	11	18.0	18	2	026062	026062 helicobacte
594	11	18.0	12	12	012114	012114 caprine art	667	11	18.0	18	4	013665	013665 homo sapien
595	11	18.0	12	12	012116	012116 caprine art	668	11	18.0	18	4	013767	013767 homo sapien
596	11	18.0	12	12	012118	012118 caprine art	669	11	18.0	18	8	034695	034695 homarus ame
597	11	18.0	12	12	012036	012036 caprine art	670	11	18.0	18	8	098674	098674 cabomba car
598	11	18.0	13	2	049230	049230 mycoplasma	671	11	18.0	18	8	0921W4	0921W4 habrobracon
599	11	18.0	13	2	051605	051605 escherichia	672	11	18.0	18	8	0921V9	0921V9 oplius kraus
600	11	18.0	13	2	09X514	09X514 enterococcu	673	11	18.0	18	8	0921V8	0921V8 aspiota sp
601	11	18.0	13	2	09WW72	09WW72 enterococcu	674	11	18.0	18	8	0921V8	0921V8 scellio fulg
602	11	18.0	13	2	09WW71	09WW71 enterococcu	675	11	18.0	18	8	0921V9	0921V9 idria sp. c
603	11	18.0	13	3	010721	010721 pseudallesc	676	11	18.0	18	8	0921V8	0921V8 gryon sp. c
604	11	18.0	13	6	018890	018890 ateles panl	677	11	18.0	18	8	0921V5	0921V5 cenocoelium

678	11	18.0	18	9	Q9XJ05	Q9xjg5 bacterioph	751	10	16.4	14	12	Q9YJ34	Q9y34 porcine cir
679	11	18.0	18	10	Q82675	O82675 cryptoglena	752	10	16.4	14	13	Q73611	O73611 gallus gall
680	11	18.0	18	11	Q63136	Q63136 rattus norv	753	10	16.4	15	2	Q52135	Q52135 enterococu
681	11	18.0	18	11	Q63506	Q63506 rattus norv	754	10	16.4	15	2	Q52586	Q52586 agrobacteri
682	11	18.0	18	12	Q88290	Q88290 small round	755	10	16.4	15	3	O14379	O14379 schizosacch
683	11	18.0	18	12	Q73557	Q73557 human immun	756	10	16.4	15	4	Q13377	Q13377 homo sapien
684	11	18.0	19	2	Q53545	Q53545 shigella so	757	10	16.4	15	10	Q41526	Q41526 triticum ae
685	11	18.0	19	4	Q16271	Q16271 homo sapien	758	10	16.4	15	11	O9XGM5	O9xgm5 arabidopsi
686	11	18.0	19	4	Q16335	Q16335 homo sapien	759	10	16.4	15	11	Q63936	Q63936 mesocricetu
687	11	18.0	19	4	Q95181	Q95181 homo sapien	760	10	16.4	15	11	Q63938	Q63938 mesocricetu
688	11	18.0	19	8	Q95181	Q95181 artemia par	761	10	16.4	15	11	Q62544	Q62544 mus apretus
689	11	18.0	19	8	Q92YW2	Q92yw2 dolopsidea	762	10	16.4	15	12	Q86128	Q86128 vesicular s
690	11	18.0	19	8	Q9XNQ3	Q9xng3 boophilus m	763	10	16.4	16	2	Q45663	Q45663 bacillus su
691	11	18.0	19	8	Q9XMB5	Q9xmb5 aegilops sq	764	10	16.4	16	4	Q16413	Q16413 homo sapien
692	11	18.0	19	9	Q38021	Q38021 bacterioph	765	10	16.4	16	5	Q23912	Q23912 dictyostell
693	11	18.0	19	9	Q38371	Q38371 bacterioph	766	10	16.4	16	12	Q07625	Q07625 rous sarcom
694	11	18.0	19	10	Q22064	Q22064 d phosphogl	767	10	16.4	16	12	Q90049	Q90049 human cytom
695	11	18.0	19	11	Q84132	Q84132 rattus norv	768	10	16.4	16	12	Q84246	Q84246 polyomaviru
696	11	18.0	19	12	Q11338	Q11338 molluscum c	769	10	16.4	17	4	Q15337	Q15337 homo sapien
697	11	18.0	19	12	Q99099	Q99099 herpes simp	770	10	16.4	17	8	Q36741	Q36741 homo sapien
698	11	18.0	19	12	Q56132	Q56132 porcine cir	771	10	16.4	17	10	Q24445	Q24445 ceratodon p
699	11	18.0	19	12	Q91329	Q91329 human immun	772	10	16.4	17	10	Q41400	Q41400 sesbania ro
700	11	18.0	19	12	Q93210	Q93210 porcine cir	773	10	16.4	17	10	Q42225	Q42225 glycine max
701	11	18.0	19	12	Q9YR03	Q9yr03 porcine cir	774	10	16.4	17	12	Q79452	Q79452 human immun
702	11	18.0	19	12	Q9YQW8	Q9yqw8 porcine cir	775	10	16.4	17	12	P90402	P90402 human immun
703	11	18.0	19	12	Q9YIT3	Q9yit3 bovine cir	776	10	16.4	18	2	Q00952	Q00952 actinobacil
704	11	18.0	19	12	Q9WJBI	Q9wjb1 human immun	777	10	16.4	18	2	Q92F30	Q92f30 salmonella
705	11	18.0	20	2	Q47614	Q47614 escherichia	778	10	16.4	18	8	Q98365	Q98365 myosorus m
706	11	18.0	20	4	Q16188	Q16188 homo sapien	779	10	16.4	18	10	Q41458	Q41458 solanum tub
707	11	18.0	20	6	Q62720	Q62720 oryctolagus	780	10	16.4	18	12	Q87587	Q87587 chimpanzee
708	11	18.0	20	8	Q34694	Q34694 homarus ame	781	10	16.4	18	12	Q84343	Q84343 simian viru
709	11	18.0	20	9	Q37868	Q37868 bacterioph	782	10	16.4	19	2	Q45558	Q45558 bacillus sp
710	11	18.0	20	11	P97907	P97907 mus musculu	783	10	16.4	19	2	Q47895	Q47895 fremyella d
711	11	18.0	20	11	Q61871	Q61871 mus musculu	784	10	16.4	19	2	O87732	O87732 streptomyce
712	11	18.0	20	11	Q62546	Q62546 mus spretus	785	10	16.4	19	2	Q52316	Q52316 escherichia
713	10	16.4	7	4	Q15903	Q15903 homo sapien	786	10	16.4	19	3	Q01057	Q01057 kluyveromyc
714	10	16.4	8	4	Q94434	Q9y4j4 homo sapien	787	10	16.4	19	10	Q39381	Q39381 brassica ol
715	10	16.4	8	5	Q94623	Q94623 manduca sex	788	10	16.4	19	10	O80997	O80997 arabidopsi
716	10	16.4	8	8	Q95213	Q95213 oryctolagus	789	10	16.4	19	11	Q63857	Q63857 mus musculu
717	10	16.4	8	8	Q34909	Q34909 locusta mig	790	10	16.4	19	12	O65747	O65747 bluetongue
718	10	16.4	9	8	Q9XNP8	Q9xnp8 boophilus m	791	10	16.4	19	12	Q84863	Q84863 unidentifie
719	10	16.4	9	6	Q9XSL0	Q9xsl0 capra hircu	792	10	16.4	19	12	Q65340	Q65340 autographa
720	10	16.4	9	12	Q89473	Q89473 human herpe	793	10	16.4	20	2	O51949	O51949 chlamydia t
721	10	16.4	9	12	Q84333	Q84333 simian viru	794	10	16.4	20	2	O51951	O51951 chlamydia t
722	10	16.4	9	12	Q88612	Q88612 middelburg	795	10	16.4	20	2	Q49132	Q49132 methylobact
723	10	16.4	11	2	Q47345	Q47345 escherichia	796	10	16.4	20	2	O69176	O69176 chlamydia t
724	10	16.4	11	2	Q68237	Q68237 borrelia bu	797	10	16.4	20	2	Q53520	Q53520 chlamydia t
725	10	16.4	11	2	Q56972	Q56972 yersinia pe	798	10	16.4	20	2	Q46416	Q46416 chlamydia t
726	10	16.4	11	2	Q9X956	Q9x956 streptomyce	799	10	16.4	20	2	O85509	O85509 chlamydia t
727	10	16.4	11	4	Q16427	Q16427 homo sapien	800	10	16.4	20	2	O85510	O85510 chlamydia t
728	10	16.4	11	4	Q94785	Q94785 homo sapien	801	10	16.4	20	2	O85512	O85512 chlamydia t
729	10	16.4	11	4	Q9Y3G2	Q9y3g2 homo sapien	802	10	16.4	20	2	O85514	O85514 chlamydia t
730	10	16.4	11	7	O77874	O77874 oreochromis	803	10	16.4	20	2	O85517	O85517 chlamydia t
731	10	16.4	11	7	O77875	O77875 oreochromis	804	10	16.4	20	2	O85519	O85519 chlamydia t
732	10	16.4	11	11	P97755	P97755 rattus norv	805	10	16.4	20	2	O85520	O85520 chlamydia t
733	10	16.4	12	2	O50303	O50303 bacillus st	806	10	16.4	20	2	O85521	O85521 chlamydia t
734	10	16.4	12	2	Q53183	Q53183 rhodococcus	807	10	16.4	20	2	O85522	O85522 chlamydia t
735	10	16.4	12	10	Q38715	Q38715 arachis hyp	808	10	16.4	20	2	O85523	O85523 chlamydia t
736	10	16.4	12	12	Q69232	Q69232 bovine herp	809	10	16.4	20	2	O85525	O85525 chlamydia t
737	10	16.4	13	2	Q47693	Q47693 escherichia	810	10	16.4	20	2	O85526	O85526 chlamydia t
738	10	16.4	13	4	Q14890	Q14890 homo sapien	811	10	16.4	20	2	O85528	O85528 chlamydia t
739	10	16.4	13	4	Q16141	Q16141 homo sapien	812	10	16.4	20	2	O85530	O85530 chlamydia t
740	10	16.4	14	3	P90342	P90342 saccharomyc	813	10	16.4	20	2	O85531	O85531 chlamydia t
741	10	16.4	14	4	Q16484	Q16484 homo sapien	814	10	16.4	20	2	O85533	O85533 chlamydia t
742	10	16.4	14	8	P92076	P92076 euhadra her	815	10	16.4	20	3	O13594	O13594 saccharomyc
743	10	16.4	14	11	O70599	O70599 rattus norv	816	10	16.4	20	4	Q9Y3G5	Q9y3g5 homo sapien
744	10	16.4	14	11	Q06415	Q06415 rattus norv	817	10	16.4	20	7	O15685	O15685 homo sapien
745	10	16.4	14	11	Q06414	Q06414 rattus norv	818	10	16.4	20	11	Q63967	Q63967 rattus norv
746	10	16.4	14	12	P91578	P91578 chorisstoneu	819	10	16.4	20	12	Q64976	Q64976 alfalfa mos
747	10	16.4	14	12	Q67112	Q67112 influenza a	820	10	16.4	20	12	Q66548	Q66548 human herpe
748	10	16.4	14	12	Q84708	Q84708 porcine epi	821	9	14.8	8	2	P72279	P72279 rhodococcus
749	10	16.4	14	12	O56127	O56127 porcine cir	822	9	14.8	8	4	O15901	O15901 homo sapien
750	10	16.4	14	12	O93202	O93202 porcine cir	823	9	14.8	8	12	Q84271	Q84271 human papil

824	9	14.8	8	12	084273	Q84273 human papill	897	9	14.8	20	2	034190	034190 ehrlichia e
825	9	14.8	9	4	045852	Q45852 clostridium	898	9	14.8	20	2	034192	034192 ehrlichia s
826	9	14.8	9	2	Q14715	Q14715 homo sapien	899	9	14.8	20	2	034629	034629 chlamydia t
827	9	14.8	9	11	Q62530	Q62530 mus spretus	900	9	14.8	20	2	09X634	09X634 serratia ma
828	9	14.8	10	2	Q44693	Q44693 bacillus am	901	9	14.8	20	2	09X632	09X632 pseudomonas
829	9	14.8	10	5	Q26093	Q26093 pisaster oc	902	9	14.8	20	2	09X630	09X630 leclercia a
830	9	14.8	11	5	Q15994	Q15994 drosophila	903	9	14.8	20	2	09X629	09X629 unidentified
831	9	14.8	11	7	078119	078119 oreochromis	904	9	14.8	20	2	09X627	09X627 escherichia
832	9	14.8	11	10	Q04131	Q04131 lycopersico	905	9	14.8	20	4	092855	092855 homo sapien
833	9	14.8	11	10	Q82070	Q82070 triticum ae	906	9	14.8	20	4	015969	015969 homo sapien
834	9	14.8	11	12	Q86556	Q86556 tomato yell	907	9	14.8	20	6	Q28830	Q28830 bos taurus
835	9	14.8	11	12	Q86864	Q86864 lymphocytic	908	9	14.8	20	8	Q95947	Q95947 saccharomyc
836	9	14.8	11	12	Q86866	Q86866 lymphocytic	909	9	14.8	20	9	Q38458	Q38458 bacterioph
837	9	14.8	11	12	Q86868	Q86868 lymphocytic	910	9	14.8	20	10	Q42485	Q42485 solanum tub
838	9	14.8	12	2	Q50019	Q50019 mycobacteri	911	9	14.8	20	10	Q62435	Q62435 mus musculu
839	9	14.8	12	6	Q46664	Q46664 macropus ro	912	9	14.8	20	11	Q64031	Q64031 cricetidae
840	9	14.8	12	6	Q9X531	Q9X531 sus scrofa	913	9	14.8	20	11	Q921F5	Q921F5 mus musculu
841	9	14.8	12	7	Q31006	Q31006 bos taurus	914	9	14.8	20	11	Q921F5	Q921F5 mus musculu
842	9	14.8	12	10	Q02319	Q02319 pinus sylve	915	9	14.8	20	12	Q85096	Q85096 punta toro
843	9	14.8	13	4	Q99931	Q99931 homo sapien	916	9	14.8	20	12	Q38539	Q38539 human torov
844	9	14.8	13	11	Q63940	Q63940 rattus norv	917	9	14.8	20	12	Q86935	Q86935 human herpe
845	9	14.8	14	2	Q47599	Q47599 escherichia	918	9	14.8	20	12	Q86936	Q86936 human herpe
846	9	14.8	14	2	Q96347	Q96347 helicobacte	919	9	14.8	20	12	Q86937	Q86937 human herpe
847	9	14.8	14	4	Q15998	Q15998 homo sapien	920	9	14.8	20	12	Q86938	Q86938 human herpe
848	9	14.8	14	4	Q95179	Q95179 homo sapien	921	9	14.8	20	12	Q86939	Q86939 human herpe
849	9	14.8	14	5	Q26100	Q26100 pratylenchu	922	9	14.8	20	12	Q86940	Q86940 human herpe
850	9	14.8	15	2	Q97249	Q97249 nitrosolobu	923	9	14.8	20	12	Q86941	Q86941 human herpe
851	9	14.8	15	2	Q05463	Q05463 nitrosolobu	924	9	14.8	20	12	Q86942	Q86942 human herpe
852	9	14.8	15	2	Q54298	Q54298 salmonella	925	9	14.8	20	12	Q41270	Q41270 spodoptera
853	9	14.8	15	2	Q47893	Q47893 fremyella d	926	8	13.1	5	5	Q42534	Q42534 brachydanio
854	9	14.8	15	2	Q05991	Q05991 staphylococ	927	8	13.1	7	2	Q54248	Q54248 streptomyc
855	9	14.8	15	2	Q9X637	Q9X637 klebsiella	928	8	13.1	7	2	Q34028	Q34028 pseudomonas
856	9	14.8	15	2	Q9X635	Q9X635 escherichia	929	8	13.1	7	8	Q99182	Q99182 pterolebias
857	9	14.8	15	4	Q78533	Q78533 homo sapien	930	8	13.1	7	12	Q9XQ10	Q9XQ10 porcine tra
858	9	14.8	15	8	Q95770	Q95770 cyciura ric	931	8	13.1	8	2	Q32560	Q32560 escherichia
859	9	14.8	15	8	Q95879	Q95879 phrynosoma	932	8	13.1	8	2	Q56429	Q56429 thermus aqu
860	9	14.8	15	8	Q35795	Q35795 saccharomyc	933	8	13.1	8	2	Q45889	Q45889 clostridium
861	9	14.8	15	9	Q80277	Q80277 bacterioph	934	8	13.1	8	3	P87225	P87225 saccharomyc
862	9	14.8	15	12	Q88881	Q88881 tobacco mos	935	8	13.1	8	5	Q15896	Q15896 babesia bov
863	9	14.8	16	2	Q54357	Q54357 bacillus am	936	8	13.1	8	6	Q28866	Q28866 megaptera n
864	9	14.8	16	2	Q10748	Q10748 clostridium	937	8	13.1	8	6	Q19957	Q19957 gossypium h
865	9	14.8	16	3	P79034	P79034 emeritella	938	8	13.1	8	8	Q19958	Q19958 gossypium h
866	9	14.8	16	5	Q26101	Q26101 pratylenchu	939	8	13.1	8	8	Q19956	Q19956 gossypium a
867	9	14.8	16	8	Q33429	Q33429 anas platyr	940	8	13.1	8	8	Q19959	Q19959 gossypium t
868	9	14.8	16	9	Q38671	Q38671 bacterioph	941	8	13.1	8	8	Q19960	Q19960 gossypium m
869	9	14.8	16	9	Q38407	Q38407 bacterioph	942	8	13.1	8	8	Q19961	Q19961 gossypium d
870	9	14.8	16	10	Q82402	Q82402 fragaria nu	943	8	13.1	8	12	Q86617	Q86617 gallid herp
871	9	14.8	16	10	Q82404	Q82404 fragaria ni	944	8	13.1	9	4	Q14277	Q14277 homo sapien
872	9	14.8	16	10	Q82405	Q82405 fragaria ii	945	8	13.1	9	4	Q00611	Q00611 homo sapien
873	9	14.8	16	10	Q82406	Q82406 fragaria mo	946	8	13.1	9	5	Q96417	Q96417 drosophila
874	9	14.8	16	10	Q82407	Q82407 fragaria vi	947	8	13.1	9	7	Q78226	Q78226 mus musculu
875	9	14.8	16	10	Q82781	Q82781 fragaria ve	948	8	13.1	9	8	Q31653	Q31653 anser caeru
876	9	14.8	16	12	Q79454	Q79454 human immun	949	8	13.1	9	10	Q42452	Q42452 triticum ae
877	9	14.8	16	12	Q79455	Q79455 human immun	950	8	13.1	9	12	P90359	P90359 barley mild
878	9	14.8	16	12	Q79460	Q79460 human immun	951	8	13.1	9	12	Q85599	Q85599 moloney mur
879	9	14.8	16	12	Q79461	Q79461 human immun	952	8	13.1	9	12	Q67605	Q67605 squash leaf
880	9	14.8	17	2	Q52210	Q52210 staphylococ	953	8	13.1	9	12	Q67606	Q67606 squash leaf
881	9	14.8	17	2	Q92632	Q92632 chlamydia t	954	8	13.1	9	12	Q70140	Q70140 human immun
882	9	14.8	17	6	P79167	P79167 equus cabal	955	8	13.1	10	2	P96305	P96305 alteromonas
883	9	14.8	17	9	Q38559	Q38559 bacterioph	956	8	13.1	10	2	P96423	P96423 pseudomonas
884	9	14.8	17	11	Q62437	Q62437 mus musculu	957	8	13.1	10	2	P96306	P96306 aeromonas s
885	9	14.8	18	2	Q92642	Q92642 chlamydia t	958	8	13.1	10	2	P96321	P96321 escherichia
886	9	14.8	18	2	P77033	P77033 escherichia	959	8	13.1	10	2	P96352	P96352 marinobacte
887	9	14.8	18	6	Q28069	Q28069 bos taurus	960	8	13.1	10	2	P74843	P74843 streptomyc
888	9	14.8	18	12	Q41588	Q41588 human immun	961	8	13.1	10	8	Q96041	Q96041 oenothera b
889	9	14.8	19	2	Q07479	Q07479 streptococ	962	8	13.1	10	8	P92576	P92576 bipes bipor
890	9	14.8	19	2	Q52033	Q52033 pseudomonas	963	8	13.1	10	11	Q63389	Q63389 rattus norv
891	9	14.8	19	2	Q53502	Q53502 lactobacill	964	8	13.1	10	12	Q87617	Q87617 chimpanzee
892	9	14.8	19	4	Q16408	Q16408 homo sapien	965	8	13.1	11	4	Q15997	Q15997 homo sapien
893	9	14.8	19	5	Q26099	Q26099 pratylenchu	966	8	13.1	11	5	Q99292	Q99292 drosophila
894	9	14.8	19	8	Q92Y76	Q92Y76 macroteleia	967	8	13.1	11	7	Q77883	Q77883 oreochromis
895	9	14.8	20	2	Q51558	Q51558 pseudomonas	968	8	13.1	11	7	Q77912	Q77912 oreochromis
896	9	14.8	20	2	Q34964	Q34964 ehrlichia p	969	8	13.1	11	8	Q32704	Q32704 nicotiana t

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970 8 13.1 11 11 Q60807
971 8 13.1 12 2 Q53358
972 8 13.1 12 8 Q36622
973 8 13.1 12 8 Q36668
974 8 13.1 12 8 Q37791
975 8 13.1 12 8 Q37071
976 8 13.1 12 10 Q02320
977 8 13.1 12 12 Q83139
978 8 13.1 12 12 Q85631
979 8 13.1 13 2 Q50476
980 8 13.1 13 2 Q53693
981 8 13.1 13 2 Q96991
982 8 13.1 13 2 Q31364
983 8 13.1 13 2 Q34622
984 8 13.1 13 2 Q34770
985 8 13.1 13 2 P74844
986 8 13.1 13 2 P94878
987 8 13.1 13 2 Q55234
988 8 13.1 13 2 Q9XBY0
989 8 13.1 13 2 Q9X3G1
990 8 13.1 13 4 Q14462
991 8 13.1 13 4 Q14461
992 8 13.1 13 11 P97622
993 8 13.1 13 11 P97344
994 8 13.1 13 12 Q9WMG5
995 8 13.1 14 2 Q44160
996 8 13.1 14 2 Q46228
997 8 13.1 14 2 Q46291
998 8 13.1 14 2 Q48878
999 8 13.1 14 2 Q56750
1000 8 13.1 14 2 Q52840

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ALIGNMENTS

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RESULT 1
Q16228 ID Q16228 PRELIMINARY; PRT; 17 AA.
AC Q16228
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE PERIPHERIN (FRAGMENT).
GN RDS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94290510.
RA GRUNING G., MILLAN J.M., MEINS M., BENEYTO M., CABALLERO M.,
RA APPELSTEDT-SYLLA E., BOSCH R., ZRENNER E., PRIETO F., GAL A.;
RT "Mutations in the human peripherin/RDS gene associated with autosomal
RT dominant retinitis pigmentosa.";
RL Hum. Mutat. 3:321-323(1994).
DR EMBL; S73627; AAB31191.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2342 MW; DCB89494 CRC32;

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Query Match 44.3%; Score 27; DB 4; Length 17;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 WNR 4
Db 1 WRWR 4

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RESULT 2
Q61714 ID Q61714 PRELIMINARY; PRT; 20 AA.

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AC Q61714;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE TRANSMEMBRANE REGION.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 84261407.
RA WIDERA G., FLAVELL R.A.;
RT "The nucleotide sequence of the murine I-E beta b immune response
RT gene: evidence for gene conversion events in class II genes of the
RT major histocompatibility complex.";
RL EMBO J. 3:1221-1225(1984).
DR EMBL; X00702; CAA25299.1; -.
KW Transmembrane.
SQ SEQUENCE 20 AA; 2289 MW; 9A27FB34 CRC32;

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Query Match 41.0%; Score 25; DB 11; Length 20;
Best Local Similarity 50.0%; Pred. No. 5.1e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 WNR 6
Db 13 WSWGLR 18

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RESULT 3
P92689 ID P92689 PRELIMINARY; PRT; 19 AA.
AC P92689;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE CYTOCHROME C OXIDASE SUBUNIT I (FRAGMENT).
GN COI.
OS Podospora anserina.
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
OC Sordariales; Sordariaceae; Podospora.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88223503.
RA KUECK U., OSIENACZ H.D., SCHMIDT U., KAPPELHOFF B., SCHULTE E.,
RA STAHL U., ESSER K.;
RT "The onset of senescence is affected by DNA rearrangements of a
RT discontinuous mitochondrial gene in Podospora anserina.";
RL Curr. Genet. 9:373-382(1985).
DR EMBL; X07122; CAA30133.1; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2635 MW; 3E9A6AF4 CRC32;

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Query Match 40.2%; Score 24.5; DB 8; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

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Qy 1 WNR-YR 6
Db 11 WNFRIYR 17

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RESULT 4
P87484 ID P87484 PRELIMINARY; PRT; 19 AA.
AC P87484;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)

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DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)
 DE BETA KERATIN (FRAGMENT).
 GN BETA KERATIN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
 RN [1]
 RP SEQUENCE OF 48-66 FROM N.A.
 RX MEDLINE; 88003561.
 RA SAWYER R.H., SHAMES R.B.;
 RT "Expression of beta-keratin genes during development of avian skin
 RT appendages.";
 RL Curr. Top. Dev. Biol. 22:235-253(1987).
 DR EMBL; M28422; AAA48631.1; -.
 FT NON_TER 1
 SQ SEQUENCE 19 AA; 2289 MW; B41AFEB8 CRC32;

Query Match 39.3%; Score 24; DB 13; Length 19;
 Best Local Similarity 37.5%; Pred. No. 7e+02; Mismatches 3; Indels 2; Gaps 0;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNWRYREY 8
 : : : : :
 Db 4 YSYRYNRY 11

RESULT 5
 ID Q99213 PRELIMINARY; PRT; 10 AA.
 AC Q99213;
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)
 DE ALBUMIN (FRAGMENT).
 OS Aegilops squarrosa.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC eurylophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
 OC Poaceae; Aegilops.
 RN [1]
 RP SEQUENCE.
 RA SHEWRY P.R., LAFIANDRA D., SALCEDO G., ARAGONCILLO C.,
 RA GARCIA-OLMEDO F., LEW E.J.-L., DIETLER M.D., KASARDA D.D.;
 RL FEBS Lett. 175:359-363(1984).
 KW Seed storage protein.
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1105 MW; 028A77EC CRC32;

Query Match 37.7%; Score 23; DB 10; Length 10;
 Best Local Similarity 66.7%; Pred. No. 5.3e+02; Mismatches 1; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 WNW 3
 : : :
 Db 4 WSW 6

RESULT 6
 ID Q45304 PRELIMINARY; PRT; 17 AA.
 AC Q45304;
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)
 DE HYPOTHETICAL 2.1 KD PROTEIN.
 OS Brevibacterium lactofermentum.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AJ12036;
 RX MEDLINE; 87277409.

RA SANO K., MATSUI K.;
 RT "Structure and function of the trp operon control regions of
 RT Brevibacterium lactofermentum, a glutamic-acid-producing bacterium.";
 RL Gene 53:191-200(1987).
 DR EMBL; M16663; AAA83988.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 17 AA; 2098 MW; 1A452574 CRC32;

Query Match 37.7%; Score 23; DB 2; Length 17;
 Best Local Similarity 75.0%; Pred. No. 8.9e+02; Mismatches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WNW 4
 : : :
 Db 12 WNW 15

RESULT 7
 ID Q73605 PRELIMINARY; PRT; 18 AA.
 AC Q73605;
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)
 DE REVERSE TRANSCRIPTASE (FRAGMENT).
 GN POL.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT P74, PCR;
 RX MEDLINE; 96242958.
 RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
 RT "Evolution of zidovudine resistance-associated genotypes in human
 RT immunodeficiency virus type 1-infected patients.";
 RL J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT P74, PCR;
 RA LEIGH BROWN A.J.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U45171; AAB04322.1; -.
 KW RNA-directed DNA polymerase.
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 2282 MW; 07CD8437 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
 Best Local Similarity 40.0%; Pred. No. 9.5e+02; Mismatches 2; Indels 2; Gaps 0;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNW 5
 : : :
 Db 3 WKWGF 7

RESULT 8
 ID Q73549 PRELIMINARY; PRT; 18 AA.
 AC Q73549;
 DT 01-NOV-1996 (TREMELREL. 01, Created)
 DT 01-NOV-1996 (TREMELREL. 01, Last sequence update)
 DT 01-NOV-1998 (TREMELREL. 08, Last annotation update)
 DE REVERSE TRANSCRIPTASE (FRAGMENT).
 GN POL.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PATIENT P74, PCR;
 RX MEDLINE; 96242958.

RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
OC Immunodeficiency virus type 1-infected patients."
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RP [2]
RC SEQUENCE FROM N.A.
RX STRAIN-PATIENT P74, PCR;
RA LEIGH BROWN A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45115; AAB04266.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
| | :
Db 3 WRWGF 7

RESULT 9
Q73573 PRELIMINARY; PRT; 18 AA.
AC Q73573;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
OC Immunodeficiency virus type 1-infected patients."
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RP [2]
RC SEQUENCE FROM N.A.
RX STRAIN-PATIENT P74, PCR;
RA LEIGH BROWN A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45139; AAB04290.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2326 MW; 4F2D8A53 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
| | :
Db 3 WRWGF 7

RESULT 10
Q73575 PRELIMINARY; PRT; 18 AA.
AC Q73575;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).

GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
OC Immunodeficiency virus type 1-infected patients."
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RP [2]
RC SEQUENCE FROM N.A.
RX STRAIN-PATIENT P74, PCR;
RA LEIGH BROWN A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45141; AAB04292.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
| | :
Db 3 WRWGF 7

RESULT 11
Q73577 PRELIMINARY; PRT; 18 AA.
AC Q73577;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
OC Immunodeficiency virus type 1-infected patients."
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RP [2]
RC SEQUENCE FROM N.A.
RX STRAIN-PATIENT P74, PCR;
RA LEIGH BROWN A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45143; AAB04294.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
| | :
Db 3 WRWGF 7

RESULT 12
Q73577 PRELIMINARY; PRT; 18 AA.
AC Q73577;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
OC Immunodeficiency virus type 1-infected patients."
RN J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 12:6-18(1996).
RP [2]
RC SEQUENCE FROM N.A.
RX STRAIN-PATIENT P74, PCR;
RA LEIGH BROWN A.J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U45143; AAB04294.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
| | :
Db 3 WRWGF 7

RESULT 12
Q73577 PRELIMINARY; PRT; 18 AA.
AC Q73577;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).

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Q73579 ID Q73579 PRELIMINARY; PRT; 18 AA.
AC Q73579;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
DR EMBL; U45145; AAB04296.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
Db 3 WKGCF 7

RESULT 13
Q73583 ID Q73583 PRELIMINARY; PRT; 18 AA.
AC Q73583;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
DR EMBL; U45145; AAB04300.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2326 MW; 4F2D8A53 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
Db 3 WKGCF 7

RESULT 14
Q73587 ID Q73587 PRELIMINARY; PRT; 18 AA.
AC Q73587;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
DR EMBL; U45153; AAB04304.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2326 MW; 4F2D8A53 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
Db 3 WKGCF 7

RESULT 15
Q73593 ID Q73593 PRELIMINARY; PRT; 18 AA.
AC Q73593;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
DR EMBL; U45159; AAB04310.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2326 MW; 4F2D8A53 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
Db 3 WKGCF 7

RESULT 16
Q73597 ID Q73597 PRELIMINARY; PRT; 18 AA.
AC Q73597;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
DR EMBL; U45159; AAB04310.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2326 MW; 4F2D8A53 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
Db 3 WKGCF 7
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QY 1 WNWRY 5
Db 3 WKGCF 7

RESULT 14
Q73587 ID Q73587 PRELIMINARY; PRT; 18 AA.
AC Q73587;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
DR EMBL; U45153; AAB04304.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2326 MW; 4F2D8A53 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
Db 3 WKGCF 7

RESULT 15
Q73593 ID Q73593 PRELIMINARY; PRT; 18 AA.
AC Q73593;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
DR EMBL; U45159; AAB04310.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2326 MW; 4F2D8A53 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
Db 3 WKGCF 7

RESULT 16
Q73597 ID Q73597 PRELIMINARY; PRT; 18 AA.
AC Q73597;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
DE REVERSE TRANSCRIPTASE (FRAGMENT).
GN POL.
OS Human immunodeficiency virus type 1.
OC Viruses; Retrov. Viruses; Retroviridae; Lentivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT P74, PCR;
RX MEDLINE; 96242958.
RA CLELAND A., WATSON H.G., ROBERTSON P., LUDLAM C.A., BROWN A.J.;
RT "Evolution of zidovudine resistance-associated genotypes in human
RL immunodeficiency virus type 1-infected patients.";
DR EMBL; U45159; AAB04310.1; -.
KW RNA-directed DNA polymerase.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 2326 MW; 4F2D8A53 CRC32;

Query Match 37.7%; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WNWRY 5
Db 3 WKGCF 7
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FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2354 MW; 7D3D0273 CRC32;

Query Match 37.78; Score 23; DB 12; Length 18;
Best Local Similarity 40.0%; Pred. No. 9.5e+02;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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| | :
Db 3 WRWGF 7

Search completed: May 2, 2000, 00:23:05
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